

PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00742259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
PR 22-MAR-2001; 2001WO-US009552.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882536.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.

(GENTH) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerlitsen WE;
PI Goddard A, Godowski PJ, Grimaldi JC, Gunney AL, Hillan KJ;
PI Kijavini IJ, Kuo SS, Napier MA, Pan J, Paoni NP, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
DR WPI; 2003-341189/32.

New genes and secreted and transmembrane polypeptides (e.g. PRO337 or PRO1559), useful for treating or diagnosing e.g. cancer, atherosclerosis, infertility, stroke, encephalitis, hepatitis or multiple sclerosis in mammals.

Example 34; Page 143; 460pp; English.

CC The invention relates to a new isolated nucleic acid molecule comprising a
CC sequence with at least 80% identity to: (a) a nucleotide encoding any of
CC 94 PRO polypeptides whose sequences are fully defined in the
CC specification; or (b) any of 94 nucleotide sequences fully defined in the
CC specification; or the full length coding sequence of any these 94
CC nucleotide sequences. Also included are an isolated PRO polypeptide
CC scoring at least 80% positives when compared to any of the PRO
CC polypeptide sequences cited above (or an isolated PRO polypeptide having
CC at least 80% amino acid sequence identity to: (a) an amino acid sequence
CC encoded by the nucleotide deposited with ATCC numbers listed in the
CC specification; (b) the PRO polypeptide, lacking its associated signal
CC peptide; or (c) an extracellular domain of the PRO polypeptide, with or
CC lacking its associated signal peptide), a vector comprising the nucleic
CC acid molecule, a host cell comprising the vector (and producing a PRO
CC polypeptide), a chimeric molecule comprising the PRO polypeptide fused
CC to a heterologous amino acid sequence and an anti-PRO antibody. The PRO
CC polypeptides or polynucleotides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioreactors. These are particularly useful for
CC detecting or treating e.g. malignancies or cancers (e.g. ovarian cancer,
CC colorectal cancer, sarcoma, leukemia or lymphoma), inflammatory disease,
CC neurosis, atherosclerosis, infertility, premature aging, psoriasis,
CC inflammatory diseases, renal disease, arthritis, immune-mediated alopecia,
CC stroke, encephalitis, hepatitis, or multiple sclerosis in mammals. The
CC PRO polypeptides are useful in drug screening, particularly as targets
CC for therapeutic intervention in these diseases, and in the diagnostic

CC determination of the presence of these diseases. The PRO polypeptides are
CC also useful as molecular weight markers, or for chromosome
CC identification. The PRO genes are useful as hybridisation probes, or for
CC screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may
CC also be used in gene therapy, particularly for replacing a defective
CC gene. The present sequence is a PCR primer used in the isolation of a
CC cDNA encoding a PRO polypeptide

XX Sequence 24 BP; 6 A; 10 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.2; DB 1; Length 24;

Best Local Similarity 87.0%; Pred. No. 7.2e+02; Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2551 CTGACGTACCAGCTGTGCCACAC 2573
|||||
Db 2 CTGACCTTCAGCTGACCCACAC 24

RESULT 858
ABV76020
ID ABV76020 standard; DNA; 24 BP.

XX ABV76020;

DT 11-FEB-2003 (first entry)

XX Cytostatic G-rich oligonucleotide T40216.

DE Cytostatic; cancer; antineoplastic; antiarthritic; antiinflammatory;

KM osteopathic; vasotropic; antiarteriosclerotic; antipsoriatic; therapy;

KW ss.

XX Synthetic.

OS Key Location/Qualifiers

XX FT misc_structure 1 /*tag= a

FT /*note= "Forms loop with bases 12, 13 and 24"

FT misc_structure 2 /*tag= b

FT /*note= "Forms quartet with bases 11, 14 and 23"

FT misc_structure 3 /*tag= c

FT /*note= "Forms quartet with bases 10, 15 and 22"

FT misc_structure 4 /*tag= d

FT /*note= "Forms quartet with bases 9, 16 and 21"

FT misc_structure 5 /*tag= e

FT /*note= "Forms quartet with bases 8, 17 and 20"

FT misc_structure 6 /*tag= f

FT /*note= "Forms loop with bases 7, 18 and 19"

FT misc_structure 8 /*tag= g

FT /*note= "Forms quartet with bases 6, 18 and 19"

FT misc_structure 9 /*tag= h

FT /*note= "Forms quartet with bases 5, 17 and 20"

FT misc_structure 10 /*tag= i

FT /*note= "Forms quartet with bases 4, 16 and 21"

FT misc_structure 11 /*tag= j

FT /*note= "Forms quartet with bases 3, 15 and 22"

FT misc_structure 12 /*tag= k

FT /*note= "Forms quartet with bases 2, 14 and 23"

FT misc_structure 12 /*tag= m

FT /*note= "Forms loop with bases 1, 12 and 24"

```

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FT      /note= "forms loop with bases 1, 13 and 24"
FT      misc_structure
FT      /*tag= n
FT      /note= "forms quartet with bases 2, 11 and 23"
FT      misc_structure
FT      /*tag= o
FT      /note= "forms quartet with bases 3, 10 and 22"
FT      misc_structure
FT      /*tag= p
FT      /note= "forms quartet with bases 4, 9 and 21"
FT      misc_structure
FT      /*tag= q
FT      /note= "forms quartet with bases 5, 8 and 20"
FT      misc_structure
FT      /*tag= r
FT      /note= "forms loop with bases 6, 7 and 19"
FT      misc_structure
FT      /*tag= s
FT      /note= "forms loop with bases 6, 7 and 18"
FT      misc_structure
FT      /*tag= t
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FT      misc_structure
FT      /*tag= u
FT      /note= "forms quartet with bases 4, 9 and 16"
FT      misc_structure
FT      /*tag= v
FT      /note= "forms quartet with bases 3, 10 and 15"
FT      misc_structure
FT      /*tag= w
FT      /note= "forms quartet with bases 2, 11 and 14"
FT      misc_structure
FT      /*tag= x
FT      /note= "forms loop with bases 1, 12 and 13"
XX      WO200276469-A1.
XX      03-OCT-2002.
XX      PD
XX      27-MAR-2002; 2002WO-US009516.
XX      XX
XX      27-MAR-2001; 2001US-0278942P.
XX      PR
XX      (BAYU ) BAYLOR COLLEGE MEDICINE.
XX      PA
XX      Jing N, Xiong W, Guan Y;
XX      PI
XX      WPI; 2003-075428/07.
XX      DR
XX      G-rich oligonucleotide composition useful for treating e.g. HIV,
XX      PT      rheumatoid arthritis, inflammatory bowel disease, osteoarthritis.
XX      PT
XX      Claim 7; Fig 1A; 76pp; English.
XX      PS
XX      The present sequence is that of G-rich oligonucleotide T40216. The
XX      CC      invention provides a method for the intracellular delivery of a G-rich
XX      CC      oligonucleotide by denaturing the oligonucleotide, mixing it with a lipid
XX      CC      to form a complex, and incubating the complex with a cell. The
XX      CC      oligonucleotide is internalised into the cell and enters the nucleus.
XX      CC      Upon internalisation, T40216 forms an intramolecular G-quartet structure
XX      CC      with 4 G-quartets in the middle and 2 G-T-G-T loops on the top and
XX      CC      bottom. The G-quartet structure inhibits a signal transducer and
XX      CC      activator of transcription (STAT). A claimed method of inhibiting
XX      CC      hyperproliferative cell growth comprises administering an oligonucleotide
XX      CC      T40216 composition which modulates a STAT protein, especially inhibiting
XX      CC      the DNA-binding activity of STAT3, in a tumour cell selected from a
XX      CC      melanoma, bladder cancer, breast cancer, lung cancer, colon cancer,
XX      CC      prostate cancer, liver cancer, pancreatic cancer, stomach cancer,
XX      CC      testicular cancer, brain cancer, ovarian cancer, lymphatic cancer, skin
XX      CC      cancer, bone cancer or soft tissue cancer cell. A claimed method of
XX      CC      treating a hyperproliferative disease comprises administering a T40216
XX      CC      composition to modulate a protein, especially STAT, involved in cell

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CC      proliferation, where the hyperproliferative disease is selected from
CC      melanoma, bladder, non-small cell lung, small cell lung, lung,
CC      hepatocarcinoma, retinoblastoma, astrocytoma, glioblastoma,
CC      neuroblastoma, head, neck, breast, pancreatic, gum, tongue, prostate,
CC      renal, bone, testicular, ovarian, mesothelioma, cervical,
CC      gastrointestinal lymphoma, brain or colon cancer, or rheumatoid
CC      arthritis, inflammatory bowel disease, osteoarthritis, leiomyoma,
CC      adenoma, lipoma, haemangioma, fibroma, vascular occlusion, restenosis,
CC      atherosclerosis, pre-neoplastic lesions, carcinoma in situ, oral hairy
CC      leukoplakia and psoriasis (all claimed). The oligonucleotide is highly
CC      stable, and the compact G-quartet structure greatly enhances resistance
CC      to nuclease digestion
XX      SQ
XX      Sequence 24 BP; 0 A; 0 C; 20 G; 4 T; 0 U; 0 Other;
XX
XX      Query Match      0.2%; Score 18.2; DB 1; Length 24;
XX      Best Local Similarity 87.0%; Pred. No. 7.2e+02;
XX      Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX      QY      3622 GGGGTGGGGGTGGAGAGAGGT 3644
XX      DB      2 GGGGTGGGGGTGGGGGTGGGT 24
XX
XX      RESULT 859
XX      ACD99368
XX      ID      ACD99368 standard; DNA; 24 BP.
XX      AC
XX      ACD99368;
XX      AC
XX      25-SEP-2003 (first entry)
XX      DT
XX      XX
XX      DE      Immunostimulatory nucleic acid #54.
XX      XX
XX      KW      Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
XX      KW      antitumor; gene therapy; vaccine; non-allergic inflammatory disease;
XX      KW      psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
XX      KW      inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX      XX
XX      OS      Synthetic.
XX      XX
XX      PN      US2003050268-A1.
XX      PD
XX      13-MAR-2003.
XX      XX
XX      29-MAR-2002; 2002US-00112653.
XX      PF
XX      29-MAR-2001; 2001US-0279642P.
XX      PR
XX      (KRIE/) KRIEG A M.
XX      PA      (BERG/) BERG D J.
XX      PT
XX      Krieg AM, Berg DJ;
XX      PI
XX      WPI; 2003-521815/49.
XX      DR
XX      Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
XX      PT      allergic contact dermatitis, latex dermatitis or inflammatory bowel
XX      PT      disease by administering an immunostimulatory nucleic acid.
XX      PS
XX      Disclosure; Page 10; 229pp; English.
XX      XX
XX      The invention describes a method of treating non-allergic inflammatory
XX      CC      disease comprising administering to a subject having or at risk of
XX      CC      developing a non-allergic inflammatory disease an immunostimulatory
XX      CC      nucleic acid for prevention or treatment of the disease. The method is
XX      CC      useful for treating non-allergic inflammatory diseases, such as
XX      CC      psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
XX      CC      inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
XX      CC      This sequence represents an immunostimulatory nucleic acid
XX      XX
XX      Sequence 24 BP; 0 A; 0 C; 3 G; 21 T; 0 U; 0 Other;
XX      SQ

```

Query Match 0.2%; Score 18.2; DB 1; Length 24;
 Best Local Similarity 87.0%; Pred. No. 7.2e+02;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4466 TTTTCTTTTCTTTTCTTTCTT 4488
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 1 TTTCTTTTCTTTTCTTTTCTT 23

Db

RESULT 860
 ADA24752
 ID ADA24752 standard; DNA; 24 BP.
 XX
 AC ADA24752;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Secreted and transmembrane PRO protein associated primer #106.
 XX
 KW Human; secreted and transmembrane protein; PRO; gene; ss; tissue typing;
 KW Chromosome identification; vaccine; cancer; retinal disorder;
 KW sports-related joint disorder; osteoarthritis; rheumatoid arthritis;
 KW wound healing; obesity; diabetes; hearing loss;
 KW cardiac insufficiency disorder; kidney disorder; nervous system disorder;
 KW haemoglobin associated disorder; expressed sequence tag; EST.
 XX
 OS Homo sapiens.
 XX
 PN US2003050241-A1.
 XX
 PD 13-MAR-2003.
 XX
 PF 16-OCT-2001; 2001US-00978564.
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 17-OCT-1997; 97US-0062250P.
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 PR 13-NOV-1997; 97US-0065311P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 10-MAR-1998; 98US-0077450P.
 PR 11-MAR-1998; 98US-0077632P.
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 PR 12-MAR-1998; 98US-0077791P.
 PR 13-MAR-1998; 98US-0078004P.
 PR 20-MAR-1998; 98US-0078886P.
 PR 20-MAR-1998; 98US-0078910P.
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 PR 05-MAY-1998; 98US-0084366P.
 PR 06-MAY-1998; 98US-0084414P.
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 PR 28-MAY-1998; 98US-0087106P.
 PR 28-MAY-1998; 98US-0087208P.
 PR 26-JUN-1998; 98US-0090863P.
 PR 26-JUN-1998; 98US-0091010P.
 PR 01-JUL-1998; 98US-0091359P.
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 PR 11-SEP-1998; 98US-0100038P.
 PR 07-OCT-1998; 98US-0100211P.
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 PR 05-JAN-1999; 98US-01300106.
 PR 08-MAR-1999; 98US-01300106.
 PR 10-MAR-1999; 98US-01300106.
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 PR 29-MAR-1999; 98US-01300106.
 PR 21-APR-1999; 98US-0130232P.
 PR 26-APR-1999; 98US-0131022P.
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 PR 14-MAY-1999; 98US-0134287P.
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 PR 16-JUN-1999; 98US-0139557P.

PR 23-JUN-1999; 99US-0141037P.
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 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028551.
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 PR 16-DEC-1999; 99WO-US030095.
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 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 22-MAR-2001; 2001WO-US009552.
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 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 30-JUL-2001; 2001US-00918585.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Botstein D, Deenyere L, Eaton DL,
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gertelzen ME,
 PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,
 PI Kijavini IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL,
 PI Stewart TA, Tumas D, Williams PM, Wood WI;
 XX
 DR MPI; 2003-521814/49.
 XX
 PT New isolated PRO polypeptides for example extracellular, secreted and
 PT membrane bound proteins, useful for modulating the biological activities
 PT of cells and for treating, for example diabetes, cancer, rheumatoid
 PT arthritis, and hearing loss.
 XX
 PS Example 34; Page 150; 461pp; English.
 XX
 CC The invention describes an isolated secreted and transmembrane (PRO)
 CC polypeptide (I). PRO337 polypeptide is useful for detecting PRO493
 CC polypeptide in a sample, and vice versa. PRO725, PRO700 and PRO739 are
 CC useful for detecting PRO1559 polypeptide in a sample, and PRO1559 is
 CC useful for detecting PRO725, PRO700 and PRO739 in a sample. PRO493 is
 CC useful for linking a bioactive molecule to a cell expressing a PRO337
 CC polypeptide, and PRO337 is useful for linking a bioactive molecule to a
 CC cell expressing a PRO493 polypeptide. PRO1559 is useful for linking a
 CC bioactive molecule to a cell expressing a PRO725, PRO700 and PRO739
 CC polypeptide, and PRO725, PRO700 and PRO739 polypeptides are useful for
 CC
 Query Match 0.2%; Score 18.2; DB 1; Length 24;
 Best Local Similarity 87.0%; Pred. No. 7.2e+02;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2551 CTGACGTACCACTGTCGACAC 2573
 DB 2 CTGACCTTCACGCTGACAC 24

RESULT 861
 ACD29785
 ID ACD29785 standard; DNA; 24 BP.
 XX
 AC ACD29785;
 XX
 DT 08-SEP-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein related primer #104.
 XX
 KW Human; secreted and transmembrane protein; PRO; cell death; neuropathy;
 KW peripheral neuropathy; diabetic peripheral neuropathy;
 KW AIDS-associated neuropathy; Charcot-Marie-Tooth disease;
 KW Refsum's disease; Abetalipoproteinemia; Tangier disease;
 KW Krabbe's disease; Metachromatic leukodystrophy; Fabry's disease;
 KW Dejerine-Sottas syndrome; Chromosome mapping; gene therapy;
 KW PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN US2003050240-A1.
 XX
 PD 13-MAR-2003.
 XX
 PF 16-OCT-2001; 2001US-00978403.
 XX
 XX 17-OCT-1997; 97US-0062250P.
 PR 03-NOV-1997; 97US-0064249P.
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 PR 21-NOV-1997; 97US-0066364P.
 PR 10-MAR-1998; 98US-0077450P.
 PR 11-MAR-1998; 98US-0077633P.
 PR 11-MAR-1998; 98US-0077641P.
 PR 11-MAR-1998; 98US-0077649P.
 PR 12-MAR-1998; 98US-0077791P.
 PR 13-MAR-1998; 98US-0078004P.
 PR 20-MAR-1998; 98US-0078886P.
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XX (GETH) GENENTECH INC.
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XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gertlisen ME,
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,
PI Kijavlin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL,
PI Stewart TA, Tumas D, Williams PM, Wood WL,
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XX WPI; 2003-503575/47.
XX
XX Novel secreted and transmembrane polypeptide for modulating biological
PT activity of cell expressing the polypeptide, identifying agonists or
PT antagonists of polypeptide, and as molecular weight markers.
XX
XX Example 34; Page 144; 459pp; English.
XX
XX The invention describes an isolated, secreted and transmembrane
CC polypeptide, termed PRO polypeptide (1). (1) is useful for detecting
CC PRO493, PRO337, PRO1559, PRO725, PRO700 or PRO739 polypeptide, and for
CC linking a bioactive molecule to a cell expressing the above polypeptides.
CC The bioactive molecule is a toxin, radiolabel or an antibody and causes
CC cell death. (1) is useful as therapeutic agent, in medical and industrial
CC applications e.g. for treating neuropathy, especially peripheral
CC neuropathy, diabetic peripheral neuropathy, AIDS-associated neuropathy,
CC Charcot-Marie-Tooth disease, Refsum's disease, Abetalipoproteinemia,
CC Tangier disease, Krabbe's disease, Metachromatic leukodystrophy, Fabry's
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Query Match 0.2%; Score 18.2; DB 1; Length 24;
Best Local Similarity 87.0%; Pred. No. 7.2e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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RESULT 862
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AC ADA12413;

XX 06-NOV-2003 (first entry)
DT Human secreted/transmembrane polypeptide PRO660 primer #2.
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DE primer; ss; inflammatory disease; organ failure; atherosclerosis;
XX cardiac injury; infertility; birth defect; premature aging; AIDS; cancer;
KW diabetic complication; tissue typing; human; PCR.
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PD 20-MAR-2003.
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XX
XX
PA (GETH ) GENENTECH INC.
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,
PI Ferreira N, Filvaroff E, Fong S, Gao W, Gerber H, Gertlisen ME;
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Best Local Similarity 87.0%; Pred. No. 7.2e+02;

Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DT 27-AUG-2003 (first entry)
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DE Novel human secreted and transmembrane protein related primer #105.
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KM Human; secreted and transmembrane protein; PRO; viral infection;
KM tumour growth; retinal disorder; injury; sight loss;
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KW retinitis pigmentosum; age-related macular degeneration;
KW 'sport-related joint problem; articular cartilage defect; osteoarthritis;
KW rheumatoid arthritis; wound healing; obesity; diabetes; insulinemia;
KW kidney disorder; mesangial cell function; Berger disease; nephropathy;
KW celiac disease; dermatitis; Crohn disease; neuropathy;
KW cardiac insufficiency disorder; peripheral neuropathy;
KW diabetic peripheral neuropathy; autonomic neuropathy;
KW reduced motility of the gastrointestinal tract;
KW atony of the urinary bladder; post polio syndrome; Krabbe's disease;
KW Charcot-Marie-Tooth disease; Fabry's disease; Tangle disease;
KW Refsum's disease; PCR; primer; ss.
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PR 16-JUN-1999; 99US-0139557P.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0142680P.

PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
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PR 30-NOV-1999; 99US-0028313.
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PR 11-FEB-2000; 2000US-0031565.
PR 18-FEB-2000; 2000US-0031565.
PR 24-FEB-2000; 2000US-0031565.
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PR 10-MAR-2000; 2000US-0031565.
PR 21-MAR-2000; 2000US-0031565.
PR 30-MAR-2000; 2000US-0031565.
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PR 22-MAY-2000; 2000US-0031705.
PR 30-MAY-2000; 2000US-0031705.
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PR 28-JUN-2000; 2000US-0031705.
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PR 08-NOV-2000; 2000US-00709238.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000US-00723749.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000US-00747259.
PR 28-FEB-2001; 2001US-00816744.
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PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854280.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00872035.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001US-00872035.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.

Query Match 0.2% Score 18.2; DB 1; Length 24;
Best Local Similarity 87.0%; Pred. No. 7.2e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2551 CTGACGTACGAGCTGTGCACAC 2573
Db 2 CTGACCTTCACGCTGACGACAC 24

RESULT 864
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ID ADB36437 standard; DNA; 24 BP.
XX
AC ADB36437;
XX
DT 04-DEC-2003, (first entry)
XX
DE Immunostimulatory nucleic acid #51.
XX
KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW hypo-responsive subject; immunostimulatory.
XX
OS Synthetic.
XX
PN US2003087848-A1.
XX
PD 08-MAY-2003.
XX

PF 02-FEB-2001; 2001US-0076479.
XX
PR 03-FEB-2000; 2000US-0179991P.
XX
PA (BRAT/) BRATZLER R L.
PA (PETE/) PETERSEN D M.
PA (FOUR/) FOURON Y.
PI Bratzler RL, Petersen DM, Fouron Y;
XX MPI; 2003-657977/62.
XX
PT Treating and/or preventing allergy or asthma using an immunostimulatory
PT nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS Disclosure; Page 6; 221pp; English.
XX
CC The invention relates to a method of treating or preventing allergy or
CC asthma which comprises administering to a subject a poly-G nucleic acid
CC in an aerosol formulation. The methods and compositions of the present
CC invention are useful for diagnosing and/or treating asthma and allergy
CC especially in a hypo-responsive subject. The present sequence represents
CC an immunostimulatory nucleic acid of the invention.
XX
SQ Sequence 24 BP; 0 A; 0 C; 3 G; 21 T; 0 U; 0 Other;
Query Match 0.2%; Score 18.2; DB 1; Length 24;
Best Local Similarity 87.0%; Pred. No. 7.2e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4466 TTTTGTGTGTGTGTGTGTGT 4488
DB 1 TTTTGTGTGTGTGTGTGTGT 23
RESULT 865
ADBT3719
ID ADB73719 standard; DNA; 24 BP.
XX
AC ADB73719;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human PRO DNA PCR primer #104.
XX
KW Human; PRO polypeptide; secreted protein; transmembrane protein;
KW cell death; neuropathy; neuropathy related disease;
KW Charcot-Marie-Tooth disorder; Refsum's disease; Krabbe's disease;
KW chromosome mapping; gene mapping; genetic disorder; septic shock;
KW antibacterial; immunosuppressive; neuroprotective; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN US2003045462-A1.
XX
PD 06-MAR-2003.
XX
PF 16-OCT-2001; 2001US-00978608.
XX
PR 17-OCT-1997; 97US-0062250P.
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PR 20-MAR-1998; 98US-0078939P.
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PR 19-JUN-2001; 2001US-00886342.
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Query Match 0.2%; Score 18.2; DB 1; Length 24;
Best Local Similarity 87.0%; Pred. No. 7.2e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2551 CTGACGTACAGCTGTGCCACAC 2573
DB 2 CTGACCTTCAGCTGACGACAC 24
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ADB76435
ID ADB76435 standard; DNA; 24 BP.
XX
XX ADB76435;
AC
XX
DT 04-DEC-2003 (first entry)
XX
XX Human PRO DNA PCR primer #104.
DE
XX
XX Human; PRO polypeptide; secreted protein; transmembrane protein;
XX
XX cell death; neuropathy; neuropathy related disease;
XX
XX Charcoid-Marie-Tooth disorder; Refsum's disease; Krabbe's disease;
XX
XX Chromosome mapping; gene mapping; genetic disorder; septic shock;
XX
XX antibacterial; immunosuppressive; neuroprotective; PCR; primer; ss.
OS
XX
XX Homo sapiens.
XX
XX US2003083248-A1.
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XX 01-MAY-2003.
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XX 16-OCT-2001; 2001US-00978757.
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PR 26-JUN-1998; 98US-0090863P.
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PR 01-JUL-1998; 98US-0091359P.
PR 30-JUL-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100038P.

PR 07-OCT-1998; 98WO-US021141.
PR 20-NOV-1998; 98US-0109304P.
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PR 05-JAN-1999; 98WO-US000106.
PR 08-MAR-1999; 98WO-US005028.
PR 10-MAR-1999; 98WO-US005190.
PR 12-MAR-1999; 98US-0123957P.
PR 29-MAR-1999; 98US-0126733P.
PR 21-APR-1999; 98US-0130232P.
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PR 28-APR-1999; 98US-0131445P.
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PR 02-JUN-1999; 98WO-US012252.
PR 16-JUN-1999; 98US-0139557P.
PR 23-JUN-1999; 98US-0141037P.
PR 07-JUL-1999; 98US-0142680P.
PR 26-JUL-1999; 98US-0145698P.
PR 28-JUL-1999; 98US-0146222P.
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PR 16-DEC-1999; 98WO-US028565.
PR 30-DEC-1999; 98WO-US030095.
PR 30-DEC-1999; 98WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
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PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
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PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
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PR 28-FEB-2001; 2001WO-US006520.
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PR 29-JUN-2001; 2001WO-US021066.
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PR 30-JUL-2001; 2001US-00918585.

(GETH) GENENTECH INC.
XX PA
XX XX
PI Ashkenazi AJ, Baker KP, Botstein D, Deanevets L, Eaton DL,
PI Peterra N, Filvaroff E, Fong S, Gao W, Gerber H, Gertisen ME,
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,
PI Klejavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL,
PI Stewart TA, Tumas D, Williams PM, Wood WI,
XX
XX WPI; 2003-755118/71.
XX
XX
PT New PRO polypeptides useful for treating peripheral neuropathy,
PT neuropathies associated with systemic disease such as post-polio syndrome
PT or AIDS-associated syndrome.
XX
XX Example 34; Page 143; 425pp; English.
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO

CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC bioactive molecules to cells expressing PRO polypeptides, for modulating
CC biological activities of cells expressing PRO polypeptides, and for
CC identifying agonists or antagonists. The bioactive molecule maybe a
CC toxin, radiolabel or antibody, and cause cell death. The PRO polypeptides
CC are useful for treating neuropathy and neuropathy related diseases such
CC as Charcot-Marie-Tooth disorder, Refsum's disease, and Krabbe's disease.
CC The polynucleotide sequences encoding PRO polypeptides are useful as
CC hybridization probes, in chromosome and gene mapping, in the generation
CC of antisense RNA and DNA, in the preparation of PRO polypeptides, for

Query Match 0.2%; Score 18.2; DB 1; Length 24;

Best Local Similarity 87.0%; Pred. No. 7.2e+02;

Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2551 CTGACGTACCAAGCTGTGCCACAC 2573
|||||
DB 2 CTGACCTTCACGCTGACCAAC 24

RESULT 867

ADCA3861
ID ADCA3861 standard; DNA; 24 BP.

XX ADCA3861;

XX 18-DEC-2003 (first entry)

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XX ophthalmological; aneurysmal; osteopathic; antithrombotic; vulnery;

KW auditory; tumour growth; retinal disorder; sports-related joint problem;

KW articular cartilage defects; osteoarthritis; rheumatoid arthritis;

XX wound healing; hearing loss; primer.

OS Homo sapiens.

XX US2003054986-A1.

XX 20-MAR-2003.

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PR 30-JUL-2001; 2001US-00918585.
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XX
Query Match 0.2%; Score 18.2; DB 1; Length 24;
Best Local Similarity 87.0%; Pred. No. 7.2e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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KW Human; ss; PCR; secreted protein; transmembrane protein; PRO; cytosratic;
KW ophthalmological; aniarthritis; osteopathic; antirheumatic; vulnerary;
KW auditory; tumour growth; retinal disorder; sports-related joint problem;
KW articular cartilage defects; osteoarthritis; rheumatoid arthritis;
KW wound healing; hearing loss; primer.
XX
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KW ophthalmological; antiarthritic; osteopathic; antirheumatic; vulneryary;
KW auditory; tumour growth; retinal disorder; sports-related joint problem;
KW articular cartilage defects; osteoarthritis; rheumatoid arthritis;
KW wound healing; hearing loss; primer.
XX
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PR 18-FEB-2000; 2000WO-US004341.
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PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
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PR 17-MAY-2000; 2000WO-US013705.
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PR 27-NOV-2000; 2000US-00723749.
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PR 20-DEC-2000; 2000US-00747259.
PR 28-FEB-2001; 2001WO-US006520.
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PR 30-JUL-2001; 2001US-00918585.
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XX
PA (GETH) GENENTECH INC.
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Query Match 0.2%; Score 18.2; DB 1; Length 24;
Best Local Similarity 87.0%; Pred. No. 7.2e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2551 CTGACGTACAGCTGTCGACAC 2573
DB 2 CTGACCTTCAGCTGACCAAC 24

RESULT 870
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XX
AC ADCC6685;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human PRO 860 PCR primer #2.
XX
KW vulnery; virucide; neuroprotective; cyostatic; gene therapy;
KW tumor cell proliferation inhibitor;
KW secreted and transmembrane protein; PRO; viral infection; wound healing;
KW tissue growth; muscle generation; muscle regeneration;
KW amyotrophic lateral sclerosis; neuropathy; AIDS-associated neuropathy;
KW diabetic peripheral neuropathy; chromosome identification; antagonist;
KW tissue typing; immunohistochemical staining; primer; ss.
XX
OS Homo sapiens.
XX
PN US2003060406-A1.
XX
PD 27-MAR-2003.
XX
PF 30-JUL-2001; 2001US-00918585.
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 PR 09-JUL-2001; 2001MO-US021735.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferreira N, Filvarov E, Fong S, Gao W, Geber H, Gerlitsen ME;
 PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
 PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL,
 PI Stewart TA, Tumas D, Williams PM, Wood WI;
 XX
 DR WPI, 2003-596568/56.
 XX
 PT Novel secreted and transmembrane polypeptides and polynucleotides
 PT encoding them, useful for treating wound healing, tissue growth and
 PT muscle generation and regeneration, amyotrophic lateral sclerosis or
 PT neuropathy.
 XX
 XX Example 34; SEQ ID NO 213; 472bp; English.
 XX
 CC The invention describes an isolated secreted and transmembrane PRO
 CC polypeptide (I). PRO polypeptide such as PRO213, PRO700, PRO320 or PRO615
 CC is useful in biotechnological and medical research, as well as in various
 CC industrial applications. PRO polypeptide such as PRO300, PRO866, PRO703,
 CC PRO708, PRO320, PRO351, PRO352, PRO381, PRO618, PRO772, PRO853,
 CC PRO860 or PRO846 is useful for therapeutic purposes. PRO363 is useful
 CC therapeutically in vivo for lessening the effects of viral infection.
 CC PRO200 is useful for the treatment of wound healing, tissue growth and
 CC muscle generation and regeneration. PRO337 is useful for treating
 CC amyotrophic lateral sclerosis, neuropathy, AIDS-associated neuropathy or
 CC diabetic peripheral neuropathy. A polynucleotide (II) encoding (I) is
 CC useful for generating transgenic animals or knockout animals which are
 CC useful in the development and screening of therapeutically useful
 CC reagents, as probes for generating a pool of sequences for identifying

CC related PRO coding sequences, and to construct hybridization probes for
 CC mapping the gene which encodes the PRO and for the genetic analysis of
 CC individuals with genetic disorders, for recombinantly expressing (I) and
 CC for chromosome identification. (I) is useful as molecular marker for
 CC protein electrophoresis purposes, and as therapeutic agents. (I) is also
 CC useful for screening compounds to identify those that mimic the PRO
 CC polypeptide (agonists) or prevent the effect of the PRO polypeptide
 CC (antagonists). (I) and (II) are useful for tissue typing. PRO antibodies
 CC are useful for immunohistochemical staining and/or assay of sample
 CC fluids. Anti-PRO antibodies are useful in diagnostic assays for PRO e.g.
 CC detecting its expression in specific cells, tissues or serum, and for
 CC affinity purification of PRO from recombinant cell culture or natural
 CC sources. This sequence represents a human secreted and transmembrane PRO
 CC protein associated primer.
 XX
 SQ Sequence 24 BP; 6 A; 10 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 0.2%; Score 18.2; DB 1; Length 24;
 Best Local Similarity 87.0%; Pred. No. 7.2e+02;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2551 CTGACGTACCAAGCTGTGCCACAC 2573
 Db 2 CTGACCTTCAGCTGACGCCACAC 24
 RESULT 871
 ID ADC68809 standard; DNA; 24 BP.
 XX
 AC ADC68809;
 DT 18-DEC-2003 (first entry)
 XX
 DE Human PRO 860 PCR primer #2.
 XX
 KW Human; ss; PCR; secreted protein; transmembrane protein; PRO; cytosolic;
 KW ophthalmological; antiarthritic; osteopathic; antineumatic; vulnery;
 KW auditory; tumour growth; retinal disorder; sports-related joint problem;
 KW articular cartilage defects; osteoarthritis; rheumatoid arthritis;
 KW wound healing; hearing loss; primer.
 XX
 OS Homo sapiens.
 XX
 PN US2003064407-A1.
 XX
 PD 03-APR-2003.
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 PF 24-OCT-2001; 2001US-0099834.
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PR 26-JUN-1998; 98US-0091010P.
PR 01-JUL-1998; 98US-0091359P.
PR 30-JUL-1998; 98US-0094651P.

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PR 07-OCT-1998; 98US-0016897H.
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PR 02-NOV-1998; 98US-00184216.
PR 06-NOV-1998; 98US-00187358.
PR 20-NOV-1998; 98US-0109304P.
PR 20-NOV-1998; 98WO-US024855.
PR 07-DEC-1998; 98US-00202054.
PR 22-DEC-1998; 98US-0021396P.
PR 23-DEC-1998; 98US-0113621P.
PR 05-JAN-1999; 98WO-US000106.
PR 05-MAR-1999; 99US-00254465.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99US-00265686.
PR 12-MAR-1999; 99WO-US005190.
PR 12-MAR-1999; 99US-00267213.
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PR 29-MAR-1999; 99US-0126773P.
PR 12-APR-1999; 99US-00284291.
PR 21-APR-1999; 99US-0130232P.
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PR 28-APR-1999; 99US-0131445P.
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PR 06-JAN-2000; 2000WO-US000219.
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PR 22-MAY-2000; 2000WO-US014042.
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PR 02-JUN-2000; 2000WO-US015264.
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XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;

Query Match 0.2%; Score 18.2; DB 1; Length 24;
Best Local Similarity 87.0%; Pred. No. 7.2e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2551 CTGACGTACCAAGCTGTGCCACAC 2573
Db 2 CTGACCTCCAGCTGAGCCACAC 24

RESULT 872
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AC ADCC2869;
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XX
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XX
XX Human; ss; PCR; secreted protein; transmembrane protein; PRO; cytosolic;
KM ophthalmological; antiarthritic; osteopathic; antineumatic; vulnery;
KM auditory; tumour growth; retinal disorder; sports-related joint problem;
KM articular cartilage defects; osteoarthritis; rheumatoid arthritis;
KM wound healing; hearing loss; primer.
XX
XX Homo sapiens.
OS
XX
PN US2003066648-A1.
PD 10-APR-2003.
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PF 25-OCT-2001; 2001US-00013921.
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PR 17-OCT-1997; 97US-0062250P.
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PR 30-MAR-1998; 98US-0079920P.
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PR 31-MAR-1998; 98US-0080105P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080165P.
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PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080328P.
PR 01-APR-1998; 98US-0080333P.

PR 01-APR-1998; 98US-0080334P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 08-APR-1998; 98US-0081071P.
PR 09-APR-1998; 98US-0081195P.
PR 09-APR-1998; 98US-0081203P.
PR 09-APR-1998; 98US-0081229P.
PR 15-APR-1998; 98US-0081817P.
PR 15-APR-1998; 98US-0081819P.
PR 15-APR-1998; 98US-0081838P.
PR 15-APR-1998; 98US-0081952P.
PR 15-APR-1998; 98US-0081955P.
PR 21-APR-1998; 98US-0082568P.
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PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 22-APR-1998; 98US-0082804P.
PR 23-APR-1998; 98US-0082796P.
PR 27-APR-1998; 98US-0083336P.
PR 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083392P.
PR 29-APR-1998; 98US-0083495P.
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PR 29-APR-1998; 98US-0083545P.
PR 29-APR-1998; 98US-0083549P.
PR 29-APR-1998; 98US-0083558P.
PR 29-APR-1998; 98US-0083559P.
PR 30-APR-1998; 98US-0083742P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 07-MAY-1998; 98US-0084598P.
PR 07-MAY-1998; 98US-0084600P.
PR 07-MAY-1998; 98US-0084627P.
PR 07-MAY-1998; 98US-0084637P.
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PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086414P.
PR 22-MAY-1998; 98US-0086430P.
PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087098P.
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PR 26-JUN-1998; 98US-0090863P.
PR 26-JUN-1998; 98US-0091010P.
PR 01-JUL-1998; 98US-0091359P.
PR 30-JUL-1998; 98US-0094651P.
PR 31-SEP-1998; 98US-0100038P.
PR 07-OCT-1998; 98WO-US021141.
PR 20-NOV-1998; 98US-0109304P.
PR 20-NOV-1998; 98WO-US024855.
PR 22-DEC-1998; 98US-0113296P.
PR 23-DEC-1998; 98US-0113621P.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 12-MAR-1999; 99US-0123957P.

PR 29-MAR-1999; 99US-0126773P.
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PR 26-APR-1999; 99US-0131022P.
PR 28-APR-1999; 99US-0131445P.
PR 14-MAY-1999; 99US-0134287P.
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PR 30-NOV-1999; 99US-0139557P.
PR 02-DEC-1999; 99US-0139557P.
PR 02-DEC-1999; 99US-0139557P.
PR 16-DEC-1999; 99US-0139557P.
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PR 05-JAN-2000; 2000US-0000219.
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PR 24-FEB-2000; 2000US-0000219.
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PR 25-MAY-2001; 2001US-0000219.
PR 01-JUN-2001; 2001US-0000219.
PR 20-JUN-2001; 2001US-0000219.
PR 29-JUN-2001; 2001US-0000219.
PR 09-JUL-2001; 2001US-0000219.
PR 30-JUL-2001; 2001US-0000219.
(GENTH) GENENTECH INC.
PA Ashkenazi AJ, Baker KP, Botstein D, Deenoyers L, Eaton DL;
XX Ferrara N, Filvaroff E, Fong S, Gao W, Garber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tumas D, Williams PM, Wood WI;
XX WPI; 2003-65924/66.
DR New isolated secreted and transmembrane PRO polypeptides, useful in the
XX preparation of a medicament for treating a condition responsive to the
PT polypeptide, and as therapeutic agents e.g. vaccines.
PT Example 34; SEQ ID NO 213; 467bp; English.
XX The invention relates to an isolated PRO polypeptide (secreted or
XX transmembrane protein) having at least 80% amino acid sequence identity
CC to an amino acid sequence chosen from 94 fully defined sequences as given
CC in the specification (including PRO lacking its associated signal
CC peptide), a PRO extracellular domain with or without its associated signal
CC peptide). Also included are nucleic acids encoding the PRO proteins
CC mentioned above, a vector comprising a PRO nucleic acid, a host cell
CC comprising the vector and producing PRO, a chimeric molecule comprising
CC PRO fused to a heterologous amino acid sequence, and an anti-PRO
CC antibody. PRO337 polypeptide is useful for detecting a PRO4993
CC polypeptide in a sample suspected of containing PRO4993 polypeptide.
CC Similarly, PRO4993 polypeptide is useful for detecting PRO337
CC polypeptide. PRO725, PRO700 or PRO739 polypeptide is useful for detecting
CC PRO1559 polypeptide, and PRO1559 polypeptide is useful for detecting
CC PRO725, PRO700 or PRO739. PRO4993 polypeptide is useful for linking a
CC bioactive molecule to a cell expressing PRO337 polypeptide. The bioactive

CC molecule is the toxin, radiolabel, or an antibody. The bioactive molecule
CC causes death of the cell. PRO337 polypeptide is useful for linking a
Query Match 0.2%; Score 18.2; DB 1; Length 24;
Best Local Similarity 87.0%; Pred. No. 7.2e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2551 CTGACGTACAGCTGTGCACAC 2573
DB 2 CTGACCTTCAGCTGACGCACAC 24
RESULT 873
ID ADC67934 standard; DNA; 24 BP.
XX ADC67934;
AC ADC67934;
DT 18-DEC-2003 (first entry)
XX
DE Human PRO 860 PCR primer #2.
XX Human; 86; PCR; secreted protein; transmembrane protein; PRO; cytostatic;
XX ophthalmological; antiarthritic; osteopathic; antirheumatic; vulnery;
XX auditory; tumour growth; retinal disorder; sports-related joint problem;
XX articular cartilage defects; osteoarthritis; rheumatoid arthritis;
XX wound healing; hearing loss; primer.
OS Homo sapiens.
XX
XX US2003069178-A1.
PN
XX
PD 10-APR-2003.
XX
PF 16-OCT-2001; 2001US-00978423.
XX
XX 17-OCT-1997; 97US-0062250P.
XX 13-NOV-1997; 97US-0064249P.
XX 21-NOV-1997; 97US-0065311P.
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XX 11-MAR-1998; 98US-0077641P.
XX 11-MAR-1998; 98US-0077649P.
XX 12-MAR-1998; 98US-0077791P.
XX 13-MAR-1998; 98US-0078004P.
XX 20-MAR-1998; 98US-0078886P.
XX 20-MAR-1998; 98US-0078910P.
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XX 01-APR-1998; 98US-0080334P.
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XX 08-APR-1998; 98US-0081070P.
XX 08-APR-1998; 98US-0081071P.
XX 09-APR-1998; 98US-0081195P.
XX 09-APR-1998; 98US-0081203P.
XX 09-APR-1998; 98US-0081229P.
XX 15-APR-1998; 98US-0081817P.
XX 15-APR-1998; 98US-0081819P.


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PR 22-APR-1998: 98US-0082704P.
PR 22-APR-1998: 98US-0082797P.
PR 22-APR-1998: 98US-0082804P.
PR 23-APR-1998: 98US-0082796P.
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PR 29-APR-1998: 98US-0083495P.
PR 29-APR-1998: 98US-0083496P.
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PR 06-MAY-1998: 98US-0084441P.
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PR 07-MAY-1998: 98US-0084627P.
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PR 30-JUL-1998: 98US-0094651P.
PR 11-SEP-1998: 98US-0100038P.
PR 07-OCT-1998: 98WO-US021141.
PR 20-NOV-1998: 98US-0109304P.
PR 20-NOV-1998: 98WO-US024855.
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PR 23-DEC-1998: 98US-0113621P.
PR 05-JAN-1999: 99WO-US000106.
PR 08-MAR-1999: 99WO-US005028.
PR 10-MAR-1999: 99WO-US005190.
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PR 29-MAR-1999: 99US-0126773P.
PR 21-APR-1999: 99US-0130232P.
PR 26-APR-1999: 99US-0131022P.
PR 28-APR-1999: 99US-0131445P.
PR 14-MAY-1999: 99US-0134287P.
PR 14-MAY-1999: 99WO-US010733.
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PR 16-JUN-1999: 99US-0139557P.

PR 23-JUN-1999: 99US-0141037P.
PR 07-JUL-1999: 99US-0142680P.
PR 26-JUL-1999: 99US-0145698P.
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PR 02-DEC-1999: 99WO-US028565.
PR 16-DEC-1999: 99WO-US030095.
PR 30-DEC-1999: 99WO-US031243.
PR 30-DEC-1999: 99WO-US031274.
PR 05-JAN-2000: 2000WO-US000219.
PR 06-JAN-2000: 2000WO-US000277.
PR 06-JAN-2000: 2000WO-US000376.
PR 11-FEB-2000: 2000WO-US003565.
PR 18-FEB-2000: 2000WO-US004341.
PR 24-FEB-2000: 2000WO-US005004.
PR 02-MAR-2000: 2000WO-US005841.
PR 10-MAR-2000: 2000WO-US006319.
PR 21-MAR-2000: 2000WO-US007532.
PR 30-MAR-2000: 2000WO-US008433.
PR 17-MAY-2000: 2000WO-US013705.
PR 22-MAY-2000: 2000WO-US014042.
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PR 24-AUG-2000: 2000WO-US023328.
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PR 01-JUN-2001: 2001WO-US017800.
PR 20-JUN-2001: 2001WO-US019692.
PR 29-JUN-2001: 2001WO-US021066.
PR 09-JUL-2001: 2001WO-US021735.
PR 30-JUL-2001: 2001US-00918585.

XX (GENTH ) GENENTECH INC.
XX
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers LJ, Eaton DL;
XX Ferrara N, Flivaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
XX Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
XX Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
XX Stewart TA, Tumas D, Williams PM, Wood WI;
XX
XX MPI; 2003-657582/62.
XX
XX
XX Novel secreted and transmembrane polypeptides, designated PRO
XX polypeptides, and polynucleotides encoding them useful for treating
XX kidney diseases, bone, cartilage and retinal disorders.
XX
XX
XX Example 34; SEQ ID NO 213; 468pp; English.
XX
XX
XX The invention relates to an isolated PRO polypeptide (secreted or
XX transmembrane protein) having at least 80% amino acid sequence identity
XX to an amino acid sequence chosen from 94 fully defined sequences as given
XX in the specification (including PRO lacking its associated signal
XX peptide, a PRO extracellular domain with or without its associated signal
XX peptide). Also included are nucleic acids encoding the PRO proteins
XX mentioned above, a vector comprising a PRO nucleic acid, a host cell
XX comprising the vector and producing PRO, a chimeric molecule comprising
XX CC PRO fused to a heterologous amino acid sequence, and an anti-PRO
XX antibody. PRO317 polypeptide is useful for detecting a PRO4993
XX polypeptide in a sample suspected of containing PRO4993 polypeptide.
XX CC Similarly, PRO4993 polypeptide is useful for detecting PRO317
XX polypeptide. PRO725, PRO700 or PRO739 polypeptide is useful for detecting
XX CC PRO1559 polypeptide, and PRO1559 polypeptide is useful for detecting
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PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
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PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
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PR 24-AUG-2000; 2000WO-US023328.
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PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001WO-US009552.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.

XX (GETH) GENENTECH INC.

PA Ashkenazi A, Baker KP, Borstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski FJ, Grimaldi JC, Gueney AU, Hillan KU;
PI Kijavlin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
PI Stewart TA, Tamas D, Williams PM, Wood WI;
XX
XX WPI; 2003-743806/70.

XX Novel isolated secreted and transmembrane PRO polypeptides, useful in the
PT preparation of a medicament for treating a condition responsive to the
PT polypeptide, and as therapeutic agents e.g. vaccines.

PS Example 34; SEQ ID NO 213; 466p; English.

XX The invention relates to an isolated PRO polypeptide (secreted or
CC transmembrane protein) having at least 80% amino acid sequence identity
CC to an amino acid sequence chosen from 94 fully defined sequences as given
CC in the specification (including PRO lacking its associated signal
CC peptide), a PRO extracellular domain with or without its associated signal
CC peptide). Also included are nucleic acids encoding the PRO proteins
CC mentioned above, a vector comprising a PRO nucleic acid, a host cell
CC comprising the vector and producing PRO, a chimeric molecule comprising
CC PRO fused to a heterologous amino acid sequence, and an anti-PRO
CC antibody. PRO337 polypeptide is useful for detecting a PRO4993
CC polypeptide in a sample suspected of containing PRO4993 polypeptide.
CC Similarly, PRO4993 polypeptide is useful for detecting PRO337

Query Match 0.2%; Score 18.2; DB 1; Length 24;
Best Local Similarity 87.0%; Pred. No. 7.2e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2551 CTGACCTACCACTGTCGCCAC 2573

DB 2 CTGACCTTCACGCTGAGCCACAC 24

RESULT 875
ADC67309

ID ADC67309 standard; DNA; 24 BP.
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AC ADC67309;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human PRO 860 PCR primer #2.
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KM vulnary; virucide; neuroprotective; cyrostatic; gene therapy;
KM tumour cell proliferation inhibitor;
KM secreted and transmembrane protein; PRO; viral infection; wound healing;
KM tissue growth; muscle generation; muscle regeneration;
KM amyotrophic lateral sclerosis; neuropathy; AIDS-associated neuropathy;
KM diabetic peripheral neuropathy; chromosome identification; antagonist;
KM tissue typing; immunohistochemical staining; primer; ss.
XX
XX Homo sapiens.
XX
PN US2003073131-A1.
XX
PD 17-APR-2003.
XX
PF 25-OCT-2001; 2001US-00016177.
XX
XX 17-OCT-1997; 97US-0062250P.
XX 03-NOV-1997; 97US-0064429P.
XX 13-NOV-1997; 97US-0065311P.
XX 21-NOV-1997; 97US-0066364P.
XX 10-MAR-1998; 98US-0077450P.
XX 11-MAR-1998; 98US-0077632P.
XX 11-MAR-1998; 98US-0077641P.
XX 12-MAR-1998; 98US-0077649P.
XX 12-MAR-1998; 98US-0077791P.
XX 13-MAR-1998; 98US-0078004P.
XX 20-MAR-1998; 98US-0078886P.
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XX 31-MAR-1998; 98US-0080107P.
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XX 01-APR-1998; 98US-0080327P.
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XX 21-APR-1998; 98US-0082569P.
XX 22-APR-1998; 98US-0082700P.
XX 22-APR-1998; 98US-0082704P.
XX 22-APR-1998; 98US-0082797P.
XX 22-APR-1998; 98US-0082804P.
XX 23-APR-1998; 98US-0082796P.

[illegible]

XX Human; ss; PCR: secreted protein; transmembrane protein; PRO; cytosolic;
KW ophthalmological; antiarthritic; osteopathic; antirheumatic; vulnery;
KW auditory; tumour growth; retinal disorder; sports-related joint problem;
KW articular cartilage defects; osteoarthritis; rheumatoid arthritis;
KW wound healing; hearing loss; primer.
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Query Match 0.2%; Score 18.2; DB 1; Length 24;
Best Local Similarity 87.0%; Pred. No. 7.2e+02;
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RESULT 877

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DT 18-DEC-2003 (first entry)

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ophthalmological; antiarthritic; osteopathic; antirheumatic; vulnery;
auditory; tumour growth; retinal disorder; sports-related joint problem;
articular cartilage defects; osteoarthritis; rheumatoid arthritis;
wound healing; hearing loss; primer.

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XX auditory; tumour growth; retinal disorder; sports-related joint problem;
XX articular cartilage defects; osteoarthritis; rheumatoid arthritis;
XX wound healing; hearing loss; primer.
OS Homo sapiens.
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PR 26-JUN-1998; 98US-00105413
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PR 26-JUN-1998; 98US-0091010P
PR 01-JUL-1998; 98US-0091359P
PR 30-JUL-1998; 98US-0094651P
PR 11-SEP-1998; 98US-0100038P
PR 07-OCT-1998; 98US-00168978
PR 07-OCT-1998; 98US-0021141
PR 06-NOV-1998; 98US-00184216
PR 20-NOV-1998; 98US-0109304P
PR 20-NOV-1998; 98US-0109304P
PR 07-DEC-1998; 98US-00202054
PR 22-DEC-1998; 98US-00218517
PR 22-DEC-1998; 98US-0113296P
PR 23-DEC-1998; 98US-0113621P
PR 05-JAN-1999; 99US-0113621P
PR 05-JAN-1999; 99US-00254465
PR 08-MAR-1999; 99US-00050028
PR 10-MAR-1999; 99US-00265686
PR 10-MAR-1999; 99US-0005190
PR 12-MAR-1999; 99US-0026721P
PR 12-MAR-1999; 99US-0123957P
PR 29-MAR-1999; 99US-0126737P
PR 12-APR-1999; 99US-00284291
PR 21-APR-1999; 99US-0130232P
PR 26-APR-1999; 99US-0131022P
PR 28-APR-1999; 99US-0131445P
PR 14-MAY-1999; 99US-00311832
PR 14-MAY-1999; 99US-0134287P
PR 14-MAY-1999; 99US-0134287P
PR 02-JUN-1999; 99US-0139557P
PR 16-JUN-1999; 99US-0141037P
PR 23-JUN-1999; 99US-0141037P
PR 07-JUL-1999; 99US-0142680P
PR 26-JUL-1999; 99US-0145698P
PR 28-JUL-1999; 99US-0146222P
PR 25-AUG-1999; 99US-00380137
PR 25-AUG-1999; 99US-00380138
PR 25-AUG-1999; 99US-00380142
PR 25-AUG-1999; 99US-0162506P
PR 30-NOV-1999; 99US-0162506P
PR 02-DEC-1999; 99US-0162506P
PR 02-DEC-1999; 99US-0162506P
PR 02-DEC-1999; 99US-0162506P
PR 16-DEC-1999; 99US-0162506P
PR 30-DEC-1999; 99US-0162506P
PR 30-DEC-1999; 99US-0162506P
PR 05-JAN-2000; 2000US0002174
PR 06-JAN-2000; 2000US0002277
PR 06-JAN-2000; 2000US000277
PR 11-FEB-2000; 2000US003565
PR 18-FEB-2000; 2000US004341
PR 24-FEB-2000; 2000US005004
PR 02-MAR-2000; 2000US005841
PR 10-MAR-2000; 2000US006319
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PR 21-MAR-2000; 2000MO-US007532.
PR 30-MAR-2000; 2000MO-US008439.
PR 17-MAY-2000; 2000MO-US013705.
PR 22-MAY-2000; 2000MO-US014042.
PR 30-MAY-2000; 2000MO-US014941.
PR 02-JUN-2000; 2000MO-US015264.
PR 28-JUL-2000; 2000MO-US020710.
PR 24-AUG-2000; 2000MO-US023328.
PR 08-NOV-2000; 2000US-00709338.
PR 27-NOV-2000; 2000US-00723749.
PR 01-DEC-2000; 2000MO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 28-FEB-2001; 2001MO-US004956.
PR 22-MAR-2001; 2001US-00816744.
PR 22-MAR-2001; 2001US-00816920.
PR 22-MAR-2001; 2001MO-US009552.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001MO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001MO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001MO-US019692.
PR 29-JUN-2001; 2001MO-US021066.
PR 09-JUL-2001; 2001MO-US021735.
PR 30-JUL-2001; 2001US-00918585.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI
Query Match 0.2%; Score 18.2; DB 1; Length 24;
Best Local Similarity 87.0%; Pred. No. 7.2e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2551 CTGACGTACCAAGCTGTGCCACAC 2573
DB 2 CTGACCTTCACGCTGAGCCACAC 24
RESULT 879
ADE16415
ID ADE16415 standard; DNA; 24 BP.
XX
AC ADE16415;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human PRO 860 PCR primer #2.
XX
XX Human; ss; PCR; secreted protein; transmembrane protein; PRO; cytosolic;
XX KM ophthalmological; antirheumatic; osteopathic; antineoplastic; vulnery;
XX KM articular; tumour growth; retinal disorder; sports-related joint problem;
XX KM articular cartilage defects; osteoarthritis; rheumatoid arthritis;
XX KM wound healing; hearing loss; primer.
XX
XX Homo sapiens.
OS
XX
XX US2003203434-A1.
XX
XX 30-OCT-2003.
XX
XX 18-OCT-2001; 2001US-00145088.
XX
XX 15-MAY-1998; 98US-0085689P.
XX 08-MAR-1999; 99MO-US005028.
XX 28-APR-1999; 99US-0131445P.
XX 25-AUG-1999; 99US-00380138.
XX 18-FEB-2000; 2000MO-US004341.
XX 30-JUL-2001; 2001US-00918585.

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XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
XX PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
XX PI Ferrara N, Filvaroff E, Fong S, Garber H, Gerritsen ME;
XX PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
XX PI Kijavitt IJ, Kuo SS, Napier MA, Pan J, Paoi NF, Roy MA, Shelton DL,
XX PI Stewart TA, Thomas D, Williams PM, Wood WI;
XX
XX WPI; 2003-875641/81.
XX
XX New genes, and its encoded secreted and transmembrane polypeptides,
XX PT useful for treating e.g. lung or breast tumors, osteoarthritis,
XX PT rheumatoid arthritis, obesity, diabetes, hyperinsulinemia,
XX PT hypoinsulinemia or wounds.
XX
XX Example 34; SEQ ID NO 213; 462pp; English.
XX
XX The invention relates to an isolated PRO polypeptide (secreted or
XX CC transmembrane protein) having at least 80% amino acid sequence identity
XX CC to an amino acid sequence chosen from 94 fully defined sequences as given
XX CC in the specification (including PRO lacking its associated signal
XX CC peptide), a PRO extracellular domain with or without its associated signal
XX CC peptide), also included are nucleic acids encoding the PRO proteins
XX CC mentioned above, a vector comprising a PRO nucleic acid, a host cell
XX CC comprising the vector and producing PRO, a chimeric molecule comprising
XX CC PRO fused to a heterologous amino acid sequence, and an anti-PRO
XX CC antibody. PRO337 polypeptide is useful for detecting a PRO4993
XX CC polypeptide in a sample suspected of containing PRO4993 polypeptide.
XX CC Similarly, PRO4993 polypeptide is useful for detecting PRO337
XX CC polypeptide. PRO725, PRO700 or PRO739 polypeptide is useful for detecting
XX CC PRO1559 polypeptide, and PRO1559 polypeptide is useful for detecting
XX CC PRO725, PRO700 or PRO739. PRO4993 polypeptide is useful for linking a
XX CC bioactive molecule to a cell expressing PRO337 polypeptide. The bioactive
XX CC molecule is the toxin, radiolabel, or an antibody. The bioactive molecule
XX CC causes death of the cell. PRO337 polypeptide is useful for linking a
XX CC bioactive molecule to a cell expressing PRO4993 polypeptide; PRO725,
XX CC PRO700 or PRO739 polypeptide are useful for linking a bioactive molecule
XX CC to a cell expressing PRO1559 polypeptide; and PRO1559 polypeptide is
XX CC useful for linking a bioactive molecule to a cell expressing PRO725,
XX CC PRO700 or PRO739 polypeptide. PRO4993 polypeptide or anti-PRO337
XX CC polypeptide is useful for modulating at least one biological activity of
XX CC the cell expressing PRO337 polypeptide, where the cell is killed. PRO337
XX CC polypeptide or anti-PRO4993 polypeptide is useful for modulating the
XX CC biological activity of the cell expressing PRO4993 polypeptide; PRO725,
XX CC PRO700 or PRO739 polypeptide or an anti-PRO1559 polypeptide is useful for
XX CC modulating the biological activity of the cell expressing PRO1559
XX CC polypeptide; and PRO1559 polypeptide or anti-PRO725, anti-PRO700 or anti-
XX CC PRO739 polypeptide is useful for modulating the biological activity of
XX CC the cell expressing PRO725, PRO700 or PRO739 polypeptide. The
XX CC polypeptides are useful for inhibiting tumour growth, retinal disorders,
XX CC sports-related joint problems, articular cartilage defects,
XX CC osteoarthritis or rheumatoid arthritis, wound healing and hearing loss in
XX CC mammals. The present sequence is a PCR primer used to isolate nucleic
XX CC acid encoding a PRO protein.
XX
XX Sequence 24 BP; 6 A; 10 C; 4 G; 4 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 18.2; DB 1; Length 24;
Best Local Similarity 87.0%; Pred. No. 7.2e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2551 CTGACGTACCAAGCTGTGCCACAC 2573
DB 2 CTGACCTTCACGCTGAGCCACAC 24
RESULT 880
ADE16415
ID ADE16415 standard; DNA; 24 BP.
XX
XX ADE16415;
AC
XX

```

29-JAN-2004 (first entry)
 Human PRO 860 PCR primer #2.
 Human; ss; PCR, secreted protein; transmembrane protein; PRO, cytosolic;
 ophthalmological; antiarthritic; osteopathic; antirheumatic; vulnery;
 auditory; tumour growth; retinal disorder; sports-related joint problem;
 articular cartilage defects; osteoarthritis; rheumatoid arthritis;
 wound healing; hearing loss; primer.
 Homo sapiens.
 US2003203435-A1.
 30-OCT-2003.
 18-OCT-2001; 2001US-00145092.
 30-APR-1998; 98US-0083742P.
 08-MAR-1999; 99WO-US005028.
 23-JUN-1999; 99US-0141037P.
 25-AUG-1999; 99US-00380138.
 18-FEB-2000; 2000WO-US004341.
 30-JUL-2001; 2001US-00918585.
 (GENTH) GENENTECH INC.
 Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
 Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
 Kijavlin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
 Stewart TA, Tumas D, Williams PM, Wood WI;
 WPI; 2003-875642/81.
 New genes, and its encoded secreted and transmembrane polypeptides,
 useful for treating e.g. lung or breast tumors, osteoarthritis,
 rheumatoid arthritis, obesity, diabetes, hyperinsulinemia,
 hypoinsulinemia or wounds.
 Example 34; SEQ ID NO 213; 452bp; English.
 The invention relates to an isolated PRO polypeptide (secreted or
 transmembrane protein) having at least 80% amino acid sequence identity
 to an amino acid sequence chosen from 94 fully defined sequences as given
 in the specification (including PRO lacking its associated signal
 peptide), a PRO extracellular domain with or without its associated signal
 peptide), also included are nucleic acids encoding the PRO proteins
 mentioned above, a vector comprising a PRO nucleic acid, a host cell
 comprising the vector and producing PRO, a chimaeric molecule comprising
 CC PRO fused to a heterologous amino acid sequence, and an anti-PRO
 antibody. PRO337 polypeptide is useful for detecting a PRO4993
 polypeptide in a sample suspected of containing PRO4993 polypeptide.
 CC Similarly, PRO4993 polypeptide is useful for detecting PRO337
 CC polypeptide. PRO725, PRO700 or PRO739 polypeptide is useful for detecting
 CC PRO1559 polypeptide, and PRO1559 polypeptide is useful for detecting
 CC PRO725, PRO700 or PRO739. PRO4993 polypeptide is useful for linking a
 CC bioactive molecule to a cell expressing PRO337 polypeptide. The bioactive
 CC molecule is the toxin, radiolabel, or an antibody. The bioactive molecule
 CC causes death of the cell. PRO337 polypeptide is useful for linking a
 CC bioactive molecule to a cell expressing PRO4993 polypeptide; PRO725,
 CC PRO700 or PRO739 polypeptide are useful for linking a bioactive molecule
 CC to a cell expressing PRO1559 polypeptide; and PRO1559 polypeptide is
 CC useful for linking a bioactive molecule to a cell expressing PRO725,
 CC PRO700 or PRO739 polypeptide. PRO4993 polypeptide or anti-PRO337
 CC polypeptide is useful for modulating at least one biological activity of
 CC the cell expressing PRO337 polypeptide, where the cell is killed. PRO337
 CC polypeptide or anti-PRO4993 polypeptide is useful for modulating the
 CC biological activity of the cell expressing PRO4993 polypeptide; PRO725,
 CC PRO700 or PRO739 polypeptide or an anti-PRO1559 polypeptide is useful for
 CC modulating the biological activity of the cell expressing PRO1559
 CC polypeptide; and PRO1559 polypeptide or anti-PRO725, anti-PRO700 or anti-
 CC PRO739 polypeptide is useful for modulating the biological activity of

the cell expressing PRO725, PRO700 or PRO739 polypeptide. The
 CC polypeptides are useful for inhibiting tumour growth, retinal disorders,
 CC sports-related joint problems, articular cartilage defects,
 CC osteoarthritis or rheumatoid arthritis, wound healing and hearing loss in
 CC mammals. The present sequence is a PCR primer used to isolate nucleic
 CC acid encoding a PRO protein.
 SQ Sequence 24 BP; 6 A; 10 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 0.2%; Score 18.2; DB 1; Length 24;
 Best Local Similarity 87.0%; Pred. No. 7.2e+02;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 2551 CTGACGTACGAGCTGTGCGACAC 2573
 Db 2 CTGACCTTCAGCTGAGCCACAC 24
 RESULT 881
 ADD73030
 ID ADD73030 standard; DNA; 24 BP.
 XX
 AC ADD73030;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human PRO 860 PCR primer #2.
 XX
 XX Human; ss; PCR, secreted protein; transmembrane protein; PRO, cytosolic;
 XX ophthalmological; antiarthritic; osteopathic; antirheumatic; vulnery;
 XX auditory; tumour growth; retinal disorder; sports-related joint problem;
 XX articular cartilage defects; osteoarthritis; rheumatoid arthritis;
 XX wound healing; hearing loss; primer.
 XX
 OS Homo sapiens.
 XX
 PN US2003203436-A1.
 XX
 PD 30-OCT-2003.
 XX
 PF 18-OCT-2001; 2001US-00145129.
 XX
 PR 22-MAY-1998; 98US-0086414P.
 PR 22-DEC-1998; 98US-0113296P.
 PR 05-JAN-1999; 99WO-US000106.
 PR 08-MAR-1999; 99WO-US005028.
 PR 12-APR-1999; 99US-00284291.
 PR 25-AUG-1999; 99US-00380138.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 30-JUL-2001; 2001US-00918585.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
 PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
 PI Kijavlin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
 PI Stewart TA, Tumas D, Williams PM, Wood WI;
 XX
 DR WPI; 2003-875643/81.
 XX
 PT New PRO genes and encoded secreted and transmembrane polypeptides, useful
 PT for treating e.g. lung or breast tumors, osteoarthritis, rheumatoid
 PT arthritis, obesity, diabetes, hyperinsulinemia, hypoinsulinemia or
 PT wounds.
 PT
 PS Example 34; SEQ ID NO 213; 453bp; English.
 XX
 CC The invention relates to an isolated PRO polypeptide (secreted or
 CC transmembrane protein) having at least 80% amino acid sequence identity
 CC to an amino acid sequence chosen from 94 fully defined sequences as given
 CC in the specification (including PRO lacking its associated signal
 CC peptide), a PRO extracellular domain with or without its associated signal

peptide). Also included are nucleic acids encoding the PRO proteins mentioned above, a vector comprising a PRO nucleic acid, a host cell comprising the vector and producing PRO, a chimeric molecule comprising PRO fused to a heterologous amino acid sequence, and an anti-PRO antibody. PRO337 polypeptide is useful for detecting a PRO4993 polypeptide in a sample suspected of containing PRO4993 polypeptide. Similarly, PRO4993 polypeptide is useful for detecting PRO337 polypeptide. PRO725, PRO700 or PRO739 polypeptide is useful for detecting PRO1559 polypeptide, and PRO1559 polypeptide is useful for detecting PRO725, PRO700 or PRO739. PRO4993 polypeptide is useful for linking a bioactive molecule to a cell expressing PRO337 polypeptide. The bioactive molecule is the toxin, radiolabel, or an antibody. The bioactive molecule causes death of the cell. PRO337 polypeptide is useful for linking a bioactive molecule to a cell expressing PRO4993 polypeptide. PRO725, PRO700 or PRO739 polypeptide are useful for linking a bioactive molecule to a cell expressing PRO1559 polypeptide, and PRO1559 polypeptide is useful for linking a bioactive molecule to a cell expressing PRO337 polypeptide. PRO4993 polypeptide is useful for modulating the biological activity of the cell expressing PRO337 polypeptide, where the cell is killed. PRO337 polypeptide or anti-PRO4993 polypeptide is useful for modulating the biological activity of the cell expressing PRO4993 polypeptide. PRO725, PRO700 or PRO739 polypeptide or an anti-PRO1559 polypeptide is useful for modulating the biological activity of the cell expressing PRO1559 polypeptide or anti-PRO725, anti-PRO700 or anti-PRO739 polypeptide is useful for modulating the biological activity of the cell expressing PRO725, PRO700 or PRO739 polypeptide. The polypeptides are useful for inhibiting tumour growth, retinal disorders, sports-related joint problems, articular cartilage defects, osteoarthritis or rheumatoid arthritis, wound healing and hearing loss in mammals. The present sequence is a PCR primer used to isolate nucleic acid encoding a PRO protein.

Sequence 24 BP; 6 A; 10 C; 4 G; 4 T; 0 U; 0 Other;
Query Match 0.2%; Score 18.2; DB 1; Length 24;
Best Local Similarity 87.0%; Pred. No. 7.2e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2551 CTGACGACGACGCTGCGCACAC 2573
2 CTGACCTTCAGCTGAGCCACAC 24

RESULT 882

ADD72388 standard; DNA; 24 BP.

AC ADD72388;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human PRO 860 PCR primer #2.
XX
XX Human; ss; PCR; secreted protein; transmembrane protein; PRO; cytosolic;
XX ophthalmological; antiarthritic; osteopathic; antineumatic; vulnery;
XX auditory; tumour growth; retinal disorder; sports-related joint problem;
XX articular cartilage defects; osteoarthritis; Rheumatoid arthritis;
XX wound healing; hearing loss; primer.
OS Homo sapiens.
XX
XX US2003194781-A1.
PN
PD 16-OCT-2003.
XX
XX 19-OCT-2001; 2001US-00164929.
PF
XX 30-MAR-1998; 98US-0079990P.
PR 07-OCT-1998; 98MO-US002141.
PR 20-NOV-1998; 98MO-US002485.
PR 05-JAN-1999; 99MO-US000106.
PR 08-MAR-1999; 99MO-US0005028.

PR 10-MAR-1999; 99MO-US005190.
PR 15-APR-1999; 99MO-US008313.
PR 14-MAY-1999; 99MO-US010733.
PR 02-JUN-1999; 99MO-US012252.
PR 25-AUG-1999; 99US-00380138.
PR 30-NOV-1999; 99MO-US028313.
PR 02-DEC-1999; 99MO-US028551.
PR 16-DEC-1999; 99MO-US030095.
PR 30-DEC-1999; 99MO-US031243.
PR 05-JAN-2000; 2000MO-US000219.
PR 06-JAN-2000; 2000MO-US000277.
PR 11-FEB-2000; 2000MO-US003565.
PR 18-FEB-2000; 2000MO-US004341.
PR 24-FEB-2000; 2000MO-US005004.
PR 02-MAR-2000; 2000MO-US005841.
PR 10-MAR-2000; 2000MO-US006319.
PR 21-MAR-2000; 2000MO-US007532.
PR 30-MAR-2000; 2000MO-US008439.
PR 17-MAY-2000; 2000MO-US013705.
PR 22-MAY-2000; 2000MO-US014042.
PR 30-MAY-2000; 2000MO-US014941.
PR 02-JUN-2000; 2000MO-US015264.
PR 28-JUN-2000; 2000MO-US020710.
PR 24-AUG-2000; 2000MO-US023328.
PR 01-DEC-2000; 2000MO-US032678.
PR 20-DEC-2000; 2000MO-US034956.
PR 28-FEB-2001; 2001MO-US006520.
PR 22-MAR-2001; 2001MO-US009552.
PR 25-MAY-2001; 2001MO-US017092.
PR 01-JUN-2001; 2001MO-US017800.
PR 20-JUN-2001; 2001MO-US019692.
PR 29-JUN-2001; 2001MO-US021066.
PR 09-JUL-2001; 2001MO-US021735.
PR 30-JUL-2001; 2001US-00918585.

(GENTH) GENTECH INC.

PA Ashkenazi AJ, Baker KP, Botstein D, Deenoyers L, Eaton DL;
XX Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gertitsen ME;
PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Kijavani IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;
XX Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI; 2003-852598/79.

New secreted and transmembrane PRO nucleic acids and polypeptides, useful for stimulating the release of tumor necrosis factor alpha from human blood and stimulating the proliferation of differentiation of chondrocyte cells.

Example 34; SEQ ID NO 213; 462bp; English.

XX The invention relates to an isolated PRO polypeptide (secreted or transmembrane protein) having at least 80 amino acid sequence identity to an amino acid sequence chosen from 94 fully defined sequences as given in the specification (including PRO lacking its associated signal peptide), a PRO extracellular domain with or without its associated signal peptide). Also included are nucleic acids encoding the PRO proteins mentioned above, a vector comprising a PRO nucleic acid, a host cell comprising the vector and producing PRO, a chimeric molecule comprising PRO fused to a heterologous amino acid sequence, and an anti-PRO antibody. PRO337 polypeptide is useful for detecting a PRO4993 polypeptide in a sample suspected of containing PRO4993 polypeptide. Similarly, PRO4993 polypeptide is useful for detecting PRO337 polypeptide. PRO725, PRO700 or PRO739 polypeptide is useful for detecting PRO1559 polypeptide, and PRO1559 polypeptide is useful for detecting PRO725, PRO700 or PRO739. PRO4993 polypeptide is useful for linking a bioactive molecule to a cell expressing PRO337 polypeptide. The bioactive molecule is the toxin, radiolabel, or an antibody. The bioactive molecule causes death of the cell. PRO337 polypeptide is useful for linking a

CC bioactive molecule to a cell expressing PRO4993 polypeptide; PRO725,
 CC PRO700 or PRO739 polypeptide are useful for linking a bioactive molecule
 CC to a cell expressing PRO1559 polypeptide; and PRO1559 polypeptide is
 CC useful for linking a bioactive molecule to a cell expressing PRO725,
 CC PRO700 or PRO739 polypeptide. PRO4993 polypeptide or anti-PRO337
 CC polypeptide is useful for modulating at least one biological activity of
 CC the cell expressing PRO337 polypeptide, where the cell is killed. PRO337
 CC polypeptide or anti-PRO4993 polypeptide is useful for modulating the
 CC biological activity of the cell expressing PRO4993 polypeptide; PRO725,
 CC PRO700 or PRO739 polypeptide or an anti-PRO1559 polypeptide is useful for
 CC modulating the biological activity of the cell expressing PRO1559
 CC polypeptide; and PRO1559 polypeptide or anti-PRO725, anti-PRO700 or anti-
 CC PRO739 polypeptide is useful for modulating the biological activity of
 CC the cell expressing PRO725, PRO700 or PRO739 polypeptide. The
 CC polypeptides are useful for inhibiting tumour growth, retinal disorders,
 CC sports-related joint problems, articular cartilage defects,
 CC osteoarthritis or rheumatoid arthritis, wound healing and hearing loss in
 CC mammals. The present sequence is a PCR primer used to isolate nucleic
 CC acid encoding a PRO protein.

SQ Sequence 24 BP; 6 A; 10 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.2; DB 1; Length 24;
 Best Local Similarity 87.0%; Pred. No. 7.2e+02;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2551 CTGACGTACCACTGTGCCACAC 2573
 Db 2 CTGACCTTCACCTGAGCCACAC 24

RESULT 883
 ADE17039
 ADE17039 standard; DNA; 24 BP.

AC ADE17039;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human PRO 860 PCR primer #2.

KW Human; ss; PCR; secreted protein; transmembrane protein; PRO; cytosstatic;
 KW ophthalmological; antiarthritic; osteopathic; antirheumatic; vulnery;
 KW auditory; tumour growth; retinal disorder; sports-related joint problem;
 KW articular cartilage defects; osteoarthritis; rheumatoid arthritis;
 KW wound healing; hearing loss; primer.

XX Homo sapiens.
 OS
 XX
 PN US2003203433-A1.
 XX
 PD 30-OCT-2003.
 XX
 PF 18-OCT-2001; 2001US-00145016.
 XX
 PR 06-MAY-1998; 98US-0084414P.
 PR 22-DEC-1998; 98US-0113296P.
 PR 05-JAN-1999; 99MO-US000106.
 PR 08-MAR-1999; 99MO-US005028.
 PR 12-APR-1999; 99US-00284291.
 PR 25-AUG-1999; 99US-00380138.
 PR 18-FEB-2000; 2000MO-US004341.
 PR 30-JUL-2001; 2001US-00918585.
 XX
 XX (GENT) GENENTECH INC.
 PA
 XX
 PI Ashkenazi AJ, Baker KP, Bolstein D, Deenoyers J, Eaton DL;
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Garber H, Gerritsen ME;
 PI Goddard A, Godowski RJ, Grimaldi JC, Gurney AL, Hillan KJ;
 PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoletti NF, Roy MA, Shelton DL;
 PI Stewart TA, Tumas D, Williams PM, Wood WI;
 XX
 DR WPI; 2003-875640/81.

XX New genes, and its encoded secreted and transmembrane polypeptides,
 PT useful for treating e.g. lung or breast tumors, osteoarthritis,
 PT rheumatoid arthritis, obesity, diabetes, hyperinsulinemia,
 PT hypotinsulinemia or wounds.

PS Example 34; SEQ ID NO 213; 459pp; English.

XX
 CC The invention relates to an isolated PRO polypeptide (secreted or
 CC transmembrane protein) having at least 80% amino acid sequence identity
 CC to an amino acid sequence chosen from 94 fully defined sequences as given
 CC in the specification (including PRO lacking its associated signal
 CC peptide, a PRO extracellular domain with or without its associated signal
 CC peptide). Also included are nucleic acids encoding the PRO proteins
 CC mentioned above, a vector comprising a PRO nucleic acid, a host cell
 CC comprising the vector and producing PRO, a chimeric molecule comprising
 CC PRO fused to a heterologous amino acid sequence, and an anti-PRO
 CC antibody. PRO337 polypeptide is useful for detecting a PRO4993
 CC polypeptide in a sample suspected of containing PRO4993 polypeptide.
 CC Similarly, PRO4993 polypeptide is useful for detecting PRO337
 CC polypeptide. PRO725, PRO700 or PRO739 polypeptide is useful for detecting
 CC PRO1559 polypeptide, and PRO1559 polypeptide is useful for detecting
 CC PRO725, PRO700 or PRO739. PRO4993 polypeptide is useful for linking a
 CC bioactive molecule to a cell expressing PRO337 polypeptide. The bioactive
 CC molecule is the toxin, radiolabel, or an antibody. The bioactive molecule
 CC causes death of the cell. PRO337 polypeptide is useful for linking a
 CC bioactive molecule to a cell expressing PRO4993 polypeptide; PRO725,
 CC PRO700 or PRO739 polypeptide are useful for linking a bioactive molecule
 CC to a cell expressing PRO1559 polypeptide; and PRO1559 polypeptide is
 CC useful for linking a bioactive molecule to a cell expressing PRO725,
 CC PRO700 or PRO739 polypeptide. PRO4993 polypeptide or anti-PRO337
 CC polypeptide is useful for modulating at least one biological activity of
 CC the cell expressing PRO337 polypeptide, where the cell is killed. PRO337
 CC polypeptide or anti-PRO4993 polypeptide is useful for modulating the
 CC biological activity of the cell expressing PRO4993 polypeptide; PRO725,
 CC PRO700 or PRO739 polypeptide or an anti-PRO1559 polypeptide is useful for
 CC modulating the biological activity of the cell expressing PRO1559
 CC polypeptide; and PRO1559 polypeptide or anti-PRO725, anti-PRO700 or anti-
 CC PRO739 polypeptide is useful for modulating the biological activity of
 CC the cell expressing PRO725, PRO700 or PRO739 polypeptide. The
 CC polypeptides are useful for inhibiting tumour growth, retinal disorders,
 CC sports-related joint problems, articular cartilage defects,
 CC osteoarthritis or rheumatoid arthritis, wound healing and hearing loss in
 CC mammals. The present sequence is a PCR primer used to isolate nucleic
 CC acid encoding a PRO protein.

XX
 SQ Sequence 24 BP; 6 A; 10 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.2; DB 1; Length 24;
 Best Local Similarity 87.0%; Pred. No. 7.2e+02;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2551 CTGACGTACCACTGTGCCACAC 2573
 Db 2 CTGACCTTCACCTGAGCCACAC 24

RESULT 884
 ADE48547
 ADE48547 standard; DNA; 24 BP.

AC ADE48547;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human PRO 860 PCR primer #2.

KW Human; ss; PCR; secreted protein; transmembrane protein; PRO; cytosstatic;
 KW ophthalmological; antiarthritic; osteopathic; antirheumatic; vulnery;
 KW auditory; tumour growth; retinal disorder; sports-related joint problem;
 KW articular cartilage defects; osteoarthritis; rheumatoid arthritis;
 KW wound healing; hearing loss; primer.

XX

OS Homo sapiens.
 XX US2003104536-A1.
 PN
 XX 05-JUN-2003.
 PD
 XX
 PF 19-OCT-2001; 2001US-00166709.
 XX
 XX 07-OCT-1998; 98MO-US021141.
 PR 20-NOV-1998; 98MO-US024855.
 PR 05-JAN-1999; 99MO-US000106.
 PR 08-MAR-1999; 99MO-US005028.
 PR 10-MAR-1999; 99MO-US005190.
 PR 14-MAY-1999; 99MO-US010733.
 PR 02-JUN-1999; 99MO-US012252.
 PR 02-NOV-1999; 99MO-US028313.
 PR 02-DEC-1999; 99MO-US028551.
 PR 02-DEC-1999; 99MO-US028565.
 PR 16-DEC-1999; 99MO-US030095.
 PR 30-DEC-1999; 99MO-US031243.
 PR 30-DEC-1999; 99MO-US031274.
 PR 05-JAN-2000; 2000MO-US000219.
 PR 06-JAN-2000; 2000MO-US000277.
 PR 11-FEB-2000; 2000MO-US003565.
 PR 18-FEB-2000; 2000MO-US004341.
 PR 24-FEB-2000; 2000MO-US005004.
 PR 02-MAR-2000; 2000MO-US005841.
 PR 10-MAR-2000; 2000MO-US006319.
 PR 21-MAR-2000; 2000MO-US007532.
 PR 30-MAR-2000; 2000MO-US008439.
 PR 17-MAY-2000; 2000MO-US013705.
 PR 22-MAY-2000; 2000MO-US014042.
 PR 30-MAY-2000; 2000MO-US014941.
 PR 02-JUN-2000; 2000MO-US015264.
 PR 28-JUL-2000; 2000MO-US020710.
 PR 24-AUG-2000; 2000MO-US023328.
 PR 01-DEC-2000; 2000MO-US032878.
 PR 20-DEC-2000; 2000MO-US034956.
 PR 28-FEB-2001; 2001MO-US006520.
 PR 22-MAR-2001; 2001MO-US009552.
 PR 25-MAY-2001; 2001MO-US017092.
 PR 01-JUN-2001; 2001MO-US017800.
 PR 20-JUN-2001; 2001MO-US019692.
 PR 29-JUN-2001; 2001MO-US021066.
 PR 09-JUL-2001; 2001MO-US021735.
 PR 30-JUL-2001; 2001US-00918585.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Geber H, Gertlisen ME,
 PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,
 PI Kijavita TJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL,
 PI Stewart TA, Tumas D, Williams PM, Wood WI,
 XX
 DR MPI; 2004-008994/01.
 XX
 XX New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO4993 or
 PT PRO337, useful in molecular biology, chromosome and gene mapping, in
 PT generating antisense RNA and DNA, and in gene therapy.
 XX
 XX Example 34; SEQ ID NO 213; 460bp; English.
 XX
 CC The invention relates to an isolated PRO polypeptide (secreted or
 CC transmembrane protein) having at least 80% amino acid sequence identity
 CC to an amino acid sequence chosen from 94 fully defined sequences as given
 CC in the specification (including PRO lacking its associated signal
 CC peptide, a PRO extracellular domain with or without its associated signal
 CC peptide). Also included are nucleic acids encoding the PRO proteins
 CC mentioned above, a vector comprising a PRO nucleic acid, a host cell
 CC comprising the vector and producing PRO, a chimeric molecule comprising
 CC PRO fused to a heterologous amino acid sequence, and an anti-PRO

CC antibody. PRO337 polypeptide is useful for detecting a PRO4993
 CC polypeptide in a sample suspected of containing PRO4993 polypeptide.
 CC Similarly, PRO4993 polypeptide is useful for detecting PRO337
 CC polypeptide. PRO725, PRO700 or PRO739 polypeptide is useful for detecting
 CC PRO1559 polypeptide, and PRO1559 polypeptide is useful for detecting
 CC PRO725, PRO700 or PRO739. PRO4993 polypeptide is useful for linking a
 CC bioactive molecule to a cell expressing PRO337 polypeptide. The bioactive
 CC molecule is the toxin, radiolabel, or an antibody. The bioactive molecule
 CC causes death of the cell. PRO337 polypeptide is useful for linking a
 CC bioactive molecule to a cell expressing PRO4993 polypeptide; PRO725,
 CC PRO700 or PRO739 polypeptide are useful for linking a bioactive molecule
 CC to a cell expressing PRO1559 polypeptide; and PRO1559 polypeptide is
 CC useful for linking a bioactive molecule to a cell expressing PRO725,
 CC PRO700 or PRO739 polypeptide. PRO4993 polypeptide or anti-PRO337
 CC polypeptide is useful for modulating at least one biological activity of
 CC the cell expressing PRO337 polypeptide, where the cell is killed. PRO337
 CC polypeptide or anti-PRO4993 polypeptide is useful for modulating the
 CC biological activity of the cell expressing PRO4993 polypeptide; PRO725,
 CC PRO700 or PRO739 polypeptide or an anti-PRO1559 polypeptide is useful for
 CC modulating the biological activity of the cell expressing PRO1559
 CC polypeptide; and PRO1559 polypeptide or anti-PRO725, anti-PRO700 or anti-
 CC PRO739 polypeptide is useful for modulating the biological activity of
 CC the cell expressing PRO725, PRO700 or PRO739 polypeptide. The
 CC polypeptides are useful for inhibiting tumour growth, retinal disorders,
 CC sports-related joint problems, articular cartilage defects,
 CC osteoarthritis or rheumatoid arthritis, wound healing and hearing loss in
 CC mammals. The present sequence is a PCR primer used to isolate nucleic
 CC acid encoding a PRO protein.
 XX
 XX Sequence 24 BP; 6 A; 10 C; 4 G; 4 T; 0 U; 0 Other;
 XX
 QY
 Db 2551 CTGACGTACACGCTGCGCACAC 2573
 2 CTGACCTTCACAGCTGACGCACAC 24
 RESULT 885
 ADE89648
 ID ADE89648 standard; DNA; 24 BP.
 AC ADE89648;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DB Human PRO 860 PCR primer #2.
 XX
 XX Human; ss; PCR; secreted protein; transmembrane protein; PRO; cytosstatic;
 KW ophthalmological; antiarthritic; osteopathic; antirheumatic; vulnery;
 KW auditory; tumour growth; retinal disorder; sports-related joint problem;
 KW articular cartilage defects; osteoarthritis; rheumatoid arthritis;
 KW wound healing; hearing loss; primer.
 XX
 OS Homo sapiens.
 XX
 PN US2003130181-A1.
 XX
 PD 10-JUL-2003.
 XX
 PF 16-OCT-2001; 2001US-00978375.
 XX
 XX 17-OCT-1997; 97US-0062250P.
 PR 03-NOV-1997; 97US-0064249P.
 PR 13-NOV-1997; 97US-0065311P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 10-MAR-1998; 98US-0077450P.
 PR 11-MAR-1998; 98US-0077632P.
 PR 11-MAR-1998; 98US-0077641P.
 PR 11-MAR-1998; 98US-0077649P.
 PR 12-MAR-1998; 98US-0077791P.

PR 13-MAR-1998; 98US-0078004P.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078933P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 30-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 31-MAR-1998; 98US-0079923P.
PR 31-MAR-1998; 98US-0080105P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080165P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080328P.
PR 01-APR-1998; 98US-0080333P.
PR 01-APR-1998; 98US-0080334P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 08-APR-1998; 98US-0081071P.
PR 09-APR-1998; 98US-0081195P.
PR 09-APR-1998; 98US-0081203P.
PR 09-APR-1998; 98US-0081229P.
PR 15-APR-1998; 98US-0081817P.
PR 15-APR-1998; 98US-0081819P.
PR 15-APR-1998; 98US-0081838P.
PR 15-APR-1998; 98US-0081952P.
PR 15-APR-1998; 98US-0081955P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082700P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
PR 23-APR-1998; 98US-0082804P.
PR 27-APR-1998; 98US-0083361P.
PR 28-APR-1998; 98US-0083322P.
PR 29-APR-1998; 98US-0083392P.
PR 29-APR-1998; 98US-0083495P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-0083500P.
PR 29-APR-1998; 98US-0083545P.
PR 29-APR-1998; 98US-0083549P.
PR 29-APR-1998; 98US-0083558P.
PR 29-APR-1998; 98US-0083559P.
PR 30-APR-1998; 98US-0083742P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 06-MAY-1998; 98US-0084411P.
PR 07-MAY-1998; 98US-0084598P.
PR 07-MAY-1998; 98US-0084600P.
PR 07-MAY-1998; 98US-0084627P.
PR 07-MAY-1998; 98US-0084637P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 13-MAY-1998; 98US-0085338P.
PR 13-MAY-1998; 98US-0085339P.
PR 15-MAY-1998; 98US-0085573P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085689P.
PR 15-MAY-1998; 98US-0085697P.
PR 15-MAY-1998; 98US-0085700P.
PR 15-MAY-1998; 98US-0085704P.

PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.
PR 22-MAY-1998; 98US-0086414P.
PR 22-MAY-1998; 98US-0086430P.
PR 22-MAY-1998; 98US-0086486P.
PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087106P.
PR 28-MAY-1998; 98US-0087208P.
PR 26-JUN-1998; 98US-0090863P.
PR 26-JUN-1998; 98US-0091010P.
PR 01-JUL-1998; 98US-0091359P.
PR 30-JUL-1998; 98US-0094651P.
PR 11-SEP-1998; 98US-0100038P.
PR 07-OCT-1998; 98WO-US021141.
PR 20-NOV-1998; 98US-0109304P.
PR 20-NOV-1998; 98WO-US024855.
PR 22-DEC-1998; 98US-0113296P.
PR 23-DEC-1998; 98US-0113621P.
PR 05-JAN-1999; 98WO-US000106.
PR 08-MAR-1999; 98WO-US005028.
PR 10-MAR-1999; 98WO-US005150.
PR 12-MAR-1999; 98US-0123957P.
PR 29-MAR-1999; 98US-0126773P.
PR 21-APR-1999; 98US-0130232P.
PR 26-APR-1999; 98US-0131022P.
PR 28-APR-1999; 98US-0131445P.
PR 14-MAY-1999; 98US-0134287P.
PR 14-MAY-1999; 98WO-US010733.
PR 02-JUN-1999; 98WO-US012252.
PR 16-JUN-1999; 98US-0139557P.
PR 23-JUN-1999; 98US-0141037P.
PR 07-JUL-1999; 98US-0144680P.
PR 26-JUL-1999; 98US-0145698P.
PR 28-JUL-1999; 98US-0146222P.
PR 29-OCT-1999; 98US-0162506P.
PR 30-NOV-1999; 98WO-US028213.
PR 02-DEC-1999; 98WO-US028551.
PR 02-DEC-1999; 98WO-US028565.
PR 16-DEC-1999; 98WO-US030095.
PR 30-DEC-1999; 98WO-US031243.
PR 30-DEC-1999; 98WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US043956.
PR 28-FEB-2001; 2001WO-US006520.
PR 22-MAR-2001; 2001WO-US009552.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
XX
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.

PA (PERR/) FERRARA N.
 PA (PIV/) PIIVAROFF E.
 PA (FONG/) FONG S.
 PA (GAOW/) GAO W.
 PA (GERB/) GERBER H.
 PA (GERR/) GERRITSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOUSKI P J.
 PA (GIRM/) GIRMALDI J C.
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLAN K J.
 PA (KLJA/) KLJAVIN I J.
 PA (KUOS/) KUO S S.
 PA (NAPI/) NAPIER M A.
 PA (PANJ/) PAN J.
 PA (PAON/) PAONI N F.
 PA (ROYM/) ROY M A.
 PA (SHEL/) SHELTON D L.
 PA (STEW/) STEWART T A.
 PA (TUMA/) TUMAS D.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 XX

Query Match 0.2%; Score 18.2; DB 1; Length 24;
 Best Local Similarity 87.0%; Pred. No. 7.2e+02;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2551 CTGACGTACCACTGTGCACAC 2573
 |||||
 2 CTGACCTTCACGCTGAGCCAC 24

RESULT 886

AAQ55856
 ID AAQ55856 standard; DNA; 25 BP.

AC AAQ55856;

DT 25-MAR-2003 (revised)
 DT 25-JUL-1994 (first entry)

XX Fragile X probe.

XX FC; foetal cells; marker; probe; hybridise; denature; dye; label;
 XX KW fluorescent; kit; detection; haemoglobin; rhesus; gamma globulin; NR;
 XX KM nitrogen reductase; ss.
 XX OS Homo sapiens.

XX WO9402646-A1.

XX 03-FEB-1994.

XX PF 19-JUL-1993; 93WO-US006628.

XX PR 17-JUL-1992; 92US-00915965.

XX PA (RERE-) RES DEV FOUND.

XX PI Aagari M, Praahad N, Cubbage ML, Ju S, Blick M, Bresser J;

XX DR WPI; 1994-048903/06.

XX PT Identifying foetal cells, conc. from maternal blood, using specific
 XX marker - e.g. surface antigen, before in situ hybridisation of target
 XX nucleic acid to detect viral infection, genetic abnormality, etc.

XX PS Disclosure; Page 73; 109pp; English.

XX Probes (AAQ55857-873) detect regions of 3 fragments of the HUMGLBN gene
 CC (AAQ64058). Bases 1-91 correspond to bases 2179-2269 of HUMGLBN, bases 92
 CC -314 are from 2393-2615 of HUMGLBN and bases 315-443 are from 3502-3630

CC OF HUMGLBN. The probes (AAQ55854-55) were used as control, positive and
 CC negative genetic testing probes. Probe (AAQ55856) was used to detect the
 CC fragile X condition (Example 14) (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX

SO Sequence 25 BP; 0 A; 9 C; 16 G; 0 T; 0 U; 0 Other;
 Query Match 0.2%; Score 18.2; DB 1; Length 25;
 Best Local Similarity 87.0%; Pred. No. 7.6e+02;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 60 CCGAGGCTGCGGCGCGCGCG 82
 |||||
 DB 1 CCGCGCGCGCGCGCGCGCG 23

RESULT 887

AAQ85271
 ID AAQ85271 standard; DNA; 25 BP.

AC AAQ85271;

DT 25-MAR-2003 (revised)
 DT 24-AUG-1995 (first entry)

XX Probe for Fragile X condition.

XX Prenatal diagnosis; fragile X; probe; ss.

XX OS Synthetic.

XX PN WO9503431-A1.

XX PD 02-FEB-1995.

XX PF 19-JUL-1994; 94WO-US008342.

XX PR 19-JUL-1993; 93US-00094710.

XX PA (APRO-) APROGENEX INC.

XX PI Bresser J, Weber WD, Ryusaki T, Praahad N, Cubbage ML, Blick M;
 XX Aagari M, Poindexter BJ;

XX DR WPI; 1995-075255/10.

XX PT Identifying foetal cells in samples contg. maternal cells - used for
 XX PT monitoring foetus status, identifying sex or detecting genetic
 XX PT abnormalities or viral infection.

XX PS Example; Page 75; 115pp; English.

XX CC In the example, Fragile X Chromosome is identified in amniocytes and in
 XX CC peripheral blood mononuclear cells. The 5' aminohexyl oligos is coupled
 XX CC to the fluorescent dye fluorescein. When an amplification of the CCG DNA
 XX CC fragment (of the X chromosome in Xq27.3) is present, there is an increase
 XX CC in the intensity of the signal. (Updated on 25-MAR-2003 to correct PN
 XX CC field.) (Updated on 25-MAR-2003 to correct PI field.)

XX SO Sequence 25 BP; 0 A; 9 C; 16 G; 0 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.2; DB 1; Length 25;
 Best Local Similarity 87.0%; Pred. No. 7.6e+02;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 60 CCGAGGCTGCGGCGCGCGCG 82
 |||||
 DB 1 CCGCGCGCGCGCGCGCGCG 23

RESULT 888

AAQ5267
 ID AAX05267 standard; DNA; 25 BP.

XX AAX05267;
AC
XX
DT 14-APR-1999 (first entry)
XX
DE Fragile X chromosome detecting probe.
XX
XX Genetic testing; foetal cell; maternal; blood; pregnant; hybridisation;
KM detection; HIV, hepatitis virus; herpes virus; chromosomal abnormality;
KW probe; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX US958649-A.
PN
XX
PD 12-JAN-1999.
XX
XX 31-DEC-1996; 96US-00775609.
PF
XX
PR 17-JUL-1992; 92US-00915765.
PR 19-JUL-1993; 93US-00094710.
PR 19-JUL-1994; 94WO-US008342.
PR 17-JAN-1995; 95US-00374144.
XX
XX (APRO-) APROGENEX INC.
PA
XX
XX Black M, Cubbage ML, Bresser J, Prashad N, Asgari M,
PI
XX
XX WPI; 1999-152096/13.
XX
XX
XX Method for distinguishing foetal cells from adult cells in blood - based
PT on amplification and detection of mRNA selectively expressed in foetal
PT cells.
PS
XX
XX Example 4, 14; Col 49; 49pp; English.

XX The invention relates to a method of enriching foetal cells from maternal
XX blood and for identifying such foetal cells. Foetal cells can be
CC distinguished from adult cells in a blood specimen by (a) treating a
CC blood specimen from a pregnant female to yield a mixture of cells
CC comprising foetal cells and adult cells; (b) amplifying one or more mRNAs
CC within the cells, the mRNAs being selectively expressed in target foetal
CC cells to be distinguished but not expressed in adult blood cells; (c)
CC performing in situ hybridisation on the cells under hybridising
CC conditions suitable to maintain cell membranes in a substantially intact
CC state and with a hybridisation medium comprising a detectably labelled
CC probe complementary to the amplified mRNA that is selectively expressed
CC in the target foetal cells but not expressed in adult blood cells; (d)
CC removing the hybridisation medium and unhybridised probe from the mixture
CC of cells to yield hybridised cells; and (e) detecting the labelled probe
CC remaining in the hybridised cells; whereby cells in which the labelled
CC probe is detected are identified as the target foetal cells; A second
CC method for determining the presence of a target nucleotide sequence in
CC individual foetal cells present in a cellular specimen is also provided.
CC The methods (especially the second) is useful for detecting HIV,
CC hepatitis viruses or herpes viruses in foetal cells, or for detecting
CC chromosomal abnormalities in foetal cells. The present sequence
CC represents a probe used for the detection of the Fragile X chromosome in
XX amniocytes and in peripheral blood mononuclear cells
XX
SQ Sequence 25 BP; 0 A; 9 C; 16 G; 0 T; 0 U; 0 Other;

Query Match 0.2%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 7.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0

60 CGAGAGCTCGGGGGCGCGCGCG 82
Gy |||||
db 1 CGGCGCGCGCGCGCGCGCGCG 23

RESULT 889

[illegible]


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PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
XX 26-APR-1999; 99EP-00303215.
XX
PA (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
XX Ulendahl P, Wong K;
XX
XX WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
XX
PS Claim 14; Page 52; 66pp; English.
XX
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16S rRNA genes in
CC particular
XX
XX Sequence 25 BP; 5 A; 3 C; 3 G; 14 T; 0 U; 0 Other;
SQ
OY 4472 TTTT TTTT TTTT TTTT GCTT GACACA 4494
DB 1 TTTT TTTT TTTT TTTT GTAT GCA GACA 23
RESULT 891
AAC96419
ID AAC96419 standard; DNA; 25 BP.
AC AAC96419;
DT 26-FEB-2001 (first entry)
XX
DE HLA DQA1 gene PCR primer #21.
XX
XX DNA sequence analysis; sequencing; protein sequence; protein structure;
XX gene typing; organ donation; bacteria identification; 16S rRNA; HLA;
XX human leukocyte antigen; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200065088-A2.
XX
XX 02-NOV-2000.
XX
XX 20-APR-2000; 2000WO-EP003636.
XX
XX 26-APR-1999; 99EP-00303215.
XX
XX (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
XX Ulendahl P, Wong K;
XX
XX WPI; 2000-679677/66.
XX
XX Identifying extendible primers for use in identification, or
XX classification of a nucleic acid of an organism, allele or gene such as
XX class 1/2 HLA comprises identifying all possible nucleotide sequences of
XX specific length.
XX

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PS Claim 14; Page 51; 66pp; English.
XX The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 3 A; 2 C; 2 G; 18 T; 0 U; 0 Other;

Query March 0.2%; Score 18.2; DB 1; Length 25;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4468 TTTTGTGCTTGA 4490
Db TTTTGTGCTTGA 23
1 TTTTGTGCTTGA 23

RESULT 892
AAC95754
ID AAC95754 standard; DNA; 25 BP.
XX
AC AAC95754;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA DQB1 gene PCR primer #25.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO20065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
XX
PS Claim 14; Page 39; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 5 A; 3 C; 3 G; 14 T; 0 U; 0 Other;

Query March 0.2%; Score 18.2; DB 1; Length 25;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4472 TTTTGTGCTTGA 4494

```

Db 1 TTTT TTTT TTTT GATGACAGACA 23

RESULT 893

ABN13915

AC ABN13915;

DT 29-MAY-2002 (first entry)

DE Human GDMLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:13907.

KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;

KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;

KW skeletal muscle disorder; amplicon; screening; ss.

OS Homo sapiens.

PN WO200192524-A2.

PD 06-DEC-2001.

PF 25-MAY-2001; 2001WO-US016981.

XX 26-MAY-2000; 2000US-0207456P.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX 30-JAN-2001; 2001WO-US000661.

XX 30-JAN-2001; 2001WO-US000662.

XX 30-JAN-2001; 2001WO-US000663.

XX 30-JAN-2001; 2001WO-US000664.

XX 30-JAN-2001; 2001WO-US000665.

XX 30-JAN-2001; 2001WO-US000666.

XX 30-JAN-2001; 2001WO-US000667.

XX 30-JAN-2001; 2001WO-US000668.

XX 30-JAN-2001; 2001WO-US000669.

XX 30-JAN-2001; 2001WO-US000670.

XX 05-FEB-2001; 2001US-0266860P.

XX (AEOM-) AECOMICA INC.

PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;

XX MPI; 2002-179446/23.

PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,

PT or as specific biomolecule capture probes for surface-enhanced laser

PT desorption ionization, comprises human myosin-like protein hGDMLP-1.

XX Disclosure; SEQ ID NO 13907; 214pp; English.

XX The present invention describes a human genome-derived myosin-like

XX protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-

XX 1 can be used in gene therapy and vaccine production. The hGDMLP-1

CC The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequence

CC SQ Sequence 25 BP; 5 A; 5 C; 12 G; 3 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 18.2; DB 1; Length 25;

XX Best Local Similarity 87.0%; Pred. No. 7.6e+02;

XX Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5542 GGTCGTCATGACATGAGAG 5564

DB 3 GGCGTCATGAGCTGAGAG 25

AC ABN13918;

DT 29-MAY-2002 (first entry)

DE Human GDMLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:13910.

KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;

KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;

KW skeletal muscle disorder; amplicon; screening; ss.

OS Homo sapiens.

PN WO200192524-A2.

PD 06-DEC-2001.

PF 25-MAY-2001; 2001WO-US016981.

XX 26-MAY-2000; 2000US-0207456P.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX 30-JAN-2001; 2001WO-US000661.

XX 30-JAN-2001; 2001WO-US000662.

XX 30-JAN-2001; 2001WO-US000663.

XX 30-JAN-2001; 2001WO-US000664.

XX 30-JAN-2001; 2001WO-US000665.

XX 30-JAN-2001; 2001WO-US000666.

XX 30-JAN-2001; 2001WO-US000667.

XX 30-JAN-2001; 2001WO-US000668.

XX 30-JAN-2001; 2001WO-US000669.

XX 30-JAN-2001; 2001WO-US000670.

XX 05-FEB-2001; 2001US-0266860P.

XX (AEOM-) AECOMICA INC.

PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;

XX MPI; 2002-179446/23.

PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,

PT or as specific biomolecule capture probes for surface-enhanced laser

PT desorption ionization, comprises human myosin-like protein hGDMLP-1.

XX Disclosure; SEQ ID NO 13910; 214pp; English.

XX The present invention describes a human genome-derived myosin-like

XX protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-

XX 1 can be used in gene therapy and vaccine production. The hGDMLP-1

XX nucleic acids can be used as probes to detect, characterise and quantify

XX hGDMLP-1 nucleic acids in samples, as amplification substrates, to

XX provide initial substrates for the recombinant engineering of hGDMLP-1

XX expressing the proteins. The hGDMLP-1 proteins or polypeptides may be

QY 5807 CCTGTCGCTATGATGATGAATC 5833
||:|||||
DB 1 CCKGTSTACCATATGAAGTGAAGC 27

RESULT 897
AAZ60441
AAZ60441 standard; DNA; 27 BP.

AC AAZ60441;
XX
XX
XX 15-SEP-2003 (revised)
DT 05-MAY-2000 (first entry)
XX

DE Tail PCR primer C used to amplify Adenovirus fiber protein DNA.
XX
XX Chimeric adenovirus; gene therapy; antigenicity; fiber protein;
KW serotype; penton protein; hexon protein; PCR primer; ss.
XX
XX unidentified adenovirus.
OS
XX WO200003029-A2.
PN
XX 20-JAN-2000.
PD
XX 08-JUL-1999; 99WO-NL000436.
PF
XX 08-JUL-1998; 98EP-00202297.
PR
XX (INTR-) INTROGENE BV.
PA
XX Havenga M, Vogels R, Bout A;
PI
XX WPI; 2000-171149/15.
DR
XX
XX New chimeric adenoviruses containing a genome derived from different
PT adenovirus serotypes, useful in gene therapy.
PR
XX
XX Example 2; Page 69; 92pp; English.

CC PCR primers AAZ60439-51 were used amplify DNA encoding the fiber proteins
CC of Adenovirus serotypes 4, 8, 9, 12, 16, 19P, 28, 32, 36, 37, 40-1, 40-2,
CC 41-8, 41-1, 49, 50 and 51. The amplified sequence is used in the course
CC of the invention to construct chimeric adenoviruses with reduced
CC antigenicity. The chimeric adenoviruses comprises at least part of a
CC fiber protein of an adenovirus serotype providing the chimeric virus
CC with a desired host range and at least part of a penton or hexon protein
CC from another, less antigenic, serotype. The chimeric adenoviruses are
CC useful for gene therapy, especially where repeated delivery is required.
CC Adenoviruses of the invention are useful can be constructed to have a
CC desired host range and a diminished capability to raise neutralizing
CC antibodies, an absence of, or decreased infection of, antigen presenting
CC cells of the immune system (e.g. macrophages), and an ability to escape
CC trapping in the liver through increased target cell specificity. (Updated
CC on 15-SEP-2003 to standardise OS field)
XX
XX
SQ Sequence 27 BP; 9 A; 6 C; 5 G; 5 T; 0 U; 2 Other;

Query Match 0.2%; Score 18.2; DB 1; Length 27;
Best Local Similarity 74.1%; Pred. No. 8.4e+02;
Matches 20; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 5807 CCTGTCGCTATGATGATGAATC 5833
||:|||||
DB 1 CCKGTSTACCATATGAAGTGAAGC 27

RESULT 898
AAF55980
ID AAF55980 standard; DNA; 27 BP.
XX
XX AAF55980;

XX 06-AUG-2003 (revised)
DT 12-APR-2001 (first entry)
XX
XX
XX Adenovirus 16 tail oligonucleotide.
DE
XX
XX Adenoviral vector; gene delivery; gene therapy; CAR-negative cell;
KW Coxsacki adenovirus receptor; fibre protein; PCR primer; ss.
XX
XX Human adenovirus type 16.
OS
XX EPI067188-A1.
PN
XX 10-JAN-2001.
PD
XX 08-JUL-1999; 99EP-00202234.
PF
XX 08-JUL-1999; 99EP-00202234.
PR
XX 08-JUL-1999; 99EP-00202234.
PA
XX (INTR-) INTROGENE BV.
PA
XX Havenga M, Vogels R;
PI
XX WPI; 2001-149351/16.
DR
XX
XX Delivering nucleic acids to host cells, useful in gene therapy, comprises
PT a chimeric adenovirus that associates with a binding site present on
PT Coxsacki adenovirus receptor negative cells.
PS
XX Example 2; Page 27; 95pp; English.

XX The present invention describes a method of delivering a nucleic acid to
CC a cell using a gene delivery vehicle based on adenovirus serotype 5. The
CC vehicle is able to bind to receptors present on cells not expressing the
CC Coxsacki adenovirus receptor (CAR) due to an altered fibre protein. The
CC method is useful in gene therapy, as the vector is able to bind to cells
CC normally resistant to adenovirus 2 and 5, including endothelial, smooth
CC muscle, dendritic, neuronal, glial, synaptic, haematopoietic and
CC macrophage cells and primary fibroblasts. (Updated on 06-AUG-2003 to
CC correct OS field.)
XX
XX
SQ Sequence 27 BP; 9 A; 6 C; 5 G; 5 T; 0 U; 2 Other;

Query Match 0.2%; Score 18.2; DB 1; Length 27;
Best Local Similarity 74.1%; Pred. No. 8.4e+02;
Matches 20; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 5807 CCTGTCGCTATGATGATGAATC 5833
||:|||||
DB 1 CCKGTSTACCATATGAAGTGAAGC 27

RESULT 899
AAF25305
ID AAF25305 standard; DNA; 27 BP.
XX
XX AAF25305;
AC
XX
XX 30-APR-2001 (first entry)
DT
XX
XX PCR primer used to amplify DNA encoding an Adenovirus fiber protein.
DE
XX Nucleic acid delivery; gene delivery vehicle; adenoviral vector;
KW Coxsacki adenovirus receptor; CAR; CAR-negative cell; PCR primer; ss.
XX
XX Mascadenovirus.
OS
XX WO200104334-A2.
PN
XX 18-JAN-2001.
PD
XX 07-JUL-2000; 2000WO-NL000481.
PF
XX

```

PR 07-JUL-1999; 99US-0142557P.
PR 08-JUL-1999; 99EP-00202234.
PA (INTR-) INTROGENE BV.
PI Havenga M, Vogels R;
XX WPI; 2001-103087/11.
DR
XX
XX PT New gene delivery vehicle, useful for delivering a nucleic acid to
XX PT Coxsacki adenovirus receptor negative cells, comprises adenoviral
XX PT subgroup D and/or F receptors present on these cells.
XX
XX PS Example 2; Page 57; 83pp; English.
XX
XX CC The specification describes a method for delivering a nucleic acid of
XX CC interest to a host cell. The method uses a gene delivery vehicle based on
XX CC adenoviral material, which delivers the nucleic acid of interest to the
XX CC host cell by associating with a binding site and/or receptor for
XX CC adenoviral subgroups D and/or F present on Coxsacki adenovirus receptor
XX CC (CAR)-negative cells. The gene delivery vehicle is useful for delivering
XX CC a nucleic acid of interest to a CAR negative cell. It is also useful as a
XX CC pharmaceutical. PCR primers AAF25303-15 were used to amplify DNA encoding
XX CC fiber proteins from different human adenovirus serotypes. The amplified
XX CC fragments were used to construct recombinant adenoviruses for use in the
XX CC method of the invention
XX
XX SQ Sequence 27 BP; 9 A; 6 C; 5 G; 5 T; 0 U; 2 Other;
XX
XX Query Match 0.2%; Score 18.2; DB 1; Length 27;
XX Best Local Similarity 74.1%; Pred. No. 8.4e+02;
XX Matches 20; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
XX
QY 5807 CCTGCTGCTATGATGATGAATC 5833
DB 1 CCKGTSTACCATATGAAGATGAAGC 27
XX
RESULT 900
AAD36010
ID AAD36010 standard; DNA; 27 BP.
XX
AC AAD36010;
XX
DT 09-AUG-2002 (first entry)
XX
DE Adenovirus serotype 5 fibre protein DNA amplifying PCR primer C.
XX
XX KM Gene delivery vehicle; stem cell; adenovirus; fibre protein; antineoplastic;
XX KM Hurlers disease; Hunters disease; Sanfilippo disease; Morquio's disease;
XX KM Niemann-Pick disease; Gaucher's disease; Fabry's disease; I-cell disease;
XX KM metachromatic leucodystrophy; Krabbe's disease; erythropoietic porphyria;
XX KM fucosidase deficiency; severe immunodeficiency syndrome; immunostimulant;
XX KM thalassemia; Jak-3 deficiency; acquired immunodeficiency syndrome; AIDS;
XX KM autoimmune disease; cardiovascular; immunosuppressive; cancer; metabolic;
XX KM cytostatic; gene therapy; PCR; primer; ss.
XX
XX OS Mastadenovirus.
XX
XX PN MO200229073-A2.
XX
XX PD 11-APR-2002.
XX
XX PF 04-OCT-2001; 2001WO-NL000731.
XX
XX PR 06-OCT-2000; 2000EP-00203471.
XX PR 06-OCT-2000; 2000US-0238830P.
XX
XX PA (CRUC-) CRUCCELL HOLLAND BV.
XX
XX PI Havenga MJE, Bout A;
XX
XX WPI; 2002-394351/42.
DR

```

```

XX
XX PT Gene delivery vehicle useful for treating, e.g., cancer and Gauchers
XX PT disease, comprises an adenovirus having tropism for stem cells provided
XX PT by nucleic acid encoding fiber protein of adenovirus B serotype and a
XX PT proteinaceous substance.
XX
XX PS Example 2; Page 46; 58pp; English.
XX
XX CC The invention relates to a gene delivery vehicle for delivering nucleic
XX CC acid to stem cells, comprises an adenovirus having tropism for stem
XX CC cells, provided by nucleic acid encoding fiber protein of adenovirus B
XX CC serotype or functional equivalent and/or homologue and a proteinaceous
XX CC substance. The gene delivery vehicle (preferably comprising a deletion in
XX CC the E1, E3, E2 or B4 regions) is used as a vehicle for delivering a
XX CC nucleic acid to stem cells. Providing an individual with a stem cell
XX CC transduced with the gene delivery vehicle is useful for the treatment of
XX CC Hurlers disease, Hunters disease, Sanfilippo disease, Niemann-Pick
XX CC disease, Morquio's disease, Gaucher's disease, Fabry's disease, Krabbe's
XX CC disease, metachromatic leucodystrophy, severe immunodeficiency syndrome,
XX CC I-cell disease, Jak-3 deficiency, fucosidase deficiency, thalassemia,
XX CC erythropoietic porphyria, AIDS, cancer and autoimmune disease. The
XX CC invention is used in gene therapy. The present sequence is a PCR primer
XX CC used in the amplification of adenovirus serotype 5 fibre protein DNA
XX
XX SQ Sequence 27 BP; 9 A; 6 C; 5 G; 5 T; 0 U; 2 Other;
XX
XX Query Match 0.2%; Score 18.2; DB 1; Length 27;
XX Best Local Similarity 74.1%; Pred. No. 8.4e+02;
XX Matches 20; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
XX
QY 5807 CCTGCTGCTATGATGATGAATC 5833
DB 1 CCKGTSTACCATATGAAGATGAAGC 27
XX
RESULT 901
ABK48880
ID ABK48880 standard; DNA; 27 BP.
XX
AC ABK48880;
XX
DT 07-AUG-2003 (revised)
XX
DT 15-JUL-2002 (first entry)
XX
DE PCR primer #3 for DNA encoding human adenovirus fibre protein.
XX
XX KM Viral vector; expressible non-viral nucleic acid; viral coat;
XX KM adenoviral vector; cell transduction; T-lymphocyte; B-cell; mast cell;
XX KM gene therapy; cytotoxic T-lymphocyte response; CTL; transgene expression;
XX KM human adenovirus fibre protein; PCR; primer; ss.
XX
XX OS Synthetic.
XX
XX PN WO200224933-A2.
XX
XX PD 28-MAR-2002.
XX
XX PF 25-SEP-2001; 2001WO-EP011086.
XX
XX PR 25-SEP-2000; 2000EP-00203375.
XX PR 11-MAY-2001; 2001US-0290403P.
XX
XX PA (GALA-) GALAPAGOS GENOMICS NV.
XX PA (CRUC-) CRUCCELL HOLLAND BV.
XX
XX PI Van Es HHG, Van Zutphen M, Ma L, Havenga MJE;
XX
XX WPI; 2002-383193/41.
XX
XX PT Introducing non-viral nucleic acid into a cell having a common non-
XX PT universal binding receptor, comprises contacting the cell with a viral
XX PT vector having coat proteins with an adenoviral sequence from serotype 35

```

PT or 51 fibre protein.

XX Example 1; Page 59; 121pp; English.

PS The present invention relates to a method of introducing an expressible
XX non-viral nucleic acid into a cell having a common non-universal binding
CC receptor. The method involves contacting the cell with a viral vector
CC containing a nucleic acid comprising the expressible non-viral nucleic
CC acid, and a modified viral coat consisting of native viral coat proteins
CC and a modified coat protein which contains an adenoviral amino acid
CC sequence from adenoviral serotype 35 or 51 fibre protein. The method is
CC useful for transducing a cell, where the a non-adenovirus nucleic acid
CC is a cDNA, where the cells are arranged in an array of subpopulations of
CC cells, and the viral vector is replication incompetent in the cell. The
CC method is also useful for ex vivo transduction of a population of cells
CC obtained from a mammal, and for administering to a human or other
CC mammalian animal subject a population of cells genetically modified ex
CC vivo with an expressible recombinant nucleic acid, where the cells
CC consist essentially of T-lymphocytes, B-cells or mast cells. The viral
CC vector is useful for preparation of a medicament for introducing an
CC expressible non-viral nucleic acid into a selected cell, in an animal for
CC the purpose of gene therapy. Unlike prior art adenoviral vectors, the
CC vectors have improved infection of a specific target cell, reduced
CC infection of non-target cells, improved stability of the virus, reduced
CC toxicity to target cells, reduced neutralisation in humans or animals,
CC reduced or increased cytotoxic T-lymphocyte (CTL) response in humans or
CC animals, better and/or prolonged transgene expression, increased
CC penetration capacity in tissues, and improved yields in packaging cell
CC lines. ABK8878-ABK4890 represent PCR primers used to amplify DNA
CC encoding fibre proteins from different human adenovirus serotypes.
CC (Updated on 07-AUG-2003 to correct OS field.)
XX SQ Sequence 27 BP; 9 A; 6 C; 5 G; 5 T; 0 U; 2 Other;

Query Match 0.2%; Score 18.2; DB 1; Length 27;
Best Local Similarity 74.1%; Pred. No. 8.4e+02;
Matches 20; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 5807 CCTGCTCGCTATGATGATGAATC 5833
DB 1 CCKGTSTACCATATGAGATGAAGC 27

RESULT 902
ABN83603
ID ABN83603 standard; DNA; 27 BP.

AC ABN83603;

DT 27-AUG-2002 (first entry)

DE Adenovirus fibre tail region PCR primer C.

XX Adenovirus; fibre protein; gene delivery; gene therapy; stem cell;
KM vector; Hunter syndrome; Hunter syndrome; Sanfilippo syndrome;
KM Niemann-Pick disease; Morquio disease; Gaucher disease; Farber syndrome;
KM Krabbe disease; metachromatic leukodystrophy; I-cell disease; AIDS;
KM cancer; severe immunodeficiency syndrome; Jak-3 deficiency;
KM fucoseidase deficiency; thalassemia; erythropoietic porphyria;
KM autoimmune disease; cytotoxic; anti-HIV; cardiovascular; antianaemic;
KM immunosuppressive; immunostimulant; metabolic; PCR; primer; ss.

OS Mastadenovirus.

XX EP1195440-A1.

PD 10-APR-2002.

PF 06-OCT-2000; 2000EP-00203471.

PR 06-OCT-2000; 2000EP-00203471.

XX 06-OCT-2000; 2000US-0238830P.

PA (INTR-) INTERGENE BV.

PI Havenga MJE, Bout A;

XX WPI; 2002-394351/42.

XX Gene delivery vehicle useful for treating, e.g., cancer and Gauchers
PT disease, comprises an adenovirus having tropism for stem cells provided
PT by nucleic acid encoding fiber protein of adenovirus B serotype and a
PT proteinaceous substance.

XX Example 2; Page 18; 40pp; English.

XX The present sequence is primer C, which is based on the tail region of
CC adenovirus fibre protein DNA. It is one of a set of tail and knob based
CC primers (see ABN83601-13) used in the amplification of fiber sequences
CC from different adenovirus serotypes. Combination of primer C with knob
CC primer 4 allowed amplification of serotype 16 fibre DNA, and the
CC combination of tail primer C and knob primer 8 amplified serotype 51
CC fibre DNA. The invention provides chimeric adenoviruses, based on
CC adenovirus serotype 5, in which the gene encoding the knob and/or fibre
CC protein has been replaced with nucleic acid derived from alternative
CC human or animal serotypes, preferably serotype B. Generation of a
CC chimeric adenovirus serotype 5 based fibre library has enabled the rapid
CC screening and detection of recombinant adenoviral vectors with preferred
CC infection characteristics for haematopoietic stem cells. Stem cells
CC transduced with a chimeric adenovirus are used in a claimed method for
CC the treatment of Hunter syndrome, Hunter syndrome, Sanfilippo syndrome,
CC Niemann-Pick disease, Morquio disease, Gaucher disease, Farber syndrome,
CC Krabbe disease, metachromatic leukodystrophy, I-cell disease, severe
CC immunodeficiency syndrome, Jak-3 deficiency, fucoseidase deficiency,
CC thalassemia, erythropoietic porphyria, AIDS, cancer and other autoimmune
CC disease (all claimed)

SQ Sequence 27 BP; 9 A; 6 C; 5 G; 5 T; 0 U; 2 Other;

Query Match 0.2%; Score 18.2; DB 1; Length 27;
Best Local Similarity 74.1%; Pred. No. 8.4e+02;
Matches 20; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 5807 CCTGCTCGCTATGATGATGAATC 5833
DB 1 CCKGTSTACCATATGAGATGAAGC 27

RESULT 903

ADCT5075/C
ID ADCT5075 standard; DNA; 27 BP.

AC ADCT5075;

DT 01-JAN-2004 (first entry)

DE Biosensor related oligonucleotide of the invention SEQ ID NO:3.

XX ss; biosensor; hybridisation.

XX Synthetic.

XX JP2003172737-A.

PN 20-JUN-2003.

PD 07-DEC-2001; 2001JP-00374764.

PF 07-DEC-2001; 2001JP-00374764.

PR (TOJO) TOYO KOHAN CO LTD.

XX WPI; 2003-819164/77.

XX Solid support body comprising crystal resonator on which a surface
PT treatment layer is formed, and a substrate whose surface treatment layer

PT is chemically modified, useful as biosensor.

XX

PS Disclosure; SEQ ID NO 3; 7bp; Japanese.

CC The invention relates to a novel solid support body comprising a crystal resonator on which a surface treatment layer is formed. The biosensor is useful for analysing biological samples e.g., gene, a protein, and a peptide, and for analysing bioactive substances. Preferably, the biosensor is useful for analysing base sequences by carrying out hybridisation. The present sequence is used in the exemplification of the invention.

CC

XX

SQ Sequence 27 BP; 19 A; 3 C; 0 G; 5 T; 0 U; 0 Other;

OY 4466 TTTTCTTTTTTTTTTGTCCTT 4488
|||||
Db 23 TTTTCTTTTTTTTTTGATT 1

RESULT 904
AAQ34110/c
ID AAQ34110 standard; DNA; 18 BP.
XX
AC AAQ34110;
XX
DT 25-MAR-2003 (revised)
DT 02-FEB-1993 (first entry)

DE Sequence of a microsatellite from clone TGLA60B.
XX
KM PCR; selection; primers; OPTIPRM; breeding; cattle; parentage;
KM genetic mapping; traits; amplification; ss.
OS
OS Bos taurus.
XX
PN MO9213102-A1.
XX
PD 06-AUG-1992.
XX
PF 15-JAN-1992; 92MO-USO00340.
PR 15-JAN-1991; 91US-00642342.
XX
PA (GENM-) GENMARK.
XX
PI Georges M, Massey JM;
XX WPI; 1992-284684/34.
DR
PT Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding.
XX
XX
PS Table 7; Page 375; 517pp; English.

CC The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MbOI DNA fragments of between 250 and 500 bp with an (AGC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MbOI sites, the frequency of (76)n >= microsatelliteness in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program OPTIPRM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also AAQ33501-34437 (Updated on 25-MAR-2003 to correct PN

[illegible]

```
QY 4464 TTTT TTTT TTTT TTTT TTTT 4481
XX ::::::::::::::::::::
XX 1 UUUUUUUUUUUUUUUUUUU 18
DB

RESULT 906
AAV21970
ID AAV21970 standard; DNA; 18 BP.
XX
XX AAT94669;
AC AAT94669;
XX
XX 27-MAR-1998 (first entry)
XX
XX Anchored poly(T) oligonucleotide polyT-AnchG.
XX
XX Flavonoid 3'-hydroxylase; pigmentation; flower colour; transgenic plant;
XX snapdragon; primer; ss.
XX
XX Synthetic.
XX
XX MO9732023-A1.
XX
XX 04-SEP-1997.
XX
XX 28-FEB-1997; 97WO-AU000124.
XX
XX 01-MAR-1996; 96AU-00008386.
XX
XX (FLOR-) FLORIGENE LTD.
XX
XX Brugliera F, Holton TA, Michael MZ;
XX
XX MPI; 1997-448691/41.
XX
XX Novel flavonoid 3'-hydroxylase(s) from flowering plants - and
XX corresponding DNA, used in the manipulation of pigmentation in plants.
XX
XX Example 15; Page 59; 234pp; English.
XX
XX Anchored poly(T) oligonucleotides polyT-ancha (AAT94667), polyT-anchc
XX (AAT94668) and polyT-anchg (AAT94669) are complementary to the upstream
XX region of a polyadenylation sequence. They were used to prime cDNA
XX synthesis from snapdragon (Antirrhinum majus) petal and leaf RNA, and
XX were also utilised in the PCR amplification of plant cytochrome P450
XX sequences (see also AAT94670-73). A cDNA clone (see AAT94657) encoding
XX flavonoid 3'-hydroxylase (see AAW35704) was isolated using a differential
XX display approach. This can be used to manipulate the pigmentation of
XX transgenic plants
XX
XX Sequence 18 BP; 0 A; 0 C; 1 G; 17 T; 0 U; 0 Other;
SQ

Query Match 0.2%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4467 TTTT TTTT TTTT TTTT TTTT 4484
XX |||||
XX 1 TTTT TTTT TTTT TTTT TTTT 18
DB

RESULT 907
AAV21970
ID AAV21970 standard; DNA; 18 BP.
XX
XX AAV21970;
AC AAV21970;
XX
XX 14-JUL-1998 (first entry)
XX
XX Nuclease resistant antisense oligo NBT 13 targeted against (T)18.
XX
XX Nuclease resistant; bacterial infection; antibiotic; target;
XX veterinary medicine; treatment; human; industrial process;
XX bacterial control; ss.
XX
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XX
XX Synthetic.
XX
XX MO9803533-A1.
XX
XX 29-JAN-1998.
XX
XX 23-JUL-1997; 97WO-US012961.
XX
XX 24-JUL-1996; 96US-00685575.
XX
XX (OLIG-) OLIGOS ETC & OLIGOS THERAPEUTICS INC.
XX
XX Arrow A, Dale RMK, Thompson TL;
XX
XX MPI; 1998-120687/11.
XX
XX Treating bacterial infections in humans or animals with
XX oligo:nucleotide(s) - resistant to nuclease and targeted to bacterial
XX nucleic acid or proteins, also conjugates of these oligo:nucleotide(s)
XX with antibiotics.
XX
XX Claim 49; Page 87; 163pp; English.
XX
XX This antisense oligonucleotide is nuclease resistant and can be used in
XX the treatment of animals, including humans, having a bacterial infection.
XX The treatment comprises administration of such nuclease resistant
XX oligonucleotides targeted to a nucleic acid or protein of the bacterium,
XX and formulated with a carrier. A compound comprising this nuclease
XX resistant oligonucleotide can be covalently linked to an antibiotic. The
XX method is used to treat infections by a wide variety of Gram-positive and
XX Gram-negative, or acid-fast, bacteria, in human and veterinary medicine.
XX The methods are particularly used in immuno-compromised individuals (e.g.
XX patients with acquired immunodeficiency syndrome or those receiving
XX chemotherapy or radiation therapy), optionally in combination with or
XX fused to, antiviral or other antimicrobial oligonucleotides. Apart from
XX therapeutic use, the oligonucleotides can be used to control bacteria in
XX laboratory cultures, foods, beverages and industrial processes. The
XX oligonucleotides are specific for bacteria, without affecting metabolism
XX in mammalian cells. They may also activate RNase H and have a general,
XX non-specific immune-stimulating effect. The oligonucleotides can be
XX administered orally, intranasally, rectally, topically or by injection,
XX optionally coupled to an agent (e.g. carbohydrate or polyamine) that
XX enhances cellular uptake
XX
XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
SQ

Query Match 0.2%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4481
XX |||||
XX 1 TTTT TTTT TTTT TTTT TTTT 18
DB

RESULT 908
AAV19943
ID AAV19943 standard; DNA; 18 BP.
XX
XX AAV19943;
AC AAV19943;
XX
XX 14-JUN-1999 (first entry)
XX
XX Primer SEQ ID NO:3 from JP11075880.
XX
XX Primer; oligonucleotide; labelling; detection; self-priming; PCR; ss.
XX
XX Synthetic.
XX
XX JP11075880-A.
XX
XX 23-MAR-1999.
XX
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XX PF 10-JUL-1998; 98JP-00195719.
XX PR 14-JUL-1997; 97JP-00205378.
XX PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX DR WPI; 1999-257710/22.
XX PT Labelling of an oligonucleotide - useful for detecting genes.
XX PS Example 1; Page 7; 10pp; Japanese.
XX CC A method has been developed for labelling an oligonucleotide having a
CC repeated sequence of (XY)n (where X and Y consists of a combination of
CC adenine and thymine or uracil or guanine and cytosine, and n is an
CC integer of 1 or more) at the 3'-terminal side in which the repeated
CC sequence is added and extended using a labelled body of the nucleotide
CC constituting the repeated sequence and a DNA polymerase lacking in 5' to
CC 3' exonuclease activity. The method can be used for detecting a gene. The
CC method can detect a gene in a sensitivity up to ten times higher than
CC prior art methods. The present sequence represents a primer used in an
CC example from the present invention
XX SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 18; DB 1; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 5.2e+02;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 4464 TTTT TTTT TTTT TTTT TTTT 4481
DB 1 TTTT TTTT TTTT TTTT TTTT 18
XX
XX RESULT 909
XX AAX19942/C
XX ID AAX19942 standard; DNA; 18 BP.
XX AC AAX19942;
XX DT 14-JUN-1999 (first entry)
XX DE Primer SEQ ID NO:2 from JP11075880.
XX KM Primer; oligonucleotide; labelling; detection; self-priming; PCR; ss.
XX OS Synthetic.
XX PN JP11075880-A.
XX PD 23-MAR-1999.
XX PF 10-JUL-1998; 98JP-00195719.
XX PR 14-JUL-1997; 97JP-00205378.
XX PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX DR WPI; 1999-257710/22.
XX PT Labelling of an oligonucleotide - useful for detecting genes.
XX PS Example 1; Page 7; 10pp; Japanese.
XX CC A method has been developed for labelling an oligonucleotide having a
CC repeated sequence of (XY)n (where X and Y consists of a combination of
CC adenine and thymine or uracil or guanine and cytosine, and n is an
CC integer of 1 or more) at the 3'-terminal side in which the repeated
CC sequence is added and extended using a labelled body of the nucleotide
CC constituting the repeated sequence and a DNA polymerase lacking in 5' to
CC 3' exonuclease activity. The method can be used for detecting a gene. The
CC method can detect a gene in a sensitivity up to ten times higher than

```

```

CC prior art methods. The present sequence represents a primer used in an
CC example from the present invention
XX SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 18; DB 1; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 5.2e+02;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 4464 TTTT TTTT TTTT TTTT TTTT 4481
DB 18 TTTT TTTT TTTT TTTT TTTT 1
XX
XX RESULT 910
XX AAX17961
XX ID AAX17961 standard; cDNA; 18 BP.
XX AC AAX17961;
XX DT 11-MAY-1999 (first entry)
XX DE Triplet repeat sequence PCR primer #11.
XX KM Primer; PCR; amplification; triplet repeat; spinobulbar atrophy;
XX myotonic dystrophy; spinocerebellar ataxia; Huntington's disease;
XX fragile X syndrome; Benet's disease; diagnosis; ss.
XX OS Synthetic.
XX PN M09856950-A1.
XX PD 17-DEC-1998.
XX PF 10-JUN-1998; 98WO-FR001187.
XX PR 11-JUN-1997; 97FR-00007225.
XX PA (DAUS-) FOND DAUSSET-CEPH JEAN.
XX PI Neri C, Cann HM;
XX DR WPI; 1999-070334/06.
XX PT DNA sequences rich in repeated nucleotide triplets - used for the
XX diagnosis and prognosis of diseases associated with trinucleotide
XX repeats.
XX PS Claim 5; Page 14; 30pp; French.
XX CC Primers AAX17951-X17974 are used to PCR amplify sequences containing the
XX triplet repeat sequences CAG/CTG or CGG/GCC. The amplified sequences can
XX be compared to sequences from a patient to determine presence of
XX additional trinucleotide repeats (TNR), specifically for assessing the
XX risk of developing a TNR-related disease (e.g. spinobulbar atrophy;
XX myotonic dystrophy; spinocerebellar ataxia; Huntington's disease; fragile
XX X syndrome or Benet's disease). The method is especially useful for
XX early diagnosis or specific monitoring, but if the disease is associated
XX with a relatively small variation in the number of repeats, it may also
XX be used to predict the onset of disease and/or its severity
XX SQ Sequence 18 BP; 3 A; 6 C; 3 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 18; DB 1; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 5.2e+02;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 7343 ACCCTGTCCAGTCGCAATG 7360
DB 1 ACCCTGTCCAGTCGCAATG 18
XX
XX RESULT 911

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```
AAZ87161/C
ID AAZ87161 standard; RNA; 18 BP.
XX
AC AAZ87161;
XX
DT 08-MAY-2000 (first entry)
XX
DE Oligoarabinonucleotide SEQ ID NO:2.
XX
XX Beta-D-arabinose; antisense; inhibition; transcription; expression;
XX reverse transcription; viral replication; RNase H cleavage;
XX triple helix formation; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..18
FT FT /tag= a
FT FT /note= "Ribose moiety replaced by beta-D-arabinose"
XX
PN WO967378-A1.
XX
PD 29-DEC-1999.
XX
PF 17-JUN-1999; 99WO-CA000571.
XX
PR 19-JUN-1998; 98CA-02241361.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Damha MJ, Parniak MA, Noronha AM, Wilde C, Borkow G, Arion D;
XX WPI; 2000-160584/14.
XX
PT Therapeutic composition containing antisense oligonucleotides that
XX include arabinose sugars, particularly for inhibiting viral replication.
XX
PS Example 1; Page 29; 91pp; English.
XX
CC The invention relates to a new composition for selective, sequence-
CC specific inhibition of gene transcription and expression in a host. The
CC composition comprises oligonucleotides containing arabinose sugars that
CC can hybridise to either a single-stranded (ss) RNA to induce RNase H
CC cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple
CC helix, thereby inhibiting DNA replication and/or transcription. The
CC oligoarabinonucleotides are used for antisense inhibition of gene
CC expression or to prevent DNA replication, or reverse transcription of RNA
CC by retroviruses. The compositions are therefore particularly used to
CC inhibit retroviral replication. The oligoarabinonucleotides can also be
CC used, in combination with RNase H, as reagents for sequence-specific
CC cleavage or RNA mapping, and additionally for the study and control of
CC gene expression in cells. The oligoarabinonucleotides have excellent
CC affinity for RNA, increased resistance to nucleases and show little if
CC any non-specific binding to cellular or serum proteins. They target ss
CC RNA, but not complementary ss DNA, so may be useful for targeting
CC retroviral genomic RNA to inhibit the early stages of viral replication.
CC Oligoarabinonucleotides containing pyrimidine bases form triple helices
CC with significantly higher thermal stability than those produced by normal
CC oligonucleotides. Sequences AAZ87160-287164 represent
CC oligoarabinonucleotides containing beta-D-arabinose used in an
CC exemplification of the present invention
XX
SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred.No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4481
DB 18 TTTT TTTT TTTT TTTT TTTT 1
```

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RESULT 912
AAZ87162
ID AAZ87162 standard; RNA; 18 BP.
XX
AC AAZ87162;
XX
DT 08-MAY-2000 (first entry)
XX
DE Oligoarabinonucleotide SEQ ID NO:3.
XX
XX Beta-D-arabinose; antisense; inhibition; transcription; expression;
XX reverse transcription; viral replication; RNase H cleavage;
XX triple helix formation; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..18
FT FT /tag= a
FT FT /note= "Ribose moiety replaced by beta-D-arabinose"
XX
PN WO967378-A1.
XX
PD 29-DEC-1999.
XX
PF 17-JUN-1999; 99WO-CA000571.
XX
PR 19-JUN-1998; 98CA-02241361.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Damha MJ, Parniak MA, Noronha AM, Wilde C, Borkow G, Arion D;
XX WPI; 2000-160584/14.
XX
PT Therapeutic composition containing antisense oligonucleotides that
XX include arabinose sugars, particularly for inhibiting viral replication.
XX
PS Example 1; Page 29; 91pp; English.
XX
CC The invention relates to a new composition for selective, sequence-
CC specific inhibition of gene transcription and expression in a host. The
CC composition comprises oligonucleotides containing arabinose sugars that
CC can hybridise to either a single-stranded (ss) RNA to induce RNase H
CC cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple
CC helix, thereby inhibiting DNA replication and/or transcription. The
CC oligoarabinonucleotides are used for antisense inhibition of gene
CC expression or to prevent DNA replication, or reverse transcription of RNA
CC by retroviruses. The compositions are therefore particularly used to
CC inhibit retroviral replication. The oligoarabinonucleotides can also be
CC used, in combination with RNase H, as reagents for sequence-specific
CC cleavage or RNA mapping, and additionally for the study and control of
CC gene expression in cells. The oligoarabinonucleotides have excellent
CC affinity for RNA, increased resistance to nucleases and show little if
CC any non-specific binding to cellular or serum proteins. They target ss
CC RNA, but not complementary ss DNA, so may be useful for targeting
CC retroviral genomic RNA to inhibit the early stages of viral replication.
CC Oligoarabinonucleotides containing pyrimidine bases form triple helices
CC with significantly higher thermal stability than those produced by normal
CC oligonucleotides. Sequences AAZ87160-287164 represent
CC oligoarabinonucleotides containing beta-D-arabinose used in an
CC exemplification of the present invention
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 0 T; 18 U; 0 Other;
XX
Query Match 0.2%; Score 18; DB 1; Length 18;
Best Local Similarity 0.0%; Pred.No. 5.2e+02;
Matches 0; Conservative 18; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4481
DB 1 UUUUUUUUUUUUUUUUUUU 18
```

Key	Location/Qualifiers
AA287166	standard; DNA; 18 BP.
AA287166;	
08-MAY-2000	(first entry)
Deoxyarabinonucleotide SEQ ID NO:7.	
2'-deoxy-2'-fluoro-beta-D-arabinose; antisense; inhibition;	
transcription; expression; reverse transcription; viral replication;	
RNase H cleavage; triple helix formation; ss.	
Synthetic.	
Key	Location/Qualifiers
modified_base	1. 18
/*tag= a	
/note= "Deoxyribose moiety replaced by 2'-deoxy-2'-	
fluoro-beta-D-arabinose"	
WO967378-A1.	
29-DEC-1999.	
17-JUN-1999;	99WO-CA000571.
19-JUN-1998;	98CA-02241361.
(UYWC-) UNIV MCGILL.	
Damha MJ, Parniak MA, Noronha AM, Wilds C, Borkow G, Arion D;	
WPI; 2000-160584/14.	
Therapeutic composition containing antisense oligonucleotides that	
include arabinose sugars, particularly for inhibiting viral replication.	
Example 2; Page 31; 91pp; English.	
The invention relates to a new composition for selective, sequence-	
specific inhibition of gene transcription and expression in a host. The	
composition comprises oligonucleotides containing arabinose sugars that	
can hybridize to either a single-stranded (ss) RNA to induce RNase H	
cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple	
helix, thereby inhibiting DNA replication and/or transcription. The	
oligoarabinonucleotides are used for antisense inhibition of gene	
expression or to prevent DNA replication, or reverse transcription of RNA	
by retroviruses. The compositions are therefore particularly used to	
inhibit retroviral replication. The oligoarabinonucleotides can also be	
used, in combination with RNase H, as reagents for sequence-specific	
cleavage or RNA mapping, and additionally for the study and control of	
gene expression in cells. The oligoarabinonucleotides have excellent	
affinity for RNA, increased resistance to nucleases and show little if	
any, but not complementary ss DNA, so may be useful for targeting	
retroviral genomic RNA to inhibit the early stages of viral replication.	
Oligoarabinonucleotides containing pyrimidine bases form triple helices	
with significantly higher thermal stability than those produced by normal	
oligonucleotides. Sequences AA287165-287169 represent	
oligoarabinonucleotides containing 2'-deoxy-2'-fluoro-beta-D-	
arabinose used in an exemplification of the present invention	
Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;	
Query Match	0.2%; Score 18; DB 1; Length 18;
Best Local Similarity	100.0%; Pred. No. 5.2e+02;
Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0

ID	AAZ87167/c	AAZ87167 standard; DNA; 18 BP.
AC	AAZ87167;	
AD	08-MAY-2000 (first entry)	
DE	Deoxyarabinonucleotide SEQ ID NO:8.	
FM	2'-deoxy-2'-fluoro-beta-D-arabinose; antisense; inhibition;	
FM	transcription; expression; reverse transcription; viral replication;	
FM	RNase H cleavage; triple helix formation; ss.	
OS	Synthetic.	
XX	Key	Location/Qualifiers
XX	modified_base	1..18
XX	/*tag= a	/note= "Deoxyribose moiety replaced by 2'-deoxy-2'-fluoro-beta-D-arabinose"
XX	MO3967378-A1.	
XX	29-DEC-1999.	
XX	17-JUN-1999;	99WO-CA000571.
XX	19-JUN-1998;	98CA-02241361.
XX	(UTMC-) UNIV MCGILL.	
XX	Damba MJ, Parniak MA, Noronha AM, Wilds C, Borkow G, Arion D;	
XX	WPI, 2000-160584/14.	
XX	Therapeutic composition containing antisense oligonucleotides that	
XX	include arabinose sugars, particularly for inhibiting viral replication.	
XX	Example 2; Page 31; 91pp; English.	
XX	The invention relates to a new composition for selective, sequence-	
XX	specific inhibition of gene transcription and expression in a host. The	
XX	composition comprises oligonucleotides containing arabinose sugars that	
XX	can hybridize to either a single-stranded (ss) RNA to induce RNase H	
XX	cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple	
XX	helix, thereby inhibiting DNA replication and/or transcription. The	
XX	oligoarabinonucleotides are used for antisense inhibition of gene	
XX	expression or to prevent DNA replication, or reverse transcription of RNA	
XX	by retroviruses. The compositions are therefore particularly used to	
XX	inhibit retroviral replication. The oligoarabinonucleotides can also be	
XX	used, in combination with RNase H, as reagents for sequence-specific	
XX	cleavage or RNA mapping, and additionally for the study and control of	
XX	gene expression in cells. The oligoarabinonucleotides have excellent	
XX	affinity for RNA, increased resistance to nucleases and show little if	
XX	any non-specific binding to cellular or serum proteins. They target ss	
XX	RNA, but not complementary ss DNA, so may be useful for targeting	
XX	retroviral genomic RNA to inhibit the early stages of viral replication.	
XX	Oligoarabinonucleotides containing pyrimidine bases form triple helices	
XX	with significantly higher thermal stability than those produced by normal	
XX	oligonucleotides. Sequences AAZ87165-287169 represent	
XX	oligodeoxyarabinonucleotides containing 2'-deoxy-2'-fluoro-beta-D-	
XX	arabinose used in an exemplification of the present invention	
XX	Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;	
XX	Query March 0.2%; Score 18; DB 1; Length 18;	
XX	Best local Similarity 100.0%; Pred. NO. 5.2e+02;	
XX	Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	

QY 4464 TTTT TTTT TTTT TTTT 4481
 |||||
 18 TTTT TTTT TTTT TTTT 1

RESULT 915
 AAD03565

ID AAD03565 standard; DNA; 18 BP.

AC AAD03565;

DT 19-JUN-2001 (first entry)

DE Oligonucleotide #6 used for the preparation of normalised cDNA libraries.

KM Rat; secreted factor; clone P00188.D12; cardiac; antiinflammatory;
 antiarhythmic; antiarteriosclerotic; antiatherosclerotic; nephropathic;
 antidiabetic; immunosuppressive; antiallergic; antitumour;
 antibacterial; osteoprotective; cerebroprotective; vasotropic; antiulcer;
 neurotropic; neuroprotective; congestive heart failure; myocarditis;
 hypertrophic cardiomyopathy; angina pectoris; myocardial infarction;
 kidney disease; acute renal failure; renal glucosuria; renal infarction;
 polycystic kidney disease; hereditary nephritis; inflammatory disease;
 tumour angiogenesis; osteoarthritis; toxic shock syndrome; psoriasis;
 stroke; neural trauma; cerebral malaria; Crohn's disease; osteoporosis;
 ulcerative colitis; Alzheimer's disease; gene therapy; ss.

OS Rattus norvegicus.

PN W0200123564-A1.

PD 05-APR-2001.

PF 27-SEP-2000; 2000MO-US026544.

PR 27-SEP-1999; 99US-0156280P.

PA (SCIO-) SCIOS INC.

PI Stanton LW, Kapoun AM;

DR WPI; 2001-266159/27.

PT Novel secreted factor encoded by clone P00188D12 which is differentially
 expressed in certain disease states, useful in diagnosing and treating
 cardiac, renal or inflammatory diseases.

PS Example 1; Page 42; 71pp; English.

CC The patent discloses novel secreted factor protein encoded by clone
 P00188.D12. The secreted factor is differentially expressed in certain
 disease states. Secreted protein, its antibodies, antagonists or
 compositions comprising them are useful in the diagnosis and treatment of
 cardiac diseases such as congestive heart failure, myocarditis,
 hypertrophic cardiomyopathy, angina pectoris, myocardial infarction,
 cardiac arrhythmia, arteriosclerosis, kidney diseases such as acute renal
 failure, renal glucosuria, renal infarction, nephrogenic diabetes
 insipidus, polycystic kidney disease, hereditary nephritis and
 inflammatory diseases such as asthma, autoimmune diabetes, tumour
 angiogenesis, rheumatoid arthritis, osteoarthritis, toxic shock syndrome,
 asthma, stroke, neural trauma, psoriasis, cerebral malaria, osteoporosis,
 Crohn's disease, ulcerative colitis, Alzheimer's disease. Secreted
 protein DNA is useful in antisense-mediated gene inhibition and in gene
 therapy. An array comprising one or more oligonucleotides complementary
 to reference RNA or DNA encoding the secreted factor is useful for
 detecting cardiac, kidney and inflammatory disease. The present DNA
 sequence is an oligonucleotide which is used in the preparation of a
 normalised cDNA library containing secreted factor DNAs. The normalised
 cDNA libraries are used in the identification of differentially expressed
 rat secreted factor P00188.D12 gene

XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.2%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 5.2e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT 4481
 |||||
 DB 1 TTTT TTTT TTTT TTTT 18

RESULT 916
 AAS13717/C

ID AAS13717 standard; DNA; 18 BP.

AC AAS13717;

DT 08-MAY-2002 (first entry)

DE Simple sequence repeat, SSR, #14.

KM Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat;
 cereal profiling; grass profiling; seed batch purity testing.

OS Poaceae.

PN NZ509193-A.

PD 25-MAY-2001.

PF 03-JAN-2001; 2001NZ-00509193.

PR 24-DEC-1999; 99AU-00004906.

PA (SAUS-) STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R.

PA (UVSC-) UNIV SOUTHERN CROSS.

PA (VICT-) STATE VICTORIA DEPT NATURAL RES & ENVIRO.

PA (UYAD-) UNIV ADELAIDE.

PA (ITWA-) INT MAIZE & WHEAT IMPROVEMENT CENT.

PI Forster JW, Jones BS;

DR WPI; 2001-512563/56.

PT New simple sequence repeats having 2 or more tandemly repeated nucleotide
 core elements isolated from ryegrass and fescue, useful for selecting of
 genes in grass or cereal breeding or profiling grass or cereal species
 varieties.

PS Claim 6; Page 51; 72pp; English.

CC The invention relates to a substantially purified or isolated nucleic
 acid (1) from ryegrass or fescue species including a simple sequence
 repeat (SSR), having 2 or more tandemly repeated nucleotide core elements
 2-6 nucleotides in length. Also included are a nucleic acid primer
 suitable for amplifying an SSR, identifying (M1) an SSR by preparing a
 library of ryegrass or fescue genomic DNA enriched for SSRs and
 identifying clones in the library containing SSRs, a library of ryegrass
 or fescue genomic DNA enriched for SSRs prepared by the M1, selecting for
 a gene in grass or cereal breeding by identifying an SSR that is closely
 associated with the gene such that the SSR and the gene are
 preferentially co-inherited, and selecting for the SSR in the breeding, a
 method for DNA profiling grass or cereal species varieties by assessing
 variation between SSR varieties and testing the purity of grass or cereal
 seed batches by assessing variation within seed batch of an SSR. The SSRs
 may be used in the selection of genes in grass or cereal breeding, for
 profiling grass or cereal species varieties, for testing the purity of
 grass or cereal seed batches, and for DNA profiling to establish the
 distinct identity, uniformity and/or stability of a cultivar. The present
 sequence is a ryegrass or fescue SSR

XX Sequence 18 BP; 0 A; 6 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 0.2%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7415 GCAGCAGCAGCAGCAGCA 7432

Db 18 GCAGCAGCAGCAGCAGCA 1

RESULT 917

AAD17014/c

ID AAD17014 standard; DNA; 18 BP.

AC AAD17014;

DT 29-NOV-2001 (first entry)

DE Oligonucleotide A18-2PEG linker.

KM Scaffold protein; antibody mimic; fibronectin type III domain;

KW randomised loop; randomised beta-sheet; diagnostic purpose;

OS Unidentified.

FM Key Location/Qualifiers

FT misc_feature 18 /tag= a

FT /note= "linked to (PEG) 2CCPurumycin"

PN WO200164942-A1.

PD 07-SEP-2001.

PF 28-FEB-2001; 2001WO-US006414.

PR 29-FEB-2000; 2000US-00515260.

PA (PHYR-) PHYLOS INC.

PI Lipovsek D, Wagner RW, Kuimelis RG;

DR WPI; 2001-557782/62.

PT Fibronectin scaffold protein array for obtaining a protein/compound which

PT binds to a compound/protein, comprises a fibronectin type III domain

PT having a randomized loop, a randomized beta-sheet or their combination.

PS Disclosure; Page 25; 67pp; English.

CC The present invention relates to an array of proteins (antibody mimics)

CC comprising a fibronectin type III domain having a randomized loop, a

CC randomised beta-sheet, or their combination, and has the capacity to bind

CC to a compound that is not bound by a corresponding naturally-occurring

CC fibronectin, immobilised onto a solid support. The antibody mimics is

CC useful for detecting a compound preferably a protein, in a biological

CC sample. It is also useful to detect one or more different analytes

CC simultaneously in a sample. Hence is useful for diagnostic purposes. It

CC is also useful for the purpose of designing proteins capable of binding

CC to virtually any compound of interest. The present sequence is an

CC oligonucleotide A18-2PEG linker used in an exemplification of the

CC invention

CC Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.2%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 5.2e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4481

Db 18 TTTT TTTT TTTT TTTT TTTT 1

RESULT 918

AA75597

ID AAF75597 standard; DNA; 18 BP.

AC AAF75597;

DT 10-MAY-2001 (first entry)

DE Binary encoded sequence tag method anchored primer #2.

KM Binary encoded sequence tag; BEST; nucleic acid analysis;

KW gene expression; adaptor; PCR primer; ss.

OS Synthetic.

PN WO200112855-A2.

PD 22-FEB-2001.

PF 11-AUG-2000; 2000WO-US022164.

PR 13-AUG-1999; 99US-0148870P.

PR 06-APR-2000; 2000US-00544713.

PA (UYVA) UNIV YALE.

PI Kaufman JC, Roth ME, Lizardi PM, Feng L, Latimer DR;

DR WPI; 2001-202878/20.

PT Producing binary sequence tags, useful for analyzing nucleic acid

PT sequence tags, gene expression or gene-expression patterns, involves

PT generating nucleic acid fragments, which are mixed with offset adaptors

PT and adaptor-indexers.

PS Disclosure; Page 100; 101pp; English.

CC The present invention describes a method of producing binary sequence

CC tags from nucleic acid fragments in a sample, involving incubating the

CC sample with cleaving reagents, mixing offset adaptors with the sample,

CC incubating with more cleaving reagents and mixing the sample with adaptor

CC -indexers where the adaptors are coupled to binary sequence tags. The

CC method is useful in sequence analysis, including analysis and comparison

CC of gene expression, nucleic acid samples and genomes

CC Sequence 18 BP; 0 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 0.2%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 5.2e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4468 TTTT TTTT TTTT TTTT TTTT 4485

Db 1 TTTT TTTT TTTT TTTT TTTT 18

RESULT 919

AA75597

ID AAF99708 standard; DNA; 18 BP.

AC AAF99708;

DT 12-JUN-2001 (first entry)

DE Immunostimulatory nucleic acid #824.

KM Vaccine; cytosolic; virucidal; bactericidal; fungicidal; anti-parasitic;

KW immunostimulatory; tumour; viral infection; bacterial infection;

KW fungal infection; parasitic infection; cancer; asthma;

KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.

OS Synthetic.

```

PN      MO200122972-A2.
PD      XX
PD      05-APR-2001.
PF      25-SEP-2000; 2000WO-US026383.
PR      25-SEP-1999; 99US-0156113P.
PR      27-SEP-1999; 99US-0156135P.
PR      23-AUG-2000; 2000US-0227436P.
XX      XX
PA      (IOWA ) UNIV IOWA RES FOUND.
PA      (COLE-) COLEY PHARM GMBH.
XX      XX
PI      Kriegl AM, Schetter C, Vollmer J;
DR      WPI, 2001-273485/28.
XX      XX
PT      Vaccinating against tumors, infectious diseases, allergies and asthma
PT      using immunostimulatory Py-rich and TG nucleic acids.
XX      XX
PS      Claim 101; Page 56; 338pp; English.
CC      The present invention relates to a method for stimulating an immune
CC      response. The method comprises administering an immunostimulatory nucleic
CC      acid to a non-rodent subject in sufficient quantity to stimulate an
CC      immune response. The present sequence is one such immunostimulatory
CC      nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC      (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC      against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC      and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC      haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC      staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC      also useful for preventing cancer, asthma, infectious disease, allergy or
CC      immune deficiency. The present sequence can also be used to redirect a
CC      Th2 to a Th1 immune response and to activate immune cells. Note: the
CC      present sequence may have a phosphorothioate backbone
XX      XX
SQ      Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
        Query Match          0.2%; Score 18; DB 1; Length 18;
        Best Local Similarity 100.0%; Pred. No. 5.2e+02;
        Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      4464 TTTTTTTTTTTTTTTTTT 4481
        |||||
        1 TTTTTTTTTTTTTTTTTT 18
        |||||

RESULT 920
AAF99734
ID      AAF99734 standard; DNA; 18 BP.
XX      XX
AC      AAF99734;
DT      12-JUN-2001 (first entry)
XX      XX
DE      Immunostimulatory nucleic acid #850.
XX      XX
KM      Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KM      immunostimulatory; tumour; viral infection; bacterial infection;
KM      fungal infection; parasitic infection; cancer; asthma;
KM      infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX      XX
OS      Synthetic.
XX      XX
PN      WO200122972-A2.
PD      XX
PD      05-APR-2001.
PF      25-SEP-2000; 2000WO-US026383.
PR      25-SEP-1999; 99US-0156113P.
PR      27-SEP-1999; 99US-0156135P.
PR      23-AUG-2000; 2000US-0227436P.
XX      XX
PA      (IOWA ) UNIV IOWA RES FOUND.
PA      (COLE-) COLEY PHARM GMBH.
XX      XX
PI      Kriegl AM, Schetter C, Vollmer J;
DR      WPI, 2001-273485/28.
XX      XX
PT      Vaccinating against tumors, infectious diseases, allergies and asthma
PT      using immunostimulatory Py-rich and TG nucleic acids.
XX      XX
PS      Claim 101; Page 56; 338pp; English.
CC      The present invention relates to a method for stimulating an immune
CC      response. The method comprises administering an immunostimulatory nucleic
CC      acid to a non-rodent subject in sufficient quantity to stimulate an
CC      immune response. The present sequence is one such immunostimulatory
CC      nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC      (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC      against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC      and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC      haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC      staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC      also useful for preventing cancer, asthma, infectious disease, allergy or
CC      immune deficiency. The present sequence can also be used to redirect a
CC      Th2 to a Th1 immune response and to activate immune cells. Note: the
CC      present sequence may have a phosphorothioate backbone
XX      XX
SQ      Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
        Query Match          0.2%; Score 18; DB 1; Length 18;
        Best Local Similarity 100.0%; Pred. No. 5.2e+02;
        Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      4464 TTTTTTTTTTTTTTTTTT 4481
        |||||
        1 TTTTTTTTTTTTTTTTTT 18
        |||||

RESULT 920
AAF99734
ID      AAF99734 standard; DNA; 18 BP.
XX      XX
AC      AAF99734;
DT      12-JUN-2001 (first entry)
XX      XX
DE      Immunostimulatory nucleic acid #850.
XX      XX
KM      Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KM      immunostimulatory; tumour; viral infection; bacterial infection;
KM      fungal infection; parasitic infection; cancer; asthma;
KM      infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX      XX
OS      Synthetic.
XX      XX
PN      WO200122972-A2.
PD      XX
PD      05-APR-2001.
PF      25-SEP-2000; 2000WO-US026383.
PR      25-SEP-1999; 99US-0156113P.
PR      27-SEP-1999; 99US-0156135P.
PR      23-AUG-2000; 2000US-0227436P.
XX      XX
PA      (IOWA ) UNIV IOWA RES FOUND.
PA      (COLE-) COLEY PHARM GMBH.
XX      XX
PI      Kriegl AM, Schetter C, Vollmer J;
DR      WPI, 2001-273485/28.
XX      XX
PT      Vaccinating against tumors, infectious diseases, allergies and asthma
PT      using immunostimulatory Py-rich and TG nucleic acids.
XX      XX
PS      Claim 101; Page 56; 338pp; English.
CC      The present invention relates to a method for stimulating an immune
CC      response. The method comprises administering an immunostimulatory nucleic
CC      acid to a non-rodent subject in sufficient quantity to stimulate an
CC      immune response. The present sequence is one such immunostimulatory
CC      nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC      (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC      against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC      and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC      haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC      staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC      also useful for preventing cancer, asthma, infectious disease, allergy or
CC      immune deficiency. The present sequence can also be used to redirect a
CC      Th2 to a Th1 immune response and to activate immune cells. Note: the
CC      present sequence may have a phosphorothioate backbone
XX      XX
SQ      Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
        Query Match          0.2%; Score 18; DB 1; Length 18;
        Best Local Similarity 100.0%; Pred. No. 5.2e+02;
        Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      4464 TTTTTTTTTTTTTTTTTT 4481
        |||||
        1 TTTTTTTTTTTTTTTTTT 18
        |||||

```

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PR 23-AUG-2000; 2000US-0227436P.
XX
XX (IOWA ) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
XX
XX Kriegl AM, Schetter C, Vollmer J;
XX WPI, 2001-273485/28.
DR
XX
XX Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids.
PS Claim 101; Page 56; 338pp; English.
XX
XX The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumor antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells. Note: the
CC present sequence may have a phosphorothioate backbone
CC
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match          0.2%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4464 TTTTTTTTTTTTTTTT 4481
        |||||
DB       1 TTTTTTTTTTTTTTTT 18

RESULT 921
AAF82472
ID   AAF82472 standard; DNA; 18 BP.
XX
XX   AAF82472;
XX
XX   DT     29-JUN-2001 (first entry)
DE   Phagemid vector pCR2.1 polylinker oligonucleotide #6.
XX
XX   KW   Phagemid vector; PCR2.1; rat; secreted factor; P00210D09; cardiant;
KW   nephrotropic; antiinflammatory; gene therapy; cardiac disease;
KW   renal disease; inflammatory disease; polylinker; ss.
XX
XX   OS   Synthetic.
XX
XX   PN   WO200123419-A2.
XX
XX   PD   05-APR-2001.
XX
XX   PF   27-SEP-2000; 2000WO-US026582.
XX
XX   PR   27-SEP-1999; 99US-0156277P.
XX
XX   PA   (SCIO-) SCIOS INC.
XX
XX   PI   Stanton LW, Kapoun AM;
XX
XX   DR   WPI, 2001-328177/34.
XX
XX   PT   Novel secreted factor encoded by clone P00210D09 useful for diagnosing,
PT   treating and/or preventing various cardiac, renal and inflammatory
PT   diseases.
```


CC useful for inhibiting angiogenesis associated with solid tumour growth,
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
 CC rubecosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
 CC neovascularisation, telangiectasia, haemophilic joints, angiodiroma,
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
 CC acid of the invention

XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

XX SQ

XX Query Match 0.2%; Score 18; DB 1; Length 18;
 XX Best Local Similarity 100.0%; Pred. No. 5.2e+02;
 XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4481
 XX |||||
 DB 1 TTTT TTTT TTTT TTTT TTTT 18

XX RESULT 924
 XX ABL39401 standard; DNA; 18 BP.

XX ID ABL39401 standard; DNA; 18 BP.

XX AC ABL39401;

XX DT 13-DEC-2002 (first entry)

XX DE Angiogenesis inhibitory oligonucleotide #913.

XX XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
 XX tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
 XX diabetic retinopathy; retinopathy of prematurity; macular degeneration;
 XX corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
 XX rubecosis; Osler-Webber Syndrome; myocardial angiogenesis;
 XX plaque neovascularisation; telangiectasia; haemophilic joints;
 XX angiodiroma; wound granulation; intestinal adhesions; atherosclerosis;
 XX scleroderma; hypertrophic scar.

XX OS Synthetic.

XX WO200253141-A2.

XX PD 11-JUL-2002.

XX PF 14-DEC-2001; 2001WO-US048458.

XX PR 14-DEC-2000; 2000US-0255534P.

XX PA (COLE-) COLEY PHARM GROUP INC.

XX PI Bratzler RL;

XX PT WPI; 2002-566690/60.

XX DR Inhibiting angiogenesis in a subject, involves administering at least one
 XX PT antiangiogenic nucleic acid molecule to the subject.

XX PS Claim 2; Page 35; 276pp; English.

XX CC The invention relates to inhibiting angiogenesis in a subject, comprising
 XX administering at least one antiangiogenic nucleic acid molecule. Also
 XX included is a kit comprising a first container housing the antiangiogenic
 XX nucleic acids, and instructions for administering them to a subject
 XX having a condition characterised by unwanted angiogenesis. The method is
 XX useful for inhibiting angiogenesis associated with solid tumour growth,
 XX tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
 XX diabetic retinopathy, retinopathy of prematurity, macular degeneration,
 XX corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
 XX rubecosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
 XX neovascularisation, telangiectasia, haemophilic joints, angiodiroma, and
 XX wound granulation, intestinal adhesions, atherosclerosis, scleroderma and

CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
 CC acid of the invention

XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

XX SQ

XX Query Match 0.2%; Score 18; DB 1; Length 18;
 XX Best Local Similarity 100.0%; Pred. No. 5.2e+02;
 XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4481
 XX |||||
 DB 1 TTTT TTTT TTTT TTTT TTTT 18

XX RESULT 925
 XX ABL39401 standard; DNA; 18 BP.

XX ID ABL39401 standard; DNA; 18 BP.

XX AC ABL39401;

XX DT 16-APR-2002 (first entry)

XX DE Immunostimulatory nucleic acid SEQ ID NO: 837.

XX XX Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
 XX angiogenesis; metastasis; cytostatic; ss.

XX OS Synthetic.

XX XX Key Location/Qualifiers
 XX FH modified_base 1..18
 XX FT /*tag= a
 XX FT /mod_base= OTHER
 XX FT /note= "phosphorochioate backbone"

XX PN WO200197843-A2.

XX PD 27-DEC-2001.

XX PF 22-JUN-2001; 2001WO-US020154.

XX PR 22-JUN-2000; 2000US-0213346P.

XX PA (IOWA) UNIV IOWA RES FOUND.

XX PI Weiner G, Hartmann G;

XX PT WPI; 2002-154611/20.

XX DR Treating or preventing cancer, such as basal cell carcinoma, comprises
 XX PT administering immunostimulatory nucleic acids that induce expression of
 XX PT cell surface antigens and antibodies to a subject having or at risk of
 XX PT developing cancer.

XX PS Disclosure; Page 308; 312pp; English.

XX CC The present invention relates to methods for treating or preventing
 XX cancer, involving administering to a subject having or at risk of
 XX developing cancer immunostimulatory nucleic acids that induce expression
 XX of cell surface antigens and antibodies. The methods are useful for
 XX treating or preventing cancer such as basal cell carcinoma, bladder
 XX cancer, bone cancer, brain and central nervous system (CNS) cancer,
 XX breast cancer, cervical cancer, colon and rectum cancer, connective
 XX tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
 XX cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
 XX Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
 XX cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
 XX cancer, stomach cancer, testicular cancer, and uterine cancer. The
 XX present sequence is an immunostimulatory oligonucleotide described in the
 XX exemplification of the invention

XX SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

RESULT	928
ABA93239	
ID	ABA93239 standard; DNA; 18 BP.
XX	
AC	ABA93239;
XX	
DT	18-APR-2002 (first entry)
XX	
DE	Adaptor oligonucleotide SEQ ID NO:2.
XX	
KW	Detection; comparative detection; adaptor; ss.
XX	
OS	Synthetic.
XX	
PN	JP2001333800-A.
XX	
PD	04-DEC-2001.
XX	
PF	30-MAY-2000; 2000JP-00160324.
XX	
PR	30-MAY-2000; 2000JP-00160324.
XX	
PA	(UNIT-) UNITECH CO LTD.
XX	
DR	WPI; 2002-135950/18.
XX	
PT	Comparative detection of the amounts of RNA and DNA.
XX	
PS	Disclosure; Page 9; 9pp; Japanese.
XX	
CC	The present invention describes a method for the comparative detection of
CC	the amount of an RNA. The method comprises: (a) cDNAs obtained by
CC	transcribing respectively from at least two tissue RNAs are respectively
CC	fragmented by using a same restriction enzyme; (b) each different adaptor
CC	and a common adaptor are added to each of the cDNA fragments derived from
CC	the same or different tissues by the step (a); (c) the resultant adaptor-
CC	added cDNAs are mixed together; (d) an adaptor primer having the common
CC	sequence to said different adaptor and a gene-specific adaptor are used
CC	to amplify said adaptor-added cDNAs containing no region derived from
CC	polyadenylic acid of the mRNA before the addition of the adaptor among
CC	the adaptor-added cDNAs prepared by the step (b); (e) the ratios of the
CC	cDNA amounts are measured between the tissues; (f) the RNA is detected
CC	from the measured result; (g) each different adaptor and a common adaptor
CC	are added to each of the genomic DNA fragments derived from a same or
CC	different individuals; (h) the resultant adaptor-added genomic DNAs are
CC	mixed together; (i) the adaptor-added genomic DNAs are amplified by using
CC	a adaptor primer having the common sequence to the different adaptor and
CC	a sequence-specific adaptor; and (j) the ratios of the amplified amounts
CC	of the genomic DNAs are measured between the individuals. The method is
CC	used for the detection of the amounts of RNA and DNA. The method is
CC	sequence represents an oligonucleotide which is used in the
CC	exemplification of the present invention
XX	
QY	Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
DB	
Query Match	0.2%; Score 18; DB 1; Length 18;
Best Local Similarity	100.0%; Pred.No. 5.2e+02;
Matches 18; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	4464 TTTT TTTTTTTTTTTTTTT 4461 TTTTTTTTTTTTTTTTTTT 18
RESULT 929	
AAD56466/c	
ID	AAD56466 standard; RNA; 18 BP.
XX	
AC	AAD56466;
XX	
DT	07-AUG-2003 (first entry)
XX	
DE	Target RNA #1 used in the exemplification of the invention.

XX	. Acyclic linker; gene expression; gene therapy; ss.
XX	unidentified.
OS	
XX	
PN	WO2003037909-A1.
XX	
PD	08-MAY-2003.
PF	29-OCT-2002; 2002WO-CA001628.
XX	
PR	29-OCT-2001; 2001US-0330719P.
XX	
PA	(UTMC-) UNIV MCGILL.
PI	Damba MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;
XX	
DR	WPI; 2003-421516/39.
XX	
PT	Novel acyclic linker-containing oligonucleotide useful for preventing or
PT	decreasing translation, reverse transcription and/or replication of a
XX	target RNA in a system, comprises a modified deoxyribonucleotide.
PS	Example 2; Fig 5; 104pp; English.
XX	
CC	The invention relates to an acyclic linker-containing oligonucleotide
CC	comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC	the invention are useful for preventing or decreasing translation,
CC	reverse transcription and/or replication of a target RNA in a system.
CC	They are useful for selectively preventing gene expression in a sequence-
CC	specific manner, for hybridising to complementary RNA such as cellular
CC	mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC	RNA. They are also useful therapeutically in formulations or medicaments
CC	to prevent or treat a disease characterised by the expression of a
CC	particular target RNA. The invention is used in gene therapy. The present
XX	sequence is a target RNA, used in the exemplification of the invention
SQ	Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match	0.2%; Score 18; DB 1; Length 18;
Best Local Similarity	100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	4464 TTTTTTTTTTTTTTTTTT 4481 18 TTTTTTTTTTTTTTTT 1
DB	
RESULT 930	
AAD56440	
ID	AAD56440 standard; DNA; 18 BP.
XX	
AC	AAD56440;
XX	
DT	07-AUG-2003 (first entry)
XX	
DE	Antisense oligo #1, to elicit RNase H degradation of target RNA.
XX	
KM	Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
XX	antisense; ss.
OS	Unidentified.
XX	
PN	WO2003037909-A1.
XX	
PD	08-MAY-2003.
XX	
PP	29-OCT-2002; 2002WO-CA001628.
XX	
PR	29-OCT-2001; 2001US-0330719P.
XX	
PA	(UTMC-) UNIV MCGILL.
XX	

PI Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;
 XX
 XX WPI; 2003-421516/39.
 DR
 PT Novel acyclic linker-containing oligonucleotide useful for preventing or
 PT decreasing translation, reverse transcription and/or replication of a
 PT target RNA in a system, comprises a modified deoxyribonucleotide.
 XX
 PS Example 2; Fig 9; 104pp; English.
 XX
 CC The invention relates to an acyclic linker-containing oligonucleotide
 CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of
 CC the invention are useful for preventing or decreasing translation,
 CC reverse transcription and/or replication of a target RNA in a system.
 CC They are useful for selectively preventing gene expression in a sequence-
 CC specific manner, for hybridising to complementary RNA such as cellular
 CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary
 CC RNA. They are also useful therapeutically in formulations or medicaments
 CC to prevent or treat a disease characterised by the expression of a
 CC particular target RNA. The invention is used in gene therapy. The present
 CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)
 CC H degradation of target RNA. This sequence is used in the exemplification
 CC of the invention
 CC
 SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
 Query Match 0.2%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 5.2e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4464 TTTT TTTT TTTT TTTT TTTT 4481
 DB 1 TTTT TTTT TTTT TTTT TTTT 18
 RESULT 931
 AAD56446 standard; DNA; 18 BP.
 ID AAD56446
 XX
 AC AAD56446;
 XX
 DT 07-AUG-2003 (first entry)
 XX
 DE 2'-F-ANA antisense oligo #1, to elicit RNase H degradation of target RNA.
 XX
 XX ACyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
 KM antisense; ss.
 KW
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..18
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "2'-deoxy-2'-fluoroarabinothymidine"
 FT
 XX
 XX WO2003037909-A1.
 XX
 XX PD 08-MAY-2003.
 XX
 XX PF 29-OCT-2002; 2002WO-CA001628.
 XX
 XX PR 29-OCT-2001; 2001US-0330719P.
 XX
 XX PA (UVMC-) UNIV MCGILL.
 XX
 PI Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;
 XX
 DR WPI; 2003-421516/39.
 XX
 PT Novel acyclic linker-containing oligonucleotide useful for preventing or
 PT decreasing translation, reverse transcription and/or replication of a
 PT target RNA in a system, comprises a modified deoxyribonucleotide.

XX
 PS Example 2; Fig 7; 104pp; English.
 XX
 CC The invention relates to an acyclic linker-containing oligonucleotide
 CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of
 CC the invention are useful for preventing or decreasing translation,
 CC reverse transcription and/or replication of a target RNA in a system.
 CC They are useful for selectively preventing gene expression in a sequence-
 CC specific manner, for hybridising to complementary RNA such as cellular
 CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary
 CC RNA. They are also useful therapeutically in formulations or medicaments
 CC to prevent or treat a disease characterised by the expression of a
 CC particular target RNA. The invention is used in gene therapy. The present
 CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)
 CC H degradation of target RNA. This sequence is used in the exemplification
 CC of the invention
 CC
 SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
 Query Match 0.2%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 5.2e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4464 TTTT TTTT TTTT TTTT TTTT 4481
 DB 1 TTTT TTTT TTTT TTTT TTTT 18
 RESULT 932
 ACH03247 standard; DNA; 18 BP.
 ID ACH03247
 XX
 AC ACH03247;
 XX
 DT 25-SEP-2003 (first entry)
 XX
 DE Immunostimulatory nucleic acid #882.
 XX
 XX Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
 KW antitumor; gene therapy; vaccine; non-allergic inflammatory disease;
 KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
 XX
 OS Synthetic.
 XX
 PN US2003050268-A1.
 XX
 XX PD 13-MAR-2003.
 XX
 XX PF 29-MAR-2002; 2002US-00112653.
 XX
 XX PR 29-MAR-2001; 2001US-0279642P.
 XX
 XX PA (KRIE/) KRIEG A M.
 XX (BERG/) BERG D J.
 XX
 XX PI Krieg AM, Berg DJ;
 XX
 XX DR WPI; 2003-521815/49.
 XX
 XX PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
 XX PT allergic contact dermatitis, latex dermatitis or inflammatory bowel
 XX PT disease by administering an immunostimulatory nucleic acid.
 XX
 XX PS Disclosure; Page 33; 229pp; English.
 XX
 CC The invention describes a method of treating non-allergic inflammatory
 CC disease comprising administering to a subject having or at risk of
 CC developing a non-allergic inflammatory disease an immunostimulatory
 CC nucleic acid for prevention or treatment of the disease. The method is
 CC useful for treating non-allergic inflammatory diseases, such as
 CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
 CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.

CC This sequence represents an immunostimulatory nucleic acid
 XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
 SQ

Query Match 0.2%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 5.2e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4481
 DB 1 TTTT TTTT TTTT TTTT TTTT 18

RESULT 933
 AAD57871
 ID AAD57871 standard; DNA; 18 BP.

AC AAD57871;
 XX
 DT 20-NOV-2003 (first entry)
 XX

DE Antisense oligo #1 used in the exemplification of the invention.

XX Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
 KW hepatitis B; gene therapy; virucide; anti-HIV; antisense; ss.

XX Unidentified.

OS WO2003064441-A2.

XX PD 07-AUG-2003.

PF 31-JAN-2003; 2003WO-CA000129.

PR 01-FEB-2002; 2002US-0352873P.

PA (UWMC-) UNIV MCGILL.

PI Damha MJ, Parniak MA;

XX WPI; 2003-689523/65.

PT New oligonucleotide, useful for preventing or treating a disease related
 PT to a target RNA in a system, e.g., AIDS or hepatitis B.
 XX

PS Example 2; Page 35; 73pp; English.

CC The present invention relates to a new oligonucleoside which comprises
 CC alternating first and second segments. The first segment comprises at
 CC least one sugar modified nucleoside. The second segment comprises at
 CC least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of
 CC each of the first and second segments, so that it comprises at least 4
 CC alternating segments. The oligonucleoside is useful for preparing a
 CC composition for inducing RNase H-mediated cleavage of a target RNA in a
 CC system, preventing or decreasing translation, transcription or
 CC replication of a target RNA in a system, detecting the presence of a
 CC target RNA in a system, validating a gene target corresponding to a
 CC target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)
 CC or hepatitis B. The invention is useful in gene therapy. The present
 CC sequence is an antisense oligonucleoside used in the exemplification of
 CC the invention
 XX

SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.2%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 5.2e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4481
 DB 1 TTTT TTTT TTTT TTTT TTTT 18

RESULT 934
 AAD57878
 ID AAD57878 standard; DNA; 18 BP.

AC AAD57878;
 XX

DT 20-NOV-2003 (first entry)
 XX

DE Antisense DNA-RNA hybrid #2 used in the exemplification of the invention.

XX Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
 KW hepatitis B; gene therapy; virucide; anti-HIV; antisense; DNA-RNA hybrid;
 KW ss.
 XX

OS Unidentified.

XX Key Location/Qualifiers

FT misc_RNA

FT misc_RNA

FT misc_RNA

FT misc_RNA

FT misc_RNA

FT misc_RNA

FT misc_RNA

FT misc_RNA

FT misc_RNA

FT misc_RNA

FT misc_RNA

FT misc_RNA

FT misc_RNA

FT misc_RNA

FT misc_RNA

FT misc_RNA

FT misc_RNA

FT misc_RNA

FT misc_RNA

FT misc_RNA

FT misc_RNA

FT misc_RNA

FT misc_RNA

FT misc_RNA

FT misc_RNA

FT misc_RNA

FT misc_RNA

FT misc_RNA

FT misc_RNA

FT misc_RNA


```

PS      Example 2; Page 35; 73pp; English.
XX
CC      The present invention relates to a new oligonucleoside which comprises
CC      alternating first and second segments. The first segment comprises at
CC      least one sugar modified nucleoside. The second segment comprises at
CC      least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of
CC      each of the first and second segments, so that it comprises at least 4
CC      alternating segments. The oligonucleotide is useful for preparing a
CC      composition for inducing RNase H-mediated cleavage of a target RNA in a
CC      system, preventing or decreasing translation, transcription or
CC      replication of a target RNA in a system, detecting the presence of a
CC      target RNA in a system, validating a gene target corresponding to a
CC      target RNA in a system or preventing or treating a disease related to a
CC      target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)
CC      or hepatitis B. The invention is useful in gene therapy. The present of
CC      sequence is an antisense DNA-RNA hybrid used in the exemplification of
CC      the invention
XX
SQ      Sequence 18 BP; 0 A; 0 C; 0 G; 9 T; 9 U; 0 Other;
XX
Query Match          0.2%; Score 18; DB 1; Length 18;
Best Local Similarity 50.0%; Pred. No. 5,2e+02;
Matches    9; Conservative    9; Mismatches    0; Indels    0; Gaps    0;
OY      4464 TTTTYYYYTTTTTTTT 4481
       :|:|:|:|:|:|:|:|:|:|
DB      1 UTUTUTUTUTUTUTUTUT 18
RESULT 937
AAD57890/C
ID      AAD57890 standard; RNA; 18 BP.
XX
AC      AAD57890;
XX
DT      20-NOV-2003 (first entry)
DS      Target RNA #1 used in RNase H assay.
XX
KW      Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
KW      hepatitis B; gene therapy; virucide; anti-HIV; ss.
XX
OS      Unidentified.
XX
WO      WO2003064441-A2.
XX
PD      07-AUG-2003.
XX
PF      31-JAN-2003; 2003WO-CANO00129.
XX
PR      01-FEB-2002; 2002US-0352873P.
XX
PA      (UYMC-) UNIV MCGILL.
XX
PI      Damha MJ, Parniak MA;
DR      WPI; 2003-689523/65.
XX
New oligonucleotide, useful for preventing or treating a disease related
PT      to a target RNA in a system, e.g., AIDS or hepatitis B.
XX
Example 4; Page 38; 73pp; English.
XX
The present invention relates to a new oligonucleoside which comprises
CC      alternating first and second segments. The first segment comprises at
CC      least one sugar modified nucleoside. The second segment comprises at
CC      least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of
CC      each of the first and second segments, so that it comprises at least 4
CC      alternating segments. The oligonucleotide is useful for preparing a
CC      composition for inducing RNase H-mediated cleavage of a target RNA in a
CC      system, preventing or decreasing translation, transcription or
CC      replication of a target RNA in a system, detecting the presence of a

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```

CC target RNA in a system, validating a gene target corresponding to a
CC target RNA in a system or preventing or treating a disease related to a
CC target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)
CC or hepatitis B. The invention is useful in gene therapy. The present
CC sequence is a target RNA used in RNase H assay. This sequence is used in
CC the exemplification of the invention
SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.2%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 4464 TTTTTTTTTTTTTTTTTT 4481
|||||
Db TTTTTTTTTTTTTTTTTT 1

RESULT 938
ADB37210
ID ADB37210 standard; DNA; 18 BP.
XX
XX ADB37210;
AC
DT 04-DEC-2003 (first entry)
DE Immunostimulatory nucleic acid #824.
XX
XX ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW hypo-responsive subject; immunostimulatory.
XX Synthetic.
OS
XX US2003087848-A1.
PN
XX 08-MAY-2003.
PD
XX 02-FEB-2001; 2001US-00776479.
PF
XX 03-FEB-2000; 2000US-0179991P.
PR
XX (BRAT/) BRATZLER R L.
XX (PETE/) PETERSEN D M.
PA (FOUR/) FOURN Y.
XX
XX Bratzler RL, Petersen DM, Fourn Y;
PI
XX WPI; 2003-657977/62.
DR
XX
XX Treating and/or preventing allergy or asthma using an immunostimulatory
XX nucleic acid alone or in combination with an asthma/allergy medicament.
XX
XX Disclosure; Page 17; 221pp; English.
XX
XX The invention relates to a method of treating or preventing allergy or
XX asthma which comprises administering to a subject a poly-G nucleic acid
XX in an aerosol formulation. The methods and compositions of the present
XX invention are useful for diagnosing and/or treating asthma and allergy
XX especially in a hypo-responsive subject. The present sequence represents
XX an immunostimulatory nucleic acid of the invention.
CC
CC
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.2%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 4464 TTTTTTTTTTTTTTTTTT 4481
|||||
Db TTTTTTTTTTTTTTTTTT 18

RESULT 939

```

ADBB37236
ID ADB37236 standard; DNA; 18 BP.
XX
AC ADB37236;
XX
DT 04-DEC-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #850.
XX
KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW hypo-responsive subject; immunostimulatory.
XX
OS Synthetic.
XX
PN US2003087848-A1.
XX
PD 08-MAY-2003.
XX
PE 02-FEB-2001; 2001US-0076479.
XX
PR 03-FEB-2000; 2000US-0179991P.
XX
PA (BRAT/) BRATZLER R L.
PA (PETE/) PETERSEN D M.
PA (FOUR/) FOURON Y.
XX
PI Bratzler RL, Petersen DM, Fouron Y;
DR WPI; 2003-657977/62.
XX
PT Treating and/or preventing allergy or asthma using an immunostimulatory
PT nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS Disclosure; Page 18; 221pp; English.
XX
SC The invention relates to a method of treating or preventing allergy or
CC asthma which comprises administering to a subject a poly-G nucleic acid
CC in an aerosol formulation. The methods and compositions of the present
CC invention are useful for diagnosing and/or treating asthma and allergy
CC especially in a hypo-responsive subject. The present sequence represents
XX an immunostimulatory nucleic acid of the invention.
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
QY Query Match; 0.2%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
4464 TTTTTTTTTTTTTTTTTT 4481
1 TTTTTTTTTTTTTTTTTT 18
RESULT 940
ADE77617/C
ID ADE77617 standard; DNA; 18 BP.
XX
AC ADE77617;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human probe NEG for elongation mediated multiplexed analysis of HLA-DR.
XX
KW probe; ss; negative control; CPTB; human leukocyte antigen; HLA;
KW genetic testing; carrier screening; genotyping; profiling; polymorphic;
KW multiplexed elongation assay; enzymatic recognition;
XX cyclic fibrosis conductance transmembrane regulator.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003034029-A2.
XX

24-APR-2003 .
15-OCT-2002; 2002MO-US033012.
15-OCT-2001; 2001US-0329427P.
15-OCT-2001; 2001US-0329428P.
15-OCT-2001; 2001US-0329619P.
15-OCT-2001; 2001US-0329620P.
14-MAR-2002; 2002US-0364416P.
(BIOA-) BIOARRAY SOLUTIONS LTD.
Li AX, Hashmi G, Seul M;
WPI; 2003-393553/37.
Concurrent interrogation of a number of polymorphic sites, useful for genetic testing, carrier screening, genetic profiling, and identity testing, comprises conducting a multiplexed elongation assay using probes.
Example 9; Page 46; 143pp; English.
This invention relates to a novel method for the concurrent interrogation of a number of polymorphic sites in the presence of, and without interference from, non-designated polymorphic sites. Specifically, it comprises conducting a multiplexed elongation assay by applying one or more temperature cycles to achieve linear amplification of the target or a combination of annealing and elongation steps under temperature-controlled conditions. Furthermore, this detection method uses probe extension or elongation and relies on enzymatic recognition, a superior technique that no longer depends on differential hybridisation. The present invention describes probes and methods useful for identifying or detecting polymorphisms at one or more designated sites, such that they can identify mutations within the cystic fibrosis conductance transmembrane regulator (CFTR) or the human leukocyte antigen (HLA) genes. In addition, concurrent interrogation of a multiplicity of polymorphic sites is useful for genetic testing, carrier screening, genotyping or genetic profiling, and identity testing. This oligonucleotide is the negative control probe used for the elongation mediated multiplexed analysis of HLA-DR, in an exemplification of the invention.
Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 0.2%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTTTTTTTTTTTTTTTT 4481
|||
DB 18 TTTTTTTTTTTTTTTTTT 1
RESULT 941
AA075548
ID AA075548 standard; DNA; 19 BP.
AC AA075548;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
XX Synthetic.
OS
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX


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XX Tailing reaction; tailed primer; primer; probe; identification;
KM detection; linear amplification scheme; chain extending enzyme;
KM telomerase; ss.
XX Synthetic.
XX Key Location/Qualifiers
FT misc_RNA 19 /tag= a
FT 19
XX US2002031776-A1.
XX 14-MAR-2002.
XX 26-JUL-2001; 2001US-00917138.
XX 28-MAY-1999; 99US-0136545P.
XX 25-MAY-2000; 2000US-00580358.
XX (TULLIS/) TULLIS R H.
XX (STREIF/) STREIFEL J A.
XX Tullis RH, Streifel JA;
XX WPI; 2002-361176/39.
XX Identifying and detecting nucleic acid, particularly DNA hybridization
PT probes, involves employing chain extending enzymes (e.g. telomerase) to
PT elongate probes to render them readily detectable.
XX Example 1; Page 5; 10pp; English.
XX The present invention describes a method for detecting a nucleic acid
CC probe, which comprises using chain extending enzymes to elongate probes.
CC The method comprises: (a) treating the sample with a chain terminating
CC reagent to prevent polynucleotide chain growth from the nucleic acid in
CC the sample; (b) contacting the sample with the probe containing a
CC terminus capable of elongation by a chain extending enzyme, where the
CC probe hybridises to the nucleic acid in the sample; (c) contacting the
CC sample with a chain extending enzyme and its substrates, which elongates
CC the probe; and (d) detecting the elongated hybridised probe. Also
CC described is a method comprising: (a) treating nucleic acid molecules or
CC modified nucleic acids in a sample with a reagent or reagents that render
CC the nucleic acid chains unextendable by a non-template-dependent enzyme;
CC (b) hybridising the treated molecules with a nucleic acid probe that
CC includes an extendable terminus, under conditions where hybrids form; and
CC (c) treating any hybrids formed with a non-template dependent chain
CC elongating enzyme and its substrates, where any hybridised probe is
CC extended. The method is useful for identifying and detecting nucleic
CC acids, particularly DNA hybridisation probes. The present sequence
CC represents a tailing reaction exemplary primer, which is used in an
CC example from the present invention
XX Sequence 19 BP; 18 A; 0 C; 0 G; 0 T; 1 U; 0 Other;
SQ
Query Match 0.2%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4464 TTTT TTTT TTTT TTTT TTTT 4481
Db 18 TTTT TTTT TTTT TTTT TTTT 1

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DE Synthetic nuclease-resistant oligomeric compound #54.
XX Nuclease resistant; ds; pharmaceutical; topical administration;
KM transdermal patch; enzymatic degradation resistant.
XX Synthetic.
XX Key Location/Qualifiers
FT modified_base 19 /tag= a
FT 19 /mod_base= OTHER
FT 19 /note= "phenoxazine"
XX WO2003004602-A2.
XX 16-JAN-2003.
XX 01-JUL-2002; 2002WO-US020934.
XX 03-JUL-2001; 2001US-0302682P.
XX 28-NOV-2001; 2001US-00962292.
XX 10-DEC-2001; 2001US-00013295.
XX (ISIS-) ISIS PHARM INC.
XX Manoharan M, Maier MA, Prakash TP, Rajeev KG;
XX WPI; 2003-256318/25.
XX Nuclease-resistant oligomeric compound useful as pharmaceuticals for
PT topical administration such as transdermal patches.
XX Disclosure; Page 234; 234pp; English.
XX The invention relates to novel nuclease-resistant oligomeric compounds.
CC The compounds of the invention are useful as pharmaceuticals for topical
CC administration such as transdermal patches. The oligomeric compound is
CC resistant to enzymatic degradation. The sequences shown in AB275345-
CC AB275399 represent the nuclease-resistant compounds of the invention
XX Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
SQ
Query Match 0.2%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4464 TTTT TTTT TTTT TTTT TTTT 4481
Db 1 TTTT TTTT TTTT TTTT TTTT 18

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RESULT 945
AB275398
ID AB275398 standard; DNA; 19 BP.
XX
AC AB275398;
XX
DT 07-MAY-2003 (first entry)
XX

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RESULT 946
AB275399
ID AB275399 standard; DNA; 19 BP.
XX
AC AB275399;
XX
DT 07-MAY-2003 (first entry)
XX
DB Synthetic nuclease-resistant oligomeric compound #55.
KM Nuclease resistant; ds; pharmaceutical; topical administration;
KM transdermal patch; enzymatic degradation resistant.
XX Synthetic.
XX Key Location/Qualifiers
FT modified_base 19 /tag= a
FT 19 /mod_base= OTHER
FT 19 /note= "G-clamp modification"
XX
XX WO2003004602-A2.

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XX 16-JAN-2003.
PD
XX 01-JUL-2002; 2002WO-US020934.
XX
XX 03-JUL-2001; 2001US-0302682P.
XX PR 28-NOV-2001; 2001US-00996292.
XX PR 10-DEC-2001; 2001US-00013295.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Maier MA, Prakash TP, Rajeev KG;
XX WPI; 2003-256318/25.
XX
XX Nuclease-resistant oligomeric compound useful as pharmaceuticals for
XX topical administration such as transdermal patches.
XX
XX Disclosure; Page 234; 234pp; English.
XX
XX The invention relates to novel nuclease-resistant oligomeric compounds.
XX The compounds of the invention are useful as pharmaceuticals for topical
XX administration such as transdermal patches. The oligomeric compound is
XX resistant to enzymatic degradation. The sequences shown in ABZ75345-
XX ABZ75399 represent the nuclease-resistant compounds of the invention
XX
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
SQ
XX
XX Query Match 0.2%; Score 18; DB 1; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 5.6e+02;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX
QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4481
DB 1 TTTT TTTT TTTT TTTT TTTT 18
XX
RESULT 947
AAQ75559
ID AAQ75559 standard; DNA; 20 BP.
XX
XX AAQ75559;
AC
XX
XX 04-AUG-1995 (first entry)
DT
XX
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
XX Synthetic.
OS
XX
XX JP06303997-A.
PN
XX
XX 01-NOV-1994.
PD
XX
XX 16-APR-1993; 93JP-00112515.
PF
XX
XX 16-APR-1993; 93JP-00112515.
PR
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX
XX WPI; 1995-018287/03.
DR
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
PT
XX
XX Disclosure; Page 5; 11pp; Japanese.
PS
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENBSEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse

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CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
CC
xx
SQ Sequence 20 BP; 0 A; 0 C; 3 G; 17 T; 0 U; 0 Other;
SQ
  Query Match          0.2%; Score 18; DB 1; Length 20;
  Best Local Similarity 100.0%; Pred. No. 6e+02;
  Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  OY 4467 TTTTTTTTTTTTTTTG 4484
      |||||
      1 TTTTTTTTTTTTTTTG 18
  DB
RESULT 948
AAQ75563
ID AAQ75563 standard; DNA; 20 BP.
XX
XX AAQ75563;
XX
XX 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX
XX WPI, 1995-018287/03.
XX
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENBSEQ files AAQ75547-075798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX
XX Sequence 20 BP; 1 A; 0 C; 2 G; 17 T; 0 U; 0 Other;
XX
  Query Match          0.2%; Score 18; DB 1; Length 20;
  Best Local Similarity 100.0%; Pred. No. 6e+02;
  Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  OY 4467 TTTTTTTTTTTTTTTG 4484
      |||||
      1 TTTTTTTTTTTTTTTG 18
  DB
RESULT 949
AAQ75572
ID AAQ75572 standard; DNA; 20 BP.
XX
XX AAQ75572;
XX

```

XX 04-AUG-1995 (first entry)
 DT Reverse transcription primer used in cDNA analysis technique.
 DE
 XX Analysis; gene expression; reverse transcription; primer; cDNA;
 KM aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX JP06303997-A.
 PN
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 5; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SO Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
 XX
 QY Query Match 0.2%; Score 18; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 TTTT TTTT TTTT TTTT TTTT G 4484
 1 TTTT TTTT TTTT TTTT TTTT G 18
 RESULT 950
 AAQ75560
 ID AAQ75560 standard; DNA; 20 BP.
 AC
 XX AAQ75560;
 DT
 XX 04-AUG-1995 (first entry)
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KM Analysis; gene expression; reverse transcription; primer; cDNA;
 KM aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX JP06303997-A.
 PN
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 DR WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 5; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SO Sequence 20 BP; 1 A; 0 C; 2 G; 17 T; 0 U; 0 Other;
 XX
 QY Query Match 0.2%; Score 18; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 TTTT TTTT TTTT TTTT TTTT G 4484
 1 TTTT TTTT TTTT TTTT TTTT G 18
 RESULT 951
 AAQ75564
 ID AAQ75564 standard; DNA; 20 BP.
 AC
 XX AAQ75564;
 DT
 XX 04-AUG-1995 (first entry)
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KM Analysis; gene expression; reverse transcription; primer; cDNA;
 KM aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX JP06303997-A.
 PN
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 5; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SO Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 U; 0 Other;
 XX
 QY Query Match 0.2%; Score 18; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4467 TTTTTTTTTTTTTTG 4484
 |||||
 XX 1 TTTTTTTTTTTTTTG 18

RESULT 952
 AAQ75565
 ID AAQ75565 standard; DNA; 20 BP.

AC AAQ75565;

DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

KW Analysis; gene expression; reverse transcription; primer; cDNA;
 aggregate; restriction enzyme; ss.

OS Synthetic.

PN JP06303997-A.

XX 01-NOV-1994.

PF 16-APR-1993; 93JP-00112515.

PR 16-APR-1993; 93JP-00112515.

PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

DR WPI; 1995-018287/03.

PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 by digestion with restriction enzymes.

PS Disclosure; Page 5; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 labelled reverse transcription primers (GENESBQ files AAQ75547-075798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily.

XX Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.2%; Score 18; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4467 TTTTTTTTTTTTTTG 4484
 |||||
 DB 1 TTTTTTTTTTTTTTG 18

RESULT 953
 AAQ75573
 ID AAQ75573 standard; DNA; 20 BP.

AC AAQ75573;

DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

KW Analysis; gene expression; reverse transcription; primer; cDNA;
 aggregate; restriction enzyme; ss.

OS Synthetic.

PN JP06303997-A.

XX 01-NOV-1994.
 PD 16-APR-1993; 93JP-00112515.
 PF 16-APR-1993; 93JP-00112515.
 PR 16-APR-1993; 93JP-00112515.
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 DR WPI; 1995-018287/03.

XX 01-NOV-1994.

PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 by digestion with restriction enzymes.

PS Disclosure; Page 5; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESBQ files AAQ75547-075798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily.

XX Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 0.2%; Score 18; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4467 TTTTTTTTTTTTTTG 4484
 |||||
 DB 1 TTTTTTTTTTTTTTG 18

RESULT 954
 AAQ75571
 ID AAQ75571 standard; DNA; 20 BP.

AC AAQ75571;

DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

KW Analysis; gene expression; reverse transcription; primer; cDNA;
 aggregate; restriction enzyme; ss.

OS Synthetic.

PN JP06303997-A.

XX 01-NOV-1994.

PF 16-APR-1993; 93JP-00112515.

PR 16-APR-1993; 93JP-00112515.

PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

DR WPI; 1995-018287/03.

PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 by digestion with restriction enzymes.

PS Disclosure; Page 5; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESBQ files AAQ75547-075798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of

CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX

XX Sequence 20 BP; 0 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 0.2%; Score 18; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4467 TTTT TTTT TTTT TTTT TTTT G 4484
 Db 1 TTTT TTTT TTTT TTTT TTTT G 18

RESULT 955
 ID AAV68372/c
 XX AAV68372 standard; DNA; 20 BP.

XX AAV68372;

XX 10-MAR-1999 (first entry)

DE Adapter primer oligonucleotide #11 for CAG repeat analysis.

KM CAG repeat; human; genome analysis; adapter primer; medical diagnostic;
 KW nucleic acid analysis; variation assessment; neurological disease;
 KM Huntington's chorea; PCR suppression; ss.

XX Synthetic.

XX WO9849345-A1.

XX 05-NOV-1998.

XX 29-APR-1998; 98WO-US008616.

XX 29-APR-1997; 97US-0045078P.

XX (UYBO-) UNIV BOSTON.

XX Smith CL;

XX WPI; 1998-594983/50.

PT Analysing nucleic acid samples - using amplification primers which
 PT contain CAG or CTG trinucleotide repeats for differential display of
 PT samples from different sources.

XX Example; Page 31; 44pp; English.

XX This sequence represents an adapter primer oligonucleotide. It was used
 CC to isolate CAG repeat containing sequences from the human genome to test
 CC the method of the invention. The method is for analysing nucleic acids in
 CC a sample, and comprises: (a) providing a sample containing nucleic acid,
 CC a first oligonucleotide primer comprising a CTG repeat, a second
 CC oligonucleotide primer comprising a CAG repeat and a polymerase and PCR
 CC reagents; (b) preparing said nucleic acid so that it is amplifiable; (c)
 CC amplifying the nucleic acid with the first and second primers; and (d)
 CC detecting the amplified product. The method is used to distinguish
 CC between the expression of genes in two or more biological samples, e.g.
 CC body fluids, cells, solid tissue or solid and liquid foods. It can be
 CC used in medical diagnostics, e.g. to differentiate between normal and
 CC diseased tissue or to assess the variation within monozygotic twin pairs.
 CC The method allows the isolation and analysis of genome subsets containing
 CC CAG repeats which are known to be important in a number of neurological
 CC diseases including Huntington's chorea. The method uses PCR suppression,
 CC in which only fragments which contain a target repeat are efficiently
 CC amplified. This allows accurate identification of differentially
 CC expressed genes in various cell types. Genome complexity is reduced by
 CC the new method which targets genomic subsets containing CAG repeats
 XX
 XX Sequence 20 BP; 1 A; 6 C; 6 G; 6 T; 0 U; 1 Other;

Query Match 0.2%; Score 18; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7413 CAGCAGCAGCAGCAGCAG 7430
 Db 20 CAGCAGCAGCAGCAGCAG 3

RESULT 956
 ID AB285312
 XX AB285312 standard; DNA; 20 BP.

XX AB285312;

XX 17-OCT-2003 (first entry)

DE Human oligonucleotide sequence.

KM Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.

XX WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIC-) EPIDERMIS PHARM INC.

XX NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.

XX Claim 15; SEQ ID NO 554; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.2%; Score 18; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4467 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
 |||||
 20 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

Db

RESULT 959
 ADD69519/C
 ID ADD69519 standard; DNA; 20 BP.
 XX
 AC ADD69519;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE ISSR-related PCR primer 6.
 XX
 KM inter-simple sequence repeat; ISSR; SSR; PCR; primer; genotyping; plant;
 KW animal; Basmati rice; ss.
 XX
 OS Unidentified.
 XX
 PN WO2003085133-A2.
 XX
 PD 16-OCT-2003.
 XX
 PF 09-JAN-2003; 2003WO-IB000041.
 XX
 PR 08-APR-2002; 2002IN-CH000260.
 XX
 PA (DNAP-) CENT DNA FINGERPRINTING & DIAGNOSTICS.
 XX
 PI Nagaraaju UG;
 XX
 DR WPI; 2003-804317/75.
 XX
 PT New set of inter-simple sequence repeats (ISSR)-PCR primers for
 PT genotyping eukaryotes, useful for genotyping diverse genomes of plant and
 PT animal systems.
 XX
 PS Disclosure; Page 19; 60pp; English.
 XX
 CC The invention relates to a novel set of inter-simple sequence repeats
 CC (ISSR)-PCR primers for genotyping eukaryotes. The primers of the
 CC invention may be useful for genotyping diverse genomes of plant and
 CC animal systems, in particular for distinguishing Basmati rice varieties
 CC from non-Basmati rice varieties and traditional Basmati rice varieties
 CC from evolved Basmati rice varieties. The current sequence is that of the
 CC ISSR-related PCR primer of the invention.
 XX
 SQ Sequence 20 BP; 1 A; 6 C; 6 G; 6 T; 0 U; 1 Other;

Query Match 0.2%; Score 18; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

7414 AGCAGCAGCAGCAGCAGC 7431
 |||||
 20 AGCAGCAGCAGCAGCAGC 3

Db

RESULT 960
 AAQ75611
 ID AAQ75611 standard; DNA; 21 BP.
 XX
 AC AAQ75611;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.

XX
 KM Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 5; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

SQ Sequence 21 BP; 1 A; 0 C; 3 G; 17 T; 0 U; 0 Other;

Query Match 0.2%; Score 18; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 6.5e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4467 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
 |||||
 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

Db

RESULT 961
 AAQ75630
 ID AAQ75630 standard; DNA; 21 BP.
 XX
 AC AAQ75630;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KM Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.

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PS Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENSEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
OY
Query Match 0.2%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0
4467 TTTTTTTTTTTTTTTG 4484
1 TTTTTTTTTTTTTTTG 18
Db
RESULT 362
AAQ75633
1D AAQ75633 standard; DNA; 21 BP.
XX
AC AAQ75633;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KM Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENSEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;
OY
Query Match 0.2%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0
4467 TTTTTTTTTTTTTTTG 4484
1 TTTTTTTTTTTTTTTG 18
Db

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RESULT	963
AAQ75609	
ID	AAQ75609 standard; DNA; 21 BP.
XX	
AC	AAQ75609;
XX	
DT	04-AUG-1995 (first entry)
XX	
DE	Reverse transcription primer used in cDNA analysis technique.
XX	
KW	Analysis; gene expression; reverse transcription; primer; cDNA;
KW	aggregate; restriction enzyme; ss.
XX	
OS	Synthetic.
XX	
PN	JP06303997-A.
XX	
PD	01-NOV-1994.
XX	
PE	16-APR-1993; 93JP-00112515.
XX	
PR	16-APR-1993; 93JP-00112515.
XX	
PA	(NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX	
DR	WPI; 1995-018287/03.
XX	
PT	Analysis of cDNA and gene expression - by amplification of mRNA followed
XX	by digestion with restriction enzymes.
XX	
PS	Disclosure; Page 5; 11pp; Japanese.
XX	
CC	A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC	double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC	labelled reverse transcription primers (GENBSEQ files AAQ7547-Q75798)
CC	and using the aggregate of mRNAs as the template for each reverse
CC	transcription primer; (b) digesting each of the prepared aggregates of
CC	the double-stranded cDNAs with restriction enzyme and; (c)
CC	electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC	method can be used to analyse gene expression rapidly and easily
XX	
SQ	Sequence 21 BP; 0 A; 0 C; 3 G; 18 T; 0 U; 0 Other;
Query Match	0.2%; Score 18; DB 1; Length 21;
Best Local Similarity	100.0%; Pred. No. 6,5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
Qy	4467 TTTTTTTTTTTTTTTTTTG 4484
Db	1 TTTTTTTTTTTTTTTTTTG 18
RESULT	964
AAQ75626	
ID	AAQ75626 standard; DNA; 21 BP.
XX	
AC	AAQ75626;
XX	
DT	04-AUG-1995 (first entry)
XX	
DE	Reverse transcription primer used in cDNA analysis technique.
XX	
KW	Analysis; gene expression; reverse transcription; primer; cDNA;
KW	aggregate; restriction enzyme; ss.
XX	
OS	Synthetic.
XX	
PN	JP06303997-A.
XX	
PD	01-NOV-1994.
XX	
PE	16-APR-1993; 93JP-00112515.


```
XX 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 6; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily.
XX
XX Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 18; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 6.5e+02;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4467 TTTTTTTTTTTTTTTTG 4484
XX 1 TTTTTTTTTTTTTTTTG 18
XX
XX RESULT 965
XX AAQ75657 standard; DNA; 21 BP.
XX
XX AAQ75657;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 6; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily.
XX
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XX Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 18; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 6.5e+02;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4467 TTTTTTTTTTTTTTTTG 4484
XX 1 TTTTTTTTTTTTTTTTG 18
XX
XX RESULT 966
XX AAQ75661 standard; DNA; 21 BP.
XX
XX AAQ75661;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 6; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily.
XX
XX Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 18; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 6.5e+02;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4467 TTTTTTTTTTTTTTTTG 4484
XX 1 TTTTTTTTTTTTTTTTG 18
XX
XX RESULT 967
XX AAQ75664 standard; DNA; 21 BP.
XX
XX AAQ75664;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
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RESULT 970
AAQ75607 standard; DNA; 21 BP.
AC
XX
AC
XX
AAQ75607;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 0 C; 4 G; 17 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4467 TTTTTTTTTTTTTTTG 4484
DB 1 TTTTTTTTTTTTTTTG 18

RESULT 971
AAQ75629 standard; DNA; 21 BP.
AC
XX
AC
XX
AAQ75629;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX

PR 16-APR-1993; 93JP-00112515.
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4467 TTTTTTTTTTTTTTTG 4484
DB 1 TTTTTTTTTTTTTTTG 18

RESULT 972
AAQ75625 standard; DNA; 21 BP.
AC
XX
AC
XX
AAQ75625;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 0.2%; Score 18; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 6.5e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4467 TTTT TTTT TTTT TTTT TTTT G 4484
 DB 1 TTTT TTTT TTTT TTTT TTTT G 18

RESULT 976

AAQ75665
 ID AAQ75665 standard; DNA; 21 BP.

XX
 AC AAQ75665;

XX 04-AUG-1995 (first entry)

XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;

KM aggregate; restriction enzyme; ss.

XX Synthetic.

OS JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-00112515.

XX 16-APR-1993; 93JP-00112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.

XX Disclosure; Page 7; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX

SQ Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;

Query Match 0.2%; Score 18; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 6.5e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4467 TTTT TTTT TTTT TTTT TTTT G 4484
 DB 1 TTTT TTTT TTTT TTTT TTTT G 18

RESULT 977

AAQ75612
 ID AAQ75612 standard; DNA; 21 BP.

XX
 AC AAQ75612;

XX 04-AUG-1995 (first entry)

XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;

KM aggregate; restriction enzyme; ss.

XX Synthetic.

OS JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-00112515.

XX 16-APR-1993; 93JP-00112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.

XX Disclosure; Page 5; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX

SQ Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 0.2%; Score 18; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 6.5e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4467 TTTT TTTT TTTT TTTT TTTT G 4484
 DB 1 TTTT TTTT TTTT TTTT TTTT G 18

RESULT 978

AAQ75608
 ID AAQ75608 standard; DNA; 21 BP.

XX
 AC AAQ75608;

XX 04-AUG-1995 (first entry)

XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;

KM aggregate; restriction enzyme; ss.

XX Synthetic.

OS JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-00112515.

XX 16-APR-1993; 93JP-00112515.


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XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 6; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESQ files AAQ75547-075798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 18; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 6.5e+02;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 4467 TTTTTTTTTTTTTTTG 4484
DB 1 TTTTTTTTTTTTTTTG 18

RESULT 982
AAQ75628
ID AAQ75628 standard; DNA; 21 BP.
AC AAQ75628;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 6; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of

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XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESQ files AAQ75547-075798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 3 A; 0 C; 1 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 18; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 6.5e+02;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 4467 TTTTTTTTTTTTTTTG 4484
DB 1 TTTTTTTTTTTTTTTG 18

RESULT 983
AAQ75610
ID AAQ75610 standard; DNA; 21 BP.
AC AAQ75610;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESQ files AAQ75547-075798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 0 A; 1 C; 3 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 18; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 6.5e+02;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 4467 TTTTTTTTTTTTTTTG 4484
DB 1 TTTTTTTTTTTTTTTG 18

RESULT 984
AAQ75632

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ID  AAQ75632 standard; DNA; 21 BP.
XX
XX  AAQ75632;
AC
XX  04-AUG-1995 (first entry)
XX
XX  Reverse transcription primer used in cDNA analysis technique.
DE
XX  Reverse transcription primer used in cDNA analysis technique.
XX
XX  Analysis; gene expression; reverse transcription; primer; cDNA;
KM  aggregate; restriction enzyme; ss.
XX
XX  Synthetic.
OS
XX  JP06303997-A.
XX
XX  01-NOV-1994.
PD
XX  16-APR-1993; 93JP-00112515.
XX
XX  16-APR-1993; 93JP-00112515.
XX
XX  16-APR-1993; 93JP-00112515.
XX
XX  (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX  WPI; 1995-018287/03.
XX
XX  Analysis of cDNA and gene expression - by amplification of mRNA followed
PT  by digestion with restriction enzymes.
XX
XX  Disclosure; Page 6; 11pp; Japanese.
XX
XX  A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC  double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC  labelled reverse transcription primers (GENESQ files AAQ75547-075798)
CC  and using the aggregate of mRNAs as the template for each reverse
CC  transcription primer; (b) digesting each of the prepared aggregates of
CC  the double-stranded cDNAs with restriction enzyme and; (c)
CC  electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC  method can be used to analyse gene expression rapidly and easily
XX
XX
SQ  Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match      0.2%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  4467 TTTT TTTT TTTT TTTT TTTT G 4484
    |||||
DB  1 TTTT TTTT TTTT TTTT TTTT G 18

RESULT 985
ID  AAQ75656 standard; DNA; 21 BP.
XX
XX  AAQ75656;
AC
XX  04-AUG-1995 (first entry)
XX
XX  Reverse transcription primer used in cDNA analysis technique.
DE
XX  Reverse transcription primer used in cDNA analysis technique.
XX
XX  Analysis; gene expression; reverse transcription; primer; cDNA;
KM  aggregate; restriction enzyme; ss.
XX
XX  Synthetic.
OS
XX  JP06303997-A.
XX
XX  01-NOV-1994.
PD
XX  16-APR-1993; 93JP-00112515.
XX
XX  16-APR-1993; 93JP-00112515.
XX
XX  16-APR-1993; 93JP-00112515.
XX
XX

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PA  (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX  WPI; 1995-018287/03.
XX
XX  Analysis of cDNA and gene expression - by amplification of mRNA followed
PT  by digestion with restriction enzymes.
XX
XX  Disclosure; Page 6; 11pp; Japanese.
XX
XX  A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC  double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC  labelled reverse transcription primers (GENESQ files AAQ75547-075798)
CC  and using the aggregate of mRNAs as the template for each reverse
CC  transcription primer; (b) digesting each of the prepared aggregates of
CC  the double-stranded cDNAs with restriction enzyme and; (c)
CC  electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC  method can be used to analyse gene expression rapidly and easily
XX
XX
SQ  Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

Query Match      0.2%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  4467 TTTT TTTT TTTT TTTT TTTT G 4484
    |||||
DB  1 TTTT TTTT TTTT TTTT TTTT G 18

RESULT 986
ID  AAQ75624 standard; DNA; 21 BP.
XX
XX  AAQ75624;
AC
XX  04-AUG-1995 (first entry)
XX
XX  Reverse transcription primer used in cDNA analysis technique.
DE
XX  Reverse transcription primer used in cDNA analysis technique.
XX
XX  Analysis; gene expression; reverse transcription; primer; cDNA;
KM  aggregate; restriction enzyme; ss.
XX
XX  Synthetic.
OS
XX  JP06303997-A.
XX
XX  01-NOV-1994.
PD
XX  16-APR-1993; 93JP-00112515.
XX
XX  16-APR-1993; 93JP-00112515.
XX
XX  16-APR-1993; 93JP-00112515.
XX
XX  (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX  WPI; 1995-018287/03.
XX
XX  Analysis of cDNA and gene expression - by amplification of mRNA followed
PT  by digestion with restriction enzymes.
XX
XX  Disclosure; Page 6; 11pp; Japanese.
XX
XX  A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC  double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC  labelled reverse transcription primers (GENESQ files AAQ75547-075798)
CC  and using the aggregate of mRNAs as the template for each reverse
CC  transcription primer; (b) digesting each of the prepared aggregates of
CC  the double-stranded cDNAs with restriction enzyme and; (c)
CC  electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC  method can be used to analyse gene expression rapidly and easily
XX
XX
SQ  Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;

Query Match      0.2%; Score 18; DB 1; Length 21;

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CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c) digesting
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4467 TTTTTTTTTTTTTTTG 4484
DB 1 TTTTTTTTTTTTTTTG 18
XX
RESULT 990
AAQ75662
ID AAQ75662 standard; DNA; 21 BP.
AC AAQ75662;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX
XX
A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4467 TTTTTTTTTTTTTTTG 4484
DB 1 TTTTTTTTTTTTTTTG 18
XX
RESULT 991
AAQ75613
ID AAQ75613 standard; DNA; 21 BP.

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```

XX
XX AAQ75613;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
XX
A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4467 TTTTTTTTTTTTTTTG 4484
DB 1 TTTTTTTTTTTTTTTG 18
XX
RESULT 992
AAF85497
ID AAF85497 standard; DNA; 23 BP.
XX
AC AAF85497;
XX
DT 23-JUL-2001 (first entry)
XX
DE PCR primer for DNA encoding kalata B1 polypeptide fragments.
XX
KW Kalata B2; transgenic plant; cotton; calcium channel binding; pain;
KM stroke; C5a binding; antiinflammatory; PCR primer; ss.
XX
OS Oldenlandia affinis.
XX
PN WO200134829-A2.
XX
PD 17-MAY-2001.
XX
PF 03-NOV-2000; 2000WO-AU001352.
XX
PR 05-NOV-1999; 99AU-00003884.
XX
PR 25-NOV-1999; 99AU-00004235.
XX

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PA (UYOU) UNIV QUEENSLAND.
 PA (UYLA-) UNIV LATROBE.
 XX
 PI Craik DJ, Anderson MA, Jennings CV;
 XX
 DR WPI; 2001-343607/36.
 XX
 PT Novel nucleic acid molecule encoding amino acid sequence capable of
 PT forming cyclic structure, for generating transgenic plants capable of
 PT producing cyclic knotted protein and resistant to pathogens such as
 PT insects.
 XX
 PS Example 10; Fig 1B; 112pp; English.
 XX
 CC PCR primers AAF55495-97 were used to amplify a DNA fragment encoding
 CC Kalata B1. Kalata B1 is a macrocyclic peptide with diverse biological
 CC activities. The Kalata B1 polynucleotide represents a nucleic acid
 CC molecule of the invention. The specification describes nucleic acid
 CC molecules which encode an amino acid sequence which is capable of being
 CC cyclised within a cell or a membrane of a cell to form a cyclic backbone.
 CC The amino acid sequence comprises sufficient disulfide bonds to confer a
 CC stabilized folded structure on the three-dimensional structure of the
 CC backbone. The nucleic acid molecules of the invention are useful for
 CC producing transgenic genetically modified food or non-food crop plants,
 CC in particular cotton. The peptides or proteins can be manipulated to
 CC introduce modulating activity, for modulating activity of calcium channel
 CC binding is useful in treatment of pain or stroke and Csa binding activity
 CC useful as an antiinflammatory agent. The nucleic acid molecules are
 CC useful in the generation of molecules having animal or plant therapeutic
 CC properties as well as in a range of diagnostic, industrial and
 CC agricultural including horticultural applications and for protecting
 CC plants such as crop plants from pest and/or pathogen infestation
 CC
 SQ Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 U; 0 Other;
 XX
 QY
 Db 4463 CTTTCTTTTCTTTTCTTTT 4480
 |||||
 6 CTTTCTTTTCTTTTCTTTT 23
 XX
 RESULT 993
 ABQ73254
 ID ABQ73254 standard; DNA; 24 BP.
 XX
 AC ABQ73254;
 XX
 DT 30-SEP-2002 (first entry)
 XX
 DE Human macro protein 17.49 PCR primer 1 SEQ ID NO.3.
 XX
 KM Human; macro protein 17.49; nerve system disorder disease;
 KM protein metabolic disorder relative disease; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN CN1339462-A.
 XX
 PD 13-MAR-2002.
 XX
 PF 21-AUG-2000; 2000CN-00119647.
 XX
 PR 21-AUG-2000; 2000CN-00119647.
 XX
 PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 XX
 PI Mao Y, Xie Y;
 XX
 DR WPI; 2002-455361/49.
 XX

PT New polypeptide-human macro protein 17.49 and polynucleotide for encoding
 PT such polypeptide.
 XX
 XX
 PS Example 2; Page 18; 32pp; Chinese.
 XX
 CC The present invention describes human macro protein 17.49 (I). Also
 CC described is a process for producing (I) using DNA recombination
 CC technology. (I) and the polynucleotide encoding it can be used for
 CC treating various diseases, such as nerve system disorder disease and
 CC protein metabolic disorder relative disease. The present sequence
 CC represents a PCR primer for (I), which is used in an example from the
 CC present invention
 CC
 SQ Sequence 24 BP; 2 A; 0 C; 4 G; 17 T; 0 U; 1 Other;
 XX
 QY
 Db 4466 TTTTCTTTTCTTTTCTTTT 4484
 |||||
 2 TTTTCTTTTCTTTTCTTTT 20
 XX
 RESULT 994
 ABK12409/C
 ID ABK12409 standard; DNA; 24 BP.
 XX
 AC ABK12409;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE RT-PCR primer #1 for cDNA encoding polypeptide-laminin B210.67.
 XX
 KM Polypeptide-laminin B210.67; embryo development teratogenesis;
 KM cytostatic; reverse transcriptase-PCR; RT-PCR; primer; ss.
 XX
 OS Unidentified.
 XX
 PN CN1328013-A.
 XX
 PD 26-DEC-2001.
 XX
 PF 14-JUN-2000; 2000CN-00116514.
 XX
 PR 14-JUN-2000; 2000CN-00116514.
 XX
 PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 XX
 PI Mao Y, Xie Y;
 XX
 DR WPI; 2002-270054/32.
 XX
 PT Polypeptide-laminin B210.67, useful for treating diseases such as embryo
 PT development teratogenesis.
 XX
 PS Example 2; Page 18 (disclosure); 33pp; Chinese.
 XX
 CC The present invention relates to the isolation of polypeptide-laminin
 CC B210.67, and the polynucleotide encoding it. Also described is the
 CC process for preparing the protein by DNA recombination. The polypeptide
 CC is useful for treating diseases such as embryo development teratogenesis.
 CC The present sequence for reverse transcriptase (RT)-PCR primer #1 is used
 CC with RT-PCR primer #2 (ABK12410) for isolating cDNA encoding polypeptide-
 CC laminin B210.67
 CC
 SQ Sequence 24 BP; 19 A; 2 C; 0 G; 3 T; 0 U; 0 Other;
 XX
 QY
 Db 4464 TTTTCTTTTCTTTTCTTTT 4481
 |||||
 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Query Match 0.2%; Score 18; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX	01-JUN-2000.
PD	
XX	24-NOV-1999; 99AU-00060643.
XX	
PR	25-NOV-1998; 98UP-00333469.
XX	
PA	(REAS-) RES ASSOC REFORESTATION TROPICAL FOREST.
XX	
PI	Hibino T, Koshiyama J;
XX	
DR	WPI; 2000-412598/36.
XX	
PT	Method for obtaining plant DNA fragments useful as novel genetic markers,
PT	comprising digesting plant DNA, subjecting fragments to genome
PT	subtraction and screening the polymorphic fragments.
XX	
PS	Example 1; Page 13; 21pp; English.
XX	
CC	The present sequence is a primer for <i>Acacia auriculiformis</i> . This sequence
CC	was used in RT-PCR reactions to produce cDNA from <i>A. auriculiformis</i> RNA.
CC	The resulting cDNA was amplified via PCR using the present sequence and
CC	another PCR primer (see AAA62141). The PCR product was used as an
CC	expression probe. The expression probe was used to obtain desired DNA
CC	fragments. The plant genetic fragments obtained by this method may be
CC	useful as markers in plant breeding. In addition, genes encoding the DNA
CC	fragments or their promoter regions may be used to modify expression.
CC	(Updated on 06-AUG-2003 to correct OS field.)
XX	
SQ	Sequence 26 BP; 1 A; 4 C; 5 G; 16 T; 0 U; 0 Other;
	Query Match 0.2%; Score 18; DB 1; Length 26;
	Best Local Similarity 80.8%; Pred. No. 8.7e+02;
	Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0
OY	.4455 GGCATGCACCTTTTCTTTTCTTTTCTTTT 4480
DB	1 GGGAGGCCCTTTTCTTTTCTTTTCTTTT 26
RESULT 998	
1D	AAA9111 standard; DNA; 26 BP.
XX	
AC	AAA9111;
XX	
DT	19-JAN-2001 (first entry)
DE	Oligonucleotide sequence #1.
XX	
XX	Cloning; sequencing; circulating subtraction; hybridisation; genetic;
KW	molecular biology; ss.
XX	
OS	Synthetic.
XX	
FN	WO200052200-A1.
XX	
PD	08-SEP-2000.
XX	
XX	25-FEB-2000; 2000WO-CN000036.
XX	
PR	26-FEB-1999; 99CN-00102450.
XX	
PA	(SHAN-) SHANGHAI BIORIGIN GENE DEV CO LTD.
XX	
PI	Mao Y, Xie Y;
XX	
DR	WPI; 2000-572191/53.
XX	
PT	Large-scale cDNA cloning and sequencing by circulating subtraction, for
PT	any cells of certain tissues or species effectively and comprehensively,
PT	applicable in genetics, molecular biology and cDNA cloning areas.
XX	

Example; Page 17; 38pp; Chinese.

The present invention describes a method for cDNA sequencing. The method comprises constructing high-quality cDNA original libraries by 0.5-3 kbase tissue cDNA fragments into a library, homogenising the libraries, choosing 5-500 clones for sequencing DNA, hybridising and subtracting the cDNA homogeneous libraries with synthesised probes basing on the sequenced cDNA clones, and repeating the selection and hybridisation steps 1-500 times. The method can be used for sequencing any cells of certain tissues or species, which is applicable in genetics, molecular biology and cDNA cloning areas. Large-scale cDNA cloning and sequencing can be performance with this method effectively and comprehensively, and a preliminary subtractive hybridisation can also be incorporated. The present sequence represents an oligonucleotide which is used in an example from the present invention

Sequence 26 BP; 3 A; 3 C; 5 G; 15 T; 0 U; 0 Other;

Query Match	0.2%;	Score 18;	DB 1;	Length 26;
Best Local Similarity	80.8%;	Pred. No. 8.7e+02;		
Matches 21;	Conservative 0;	Mismatches 5;	Indels 0;	Gaps

4452 GGTCGATGGACCTTTTTTTTTTTT 4477
1 GGCCGACAGAAATTTTTTTTTTTT 26

RESULT 999
AAK98642/c
ID AAK98642 standard; DNA; 26 BP.
XX AAK98642;
XX
DT 03-MAY-2002 (first entry)
XX
DE Caryopsis specific promoter sequence #2.
XX
KW Caryopsis specific promoter; transgenic plant; plant metabolism;
KM starch biosynthesis; seed development; ds.
XX
OS Unidentified.
XX
PN WO200202785-A1.
XX
PD 10-JAN-2002.
XX
PT 03-JUL-2001; 2001MO-EP007592.
XX
PR 06-JUL-2000; 2000DE-01032379.
PR 26-AUG-2000; 2000DE-01041861.
XX
PA (AVBT) AVENTIS CROPS SCIENCE GMBH.
XX
PI Sprunck S, Kluth A, Becker D, Luetticke S, Loerz H;
XX
DR WPI; 2002-164537/21.
XX
PT New nucleic acid that functions as caryopsis-specific promoter, useful
XX for tissue-selective gene expression or suppression in plants, also
XX related transgenic plants.
XX
PS Claim 1; Page 44; 57pp; German.
XX
CC The present invention provides a number of caryopsis specific promoter
CC sequences. These can be used to provide caryopsis specific expression or
CC suppression of genes in genetically modified plants, particularly
CC monocotyledonous plants. Particularly they are used for targeted
CC alteration of plant metabolism, most particularly for biosynthesis of
CC starch with altered properties, but also modification of other storage
CC substances (polysaccharides, fats, proteins and biopolymeric plastics),
CC especially by regulating genes during seed development. The present
CC sequence is a caryopsis specific promoter of the invention


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XX 01-MAY-1997.
PD 25-OCT-1996; 96WO-US017480.
PF 26-OCT-1995; 95US-0005974P.
PR 11-JAN-1996; 96US-00584040.
XX (RIBO-) RIBOZYME PHARM INC.
PA (CHIR ) CHIRON CORP.
XX
PI Pavco P, Mcswigen J, Stinchcomb D, Escobedo J,
DR WPI; 1997-259017/23.
XX
PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
PS Claim 9; Page 180; 218pp; English.
XX
CC The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX
SQ Sequence 27 BP; 8 A; 4 C; 8 G; 0 T; 6 U; 1 Other;
XX
QY Query Match 0.2%; Score 18; DB 1; Length 27;
Best Local Similarity 59.3%; Pred. No. 9.1e+02;
Matches 16; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
Db 1343 TCAGTCGCTGATGAGATGCCAGCT 1369
1 UAAGUGGCGCUGANGAAGCAAGCUCU 27
XX
RESULT 1003
AAX68333
ID AAX68333 standard; RNA; 27 BP.
XX
AC AAX68333;
XX
DT 28-JUL-1999 (first entry)
XX
DE Human flt1 VEGF receptor hammethead ribozyme #1059.
XX
KM Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KM KDR; hammethead ribozyme; hairpin ribozyme; cleavage;
KM tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KM fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KM foetal liver kinase 1; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9715662-A2.
XX
PD 01-MAY-1997.
XX
PF 25-OCT-1996; 96WO-US017480.
XX
PR 26-OCT-1995; 95US-0005974P.
PR 11-JAN-1996; 96US-00584040.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (CHIR ) CHIRON CORP.

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XX Pavco P, Mcswigen J, Stinchcomb D, Escobedo J;
PI WPI; 1997-259017/23.
XX
PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
PS Claim 9; Page 78; 218pp; English.
XX
CC The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX
SQ Sequence 27 BP; 5 A; 7 C; 7 G; 0 T; 7 U; 1 Other;
XX
QY Query Match 0.2%; Score 18; DB 1; Length 27;
Best Local Similarity 63.0%; Pred. No. 9.1e+02;
Matches 17; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
Db 1343 TCAGTCGCTGATGAGATGCCAGCT 1369
1 UCUGGCGCUGANGAAGCAAGCUCU 27
XX
RESULT 1004
AAX29821/c
ID AAX29821 standard; cDNA; 27 BP.
XX
AC AAX29821;
XX
DT 14-SEP-1998 (first entry)
XX
DE Galectin 9 5' PCR primer.
XX
KM Galectin 9; lectin; human; autoimmune disease; inflammatory disease;
KM asthma; allergy; PCR; primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9815624-A1.
XX
PD 16-APR-1998.
XX
PF 09-OCT-1997; 97WO-US018261.
XX
PR 09-OCT-1996; 96US-0028093P.
PR 09-OCT-1996; 96WO-US015655.
XX
PA (HUMA-) HUMAN GENOME SCI. INC.
XX
PI Ni J, Gentz RL, Ruben SM;
XX
DR WPI; 1998-240812/21.
XX
PT Galectin 8, 9, 10 and 10SV polynucleotides - used for treating cancer,
PT autoimmune diseases, inflammatory diseases, asthma, and allergic
PT diseases.
XX
PS Example 2; Page 37; 118pp; English.
XX
CC This oligonucleotide primer contains a 5' SmaI site followed by
CC nucleotides 19-36 of the novel human galectin 9 protein coding sequence
CC (see AAX29786). It was used as a 5' PCR primer, together with a galectin

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CC 9 3' primer (see AAV29822), to amplify galactin 9 DNA from cDNA clone
 CC ATCC 97733. The PCR product was ligated into vector pA2-GP, and galactin
 CC 9 (see AAW56504) was expressed in *Spodoptera frugiperda* Sf9 insect cells
 CC using a baculovirus expression system. Novel galactins 8, 9, 10 and 10Sv
 CC (see AAW56503-06) are useful for treating cancer, autoimmune diseases,
 CC inflammatory diseases, asthma and allergic diseases
 CC
 SQ Sequence 27 BP; 2 A; 12 C; 9 G; 4 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 18; DB 1; Length 27;
 Best Local Similarity 80.8%; Pred. No. 9.1e+02;
 Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 27 TGGAGCTGCTGCAGGCTCCGCGCGC 52
 DB 26 TGGGAAACCGCTGAAGCCCGGAGCG 1
 RESULT 1005
 AAF74933/c
 ID AAF74933 standard; DNA; 27 BP.
 XX
 AC AAF74933;
 XX
 DT 23-MAY-2001 (first entry)
 XX
 DE CD40L poly-A tract sequence SEQ ID NO:30.
 XX
 KW Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
 KW diagnosis; antiarthritic; antirheumatic; immunosuppressive;
 KW antiinflammatory; inflammatory disease; autoimmune disease; ds.
 XX
 OS Homo sapiens.
 XX
 PI WO200119844-A1.
 XX
 PD 22-MAR-2001.
 XX
 PF 13-SEP-2000; 2000MO-US024966.
 XX
 PR 13-SEP-1999; 99US-0153625P.
 XX
 PA (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
 XX
 PI Crow MK, Li Y;
 XX
 DR WPI; 2001-244776/25.
 XX
 PT New altered CD40L promoter for use in the study, diagnosis and treatment
 PT of a variety of inflammatory disorders and autoimmune diseases, such as
 PT rheumatoid arthritis.
 XX
 PS Example 1; Fig 3; 90pp; English.
 XX
 CC The present invention describes an isolated, purified nucleic acid, which
 CC is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
 CC residues 331-455 of the sequence comprising 455 nucleotides given in
 CC AAF74905 where A in the wild type sequence at position 331 (corresponding
 CC to position -155) is replaced with C. (I) has antiarthritic,
 CC antirheumatic, immunosuppressive and antiinflammatory activities, and can
 CC be used in gene therapy. (I) is useful in the study, diagnosis and
 CC treatment of inflammatory and autoimmune diseases, as well as diseases in
 CC which elevated expression of CD40L is a factor, e.g., rheumatoid
 CC arthritis. The present sequence represents a CD40L poly-A tract sequence
 CC which is used in an example from the present invention
 CC
 SQ Sequence 27 BP; 20 A; 3 C; 1 G; 3 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 18; DB 1; Length 27;
 Best Local Similarity 80.8%; Pred. No. 9.1e+02;
 Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 4458 ATGGACTTTTTTTTTTTTTTTTTT 4483

DB 26 AAGGTTTCGTTTTTTTTTTTTTT 1
 RESULT 1006
 ABK49262/c
 ID ABK49262 standard; DNA; 27 BP.
 XX
 AC ABK49262;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE Human coagulation Factor VII variant [M298K]-FVII primer #2.
 XX
 KW Human; coagulation factor VII; haemostatic; bleeding disorder; primer;
 KW clotting factor deficiency; haemophilia; defective platelet function;
 KW thrombocytopenia; von Willebrand's disease; tissue factor; ss;
 KW site-directed mutagenesis.
 XX
 OS Homo sapiens.
 XX
 PI WO200222776-A2.
 XX
 PD 21-MAR-2002.
 XX
 PF 13-SEP-2001; 2001WO-DK000596.
 XX
 PR 13-SEP-2000; 2000DK-00001361.
 XX
 PR 29-SEP-2000; 2000US-0236455P.
 XX
 PA (NOVO) NOVO NORDISK AS.
 XX
 PI Persson E, Olsen OH;
 XX
 DR WPI; 2002-351879/38.
 XX
 PT New human coagulation factor VII variants having coagulant activity,
 PT useful for treatment or prophylaxis of bleeding disorders in a subject or
 PT for enhancing normal hemostatic system.
 XX
 PS Example 1; Page 38; 64pp; English.
 XX
 CC The invention relates to the human coagulation Factor VII polypeptide and
 CC variants of the amino acid sequence. The protein of the invention is
 CC useful for preparing for medicament for treating a bleeding episode or
 CC for the enhancement of the normal haemostatic system. The protein is
 CC useful for treatment of bleeding disorders in a subject or for the
 CC enhancement of the normal haemostatic system. The factor VII variants may
 CC be used to control bleeding disorders which have several causes such as
 CC clotting factor deficiencies (e.g., haemophilia A and B or deficiency of
 CC coagulation factors XI or VII) or clotting factor inhibitors, or they may
 CC be used to control excessive bleeding occurring in subjects with a
 CC normally functioning blood clotting cascade (no clotting factor
 CC deficiencies or inhibitors against any of the coagulation factors). The
 CC bleedings may be caused by a defective platelet function,
 CC thrombocytopenia or von Willebrand's disease. Factor VIIa variants
 CC exhibit an inherent activity which may be therapeutically useful in
 CC situations where the procoagulant activity is independent of tissue
 CC factor. This sequence represents a primer used to introduce a mutation to
 CC DNA encoding a human coagulation factor VII variant polypeptide
 CC
 SQ Sequence 27 BP; 5 A; 9 C; 8 G; 5 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 18; DB 1; Length 27;
 Best Local Similarity 80.8%; Pred. No. 9.1e+02;
 Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 983 CCAAGAGATCAAGGCTGAAGGTG 1008
 DB 26 CCTGAGCTCAAGGTCTTCAAGGTG 1
 RESULT 1007

AD3511/C
 ID AAD3511 standard; DNA; 27 BP.
 XX
 AC AAD3511;
 XX
 DT 01-JUL-2002 (first entry)
 XX
 DE TTT18Apad_P820-27-0003 probe for calibration of molecular array data.
 XX
 KM Molecular array; probe; ss.
 XX
 OS Unidentified.
 XX
 PN EPL186673-A2.
 XX
 PD 13-MAR-2002.
 XX
 PF 10-SEP-2001; 2001EP-00307665.
 XX
 PR 11-SEP-2000; 2000US-00659173.
 XX
 PA (AGIL-) AGILENT TECHNOLOGIES INC.
 XX
 PI Mabler PK, Delenstarr GC;
 XX
 DR WPI; 2002-282886/33.
 XX
 PT Calibration of molecular array data by employing calibration probes that
 PT generate signals proportional to total concentrations of labeled target
 PT molecules, and molecular arrays incorporating sets of calibration probes.
 XX
 PS Disclosure; Page 14; 32pp; English.
 XX
 CC The invention relates to a method for calibrating data scanned from a
 CC molecular array. The method involves employing calibration probes that
 CC generate signals proportional to the total concentrations of labelled
 CC target molecules to which the molecular array probes are directed over an
 CC entire range of sample solutions and molecular arrays incorporating sets
 CC of calibration probes. Method is useful for calibrating different types
 CC of signals scanned from a molecular array, or calibrating signals scanned
 CC from different molecular arrays. The present sequence is poly (A)
 CC normalisation probe used in calibration of molecular array data
 XX
 SQ Sequence 27 BP; 21 A; 4 C; 0 G; 2 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 18; DB 1; Length 27;
 Best Local Similarity 80.8%; Pred. No. 9.1e+02;
 Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 6454 TTTTGGATCTTTTTCGTT 6479
 DB 26 TTTTGGAGATTTTTCGTTT 1
 XX
 RESULT 1008
 ID AAO75738 standard; DNA; 21 BP.
 XX
 AC AAO75738;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KM Analysis; gene expression; reverse transcription; primer; cDNA;
 KM aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX

PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 8; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESBQ files AAO7547-075798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 17.8; DB 1; Length 21;
 Best Local Similarity 90.5%; Pred. No. 7e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4466 TTTTTCGTTTTCGTC 4486
 DB 1 TTTTTCGTTTTCGTC 21
 XX
 RESULT 1009
 ID AAO75762 standard; DNA; 21 BP.
 XX
 AC AAO75762;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KM Analysis; gene expression; reverse transcription; primer; cDNA;
 KM aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 8; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESBQ files AAO7547-075798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

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XX      SQ      Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;
KM      Query Match      0.2%; Score 17.8; DB 1; Length 21;
KW      Best Local Similarity 90.5%; Pred. No. 7e+02;
XX      Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      4466 TTTTGTGTC 4486
DB      1 TTTTTCATC 21

RESULT 1010
AAQ75675
ID      AAQ75675 standard; DNA; 21 BP.
XX
XX      AAQ75675;
XX
XX      04-AUG-1995 (first entry)
XX
DE      Reverse transcription primer used in cDNA analysis technique.
XX
XX      Analysis; gene expression; reverse transcription; primer; cDNA;
KW      aggregate; restriction enzyme; ss.
XX
XX      Synthetic.
XX
XX      OS
XX      JP06303997-A.
XX
XX      PN
XX      01-NOV-1994.
XX
XX      PD
XX      16-APR-1993; 93JP-00112515.
XX
XX      PF
XX      16-APR-1993; 93JP-00112515.
XX
XX      PR
XX      16-APR-1993; 93JP-00112515.
XX
XX      PA      (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX      DR      WPI; 1995-018287/03.
XX
XX      Analysis of cDNA and gene expression - by amplification of mRNA followed
PT      by digestion with restriction enzymes.
XX
XX      PS      Disclosure; Page 7; 11pp; Japanese.
XX
XX      CC      A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC      double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC      labelled reverse transcription primers (GENSEQ files AAQ75547-Q75798)
CC      and using the aggregate of mRNAs as the template for each reverse
CC      transcription primer; (b) digesting each of the prepared aggregates of
CC      the double-stranded cDNAs with restriction enzyme and; (c)
CC      electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC      method can be used to analyse gene expression rapidly and easily
XX
XX      SQ      Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
QY      Query Match      0.2%; Score 17.8; DB 1; Length 21;
KM      Best Local Similarity 90.5%; Pred. No. 7e+02;
XX      Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      4464 TTTTGTG 4484
DB      1 TTTTATAG 21

RESULT 1011
AAQ75733
ID      AAQ75733 standard; DNA; 21 BP.
XX
XX      AAQ75733;
XX
XX      04-AUG-1995 (first entry)
XX
DE      Reverse transcription primer used in cDNA analysis technique.

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XX      XX      Analysis; gene expression; reverse transcription; primer; cDNA;
KW      aggregate; restriction enzyme; ss.
XX
XX      Synthetic.
XX
XX      OS
XX      JP06303997-A.
XX
XX      PN
XX      01-NOV-1994.
XX
XX      PD
XX      16-APR-1993; 93JP-00112515.
XX
XX      PF
XX      16-APR-1993; 93JP-00112515.
XX
XX      PR
XX      16-APR-1993; 93JP-00112515.
XX
XX      PA      (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX      DR      WPI; 1995-018287/03.
XX
XX      Analysis of cDNA and gene expression - by amplification of mRNA followed
PT      by digestion with restriction enzymes.
XX
XX      PS      Disclosure; Page 8; 11pp; Japanese.
XX
XX      CC      A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC      double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC      labelled reverse transcription primers (GENSEQ files AAQ75547-Q75798)
CC      and using the aggregate of mRNAs as the template for each reverse
CC      transcription primer; (b) digesting each of the prepared aggregates of
CC      the double-stranded cDNAs with restriction enzyme and; (c)
CC      electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC      method can be used to analyse gene expression rapidly and easily
XX
XX      SQ      Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;
QY      Query Match      0.2%; Score 17.8; DB 1; Length 21;
KM      Best Local Similarity 90.5%; Pred. No. 7e+02;
XX      Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      4467 TTTTGTGCT 4487
DB      1 TTTTAACT 21

RESULT 1012
AAQ75771
ID      AAQ75771 standard; DNA; 21 BP.
XX
XX      AAQ75771;
XX
XX      04-AUG-1995 (first entry)
XX
DE      Reverse transcription primer used in cDNA analysis technique.
XX
XX      Analysis; gene expression; reverse transcription; primer; cDNA;
KW      aggregate; restriction enzyme; ss.
XX
XX      Synthetic.
XX
XX      OS
XX      JP06303997-A.
XX
XX      PN
XX      01-NOV-1994.
XX
XX      PD
XX      16-APR-1993; 93JP-00112515.
XX
XX      PF
XX      16-APR-1993; 93JP-00112515.
XX
XX      PR
XX      16-APR-1993; 93JP-00112515.
XX
XX      PA      (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX      DR      WPI; 1995-018287/03.
XX
XX      Analysis of cDNA and gene expression - by amplification of mRNA followed
PT      by digestion with restriction enzymes.

```

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PS Disclosure; Page 9; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
Query Match 0.2%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4464 TTTTCTTTTCTTTTCTG 4484
DB 1 TTTTCTTTTCTTTTCTG 21

RESULT 1013
AAQ75730
ID AAQ75730 standard; DNA; 21 BP.
XX
AC AAQ75730;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KM Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;
Query Match 0.2%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4466 TTTTCTTTTCTTTTCTG 4486
DB 1 TTTTCTTTTCTTTTCTG 21

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RESULT 1014
AAQ75773
ID AAQ75773 standard; DNA; 21 BP.
XX
AC AAQ75773;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KM Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 9; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;
Query Match 0.2%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4465 TTTTCTTTTCTTTTCTG 4485
DB 1 TTTTCTTTTCTTTTCTG 21

RESULT 1015
AAQ75793
ID AAQ75793 standard; DNA; 21 BP.
XX
AC AAQ75793;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KM Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.

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XX 16-APR-1993; 93JP-00112515.
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 9; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESQ files AAQ75547-075798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX
XX SQ Sequence 21 BP; 0 A; 2 C; 0 G; 19 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 17.8; DB 1; Length 21;
XX Best Local Similarity 90.5%; Pred. No. 7e+02;
XX Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 4468 TTTTCTTTTCTTCTT 4488
XX 1 TTTTCTTTTCTTCTT 21
XX
XX RESULT 1016
XX ID AAQ75794 standard; DNA; 21 BP.
XX AAQ75794;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX KM aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 9; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESQ files AAQ75547-075798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX

SQ Sequence 21 BP; 0 A; 3 C; 0 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 17.8; DB 1; Length 21;
XX Best Local Similarity 90.5%; Pred. No. 7e+02;
XX Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 4466 TTTTCTTTTCTTCTT 4486
XX 1 TTTTCTTTTCTTCTT 21
XX
XX RESULT 1017
XX ID AAQ75695 standard; DNA; 21 BP.
XX AAQ75695;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX KM aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 7; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESQ files AAQ75547-075798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX
XX SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 17.8; DB 1; Length 21;
XX Best Local Similarity 90.5%; Pred. No. 7e+02;
XX Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 4464 TTTTCTTTTCTTCTT 4484
XX 1 TTTTCTTTTCTTCTT 21
XX
XX RESULT 1018
XX ID AAQ75718 standard; DNA; 21 BP.
XX AAQ75718;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX


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RESULT 1021
AAQ75791
ID AAQ75791 standard; DNA; 21 BP.
XX
XX
AC AAQ75791;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KM Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 9; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT G 4484
DB 1 TTTT TTTT TTTT TTTT TTTT CCG 21

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PR 16-APR-1993; 93JP-00112515.
XX
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT G 4484
DB 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT AATG 21

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RESULT 1023
AAQ75797
ID AAQ75797 standard; DNA; 21 BP.
XX
XX
AC AAQ75797;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KM Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 9; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 3 C; 0 G; 18 T; 0 U; 0 Other;

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CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESSEQ files AAQ75547-075798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX

SO Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.8; DB 1; Length 21;
 Best Local Similarity 90.5%; Pred. No. 7e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4465 TTTTGTGCTT 4485
 DB 1 TTTTGTGCTT 21

RESULT 1027
 ID AAQ75697 standard; DNA; 21 BP.
 AC AAQ75697;
 XX

DT 04-AUG-1995 (first entry)
 XX

DE Reverse transcription primer used in cDNA analysis technique.

KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KM aggregate; restriction enzyme; ss.
 XX

OS Synthetic.

PN JP06303997-A.
 XX

PD 01-NOV-1994.
 XX

PF 16-APR-1993; 93JP-00112515.
 XX

PR 16-APR-1993; 93JP-00112515.
 XX

PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX

DR WPI; 1995-018287/03.
 XX

PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX

PS Disclosure; Page 7; 11pp; Japanese.
 XX

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESSEQ files AAQ75547-075798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX

SO Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.8; DB 1; Length 21;
 Best Local Similarity 90.5%; Pred. No. 7e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4468 TTTTGTGCTT 4488
 DB 1 TTTTGTGCTT 21

RESULT 1028

AAQ75706
 ID AAQ75706 standard; DNA; 21 BP.
 XX

AC AAQ75706;
 XX

DT 04-AUG-1995 (first entry)
 XX

DE Reverse transcription primer used in cDNA analysis technique.

KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KM aggregate; restriction enzyme; ss.
 XX

OS Synthetic.

PN JP06303997-A.
 XX

PD 01-NOV-1994.
 XX

PF 16-APR-1993; 93JP-00112515.
 XX

PR 16-APR-1993; 93JP-00112515.
 XX

PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX

DR WPI; 1995-018287/03.
 XX

PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX

PS Disclosure; Page 7; 11pp; Japanese.
 XX

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESSEQ files AAQ75547-075798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX

SO Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.8; DB 1; Length 21;
 Best Local Similarity 90.5%; Pred. No. 7e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4466 TTTTGTGCTC 4486
 DB 1 TTTTGTGCTC 21

RESULT 1029

ID AAQ75785 standard; DNA; 21 BP.
 XX

AC AAQ75785;
 XX

DT 04-AUG-1995 (first entry)
 XX

DE Reverse transcription primer used in cDNA analysis technique.

KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KM aggregate; restriction enzyme; ss.
 XX

OS Synthetic.

PN JP06303997-A.
 XX

PD 01-NOV-1994.
 XX

PF 16-APR-1993; 93JP-00112515.
 XX

PR 16-APR-1993; 93JP-00112515.
 XX

XX	PA	(NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX	DR	WPI, 1995-018287/03.
XX	PT	Analysis of cDNA and gene expression - by amplification of mRNA followed
XX	PT	by digestion with restriction enzymes.
XX	PS	Disclosure; Page 9, 11pp; Japanese.
XX	CC	A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX	CC	double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX	CC	labelled reverse transcription primers (GENESBQ files AAQ75547-075798)
XX	CC	and using the aggregate of mRNAs as the template for each reverse
XX	CC	transcription primer; (b) digesting each of the prepared aggregates of
XX	CC	the double-stranded cDNAs with restriction enzyme and; (c)
XX	CC	electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX	CC	method can be used to analyse gene expression rapidly and easily
XX	SQ	Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;
QY	Query Match	0.2%; Score 17.8; DB 1; Length 21;
Db	Best Local Similarity	90.5%; . Pred. No. 76+02;
	Matches 19; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
	4465	TTTTTTTTTTTTTTTTTTTGT 4465
	1	TTTTTTTTTTTTTTTCGT 21
RESULT 1030		
AAQ75698		
ID	AAQ75698	standard; DNA; 21 BP.
AC	AAQ75698;	
DT	04-AUG-1995	(first entry)
DE	Reverse transcription primer used in cDNA analysis technique.	
XX	XX	
XX	XX	Analysis; gene expression; reverse transcription; primer; cDNA;
XX	XX	aggregate; restriction enzyme; ss.
XX	OS	Synthetic.
XX	PN	JP06303997-A.
XX	PD	01-NOV-1994.
XX	PR	16-APR-1993; 93JP-00112515.
XX	PR	16-APR-1993; 93JP-00112515.
XX	PA	(NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX	DR	WPI, 1995-018287/03.
XX	PT	Analysis of cDNA and gene expression - by amplification of mRNA followed
XX	PT	by digestion with restriction enzymes.
XX	PS	Disclosure; Page 7, 11pp; Japanese.
XX	CC	A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX	CC	double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX	CC	labelled reverse transcription primers (GENESBQ files AAQ75547-075798)
XX	CC	and using the aggregate of mRNAs as the template for each reverse
XX	CC	transcription primer; (b) digesting each of the prepared aggregates of
XX	CC	the double-stranded cDNAs with restriction enzyme and; (c)
XX	CC	electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX	CC	method can be used to analyse gene expression rapidly and easily
XX	SQ	Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

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Query Match          0.2%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred.No. 7e+02; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 2;

QY      4466 TTTTTCCTTTTTTTTGTC 4486
        |||
DB       1 TTTTTCCTTTTTTTTACTC 21

RESULT 1031
AAQ75717
ID AAQ75717 standard; DNA; 21 BP.
AC AAQ75717;
DT 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.
KW Analysis; gene expression; reverse transcription; primer; cDNA;
   aggregate; restriction enzyme; 88.
XX Synthetic.
OS
XX JP06303997-A.
EN
XX 01-NOV-1994.
PD
XX 16-APR-1993; 93JP-00112515.
PE
XX 16-APR-1993; 93JP-00112515.
PR
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; 11pp; Japanese.

A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
electrophoresing the digested aggregate of cDNAs in separate lanes. The
method can be used to analyse gene expression rapidly and easily
CC
CX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match          0.2%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred.No. 7e+02; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 2;

QY      4467 TTTTTCCTTTTTTTTGTC 4487
        |||
DB       1 TTTTTCCTTTTTTTTACTC 21

RESULT 1032
AAQ75759
ID AAQ75759 standard; DNA; 21 BP.
AC AAQ75759;
DT 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.
KW Analysis; gene expression; reverse transcription; primer; cDNA;
   aggregate; restriction enzyme; 88.
XX

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XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX DR Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 8; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESSEQ files AAQ75547-075798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily.
XX SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match      0.2%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTG 4484
DB 1 TTTT TTTT TTTT TTTT TTTT CATG 21

RESULT 1033
AAQ75750
ID AAQ75750 standard; DNA; 21 BP.
XX AC AAQ75750;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KM Analysis; gene expression; reverse transcription; primer; cDNA;
XX KM aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX DR Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 8; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of

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XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESSEQ files AAQ75547-075798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily.
XX SQ Sequence 21 BP; 0 A; 3 C; 1 G; 17 T; 0 U; 0 Other;

Query Match      0.2%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4466 TTTT TTTT TTTT TTTT TTTT TTTGTC 4486
DB 1 TTTT TTTT TTTT TTTT TTTT TTTGCCC 21

RESULT 1034
AAQ75677
ID AAQ75677 standard; DNA; 21 BP.
XX AC AAQ75677;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KM Analysis; gene expression; reverse transcription; primer; cDNA;
XX KM aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX DR Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 7; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESSEQ files AAQ75547-075798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily.
XX SQ Sequence 21 BP; 2 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match      0.2%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4465 TTTT TTTT TTTT TTTT TTTT TTTGT 4485
DB 1 TTTT TTTT TTTT TTTT TTTT TTTAT 21

RESULT 1035
AAQ75710

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ID AAQ75710 standard; DNA; 21 BP.
XX
AC AAQ75710;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KM Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PS (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
PT WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily.
XX
SQ Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4466 TTTT TTTT TTTT TTTT TTTT GTC 4486
Db 1 TTTT TTTT TTTT TTTT TAGAC 21
XX
RESULT 1036
AAQ75749
ID AAQ75749 standard; DNA; 21 BP.
XX
AC AAQ75749;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KM Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PS WPI; 1993-00112515.
XX

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PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily.
XX
SQ Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4467 TTTT TTTT TTTT TTTT TTTT GCT 4487
Db 1 TTTT TTTT TTTT TTTT TTTT GCT 21
XX
RESULT 1037
AAQ75765
ID AAQ75765 standard; DNA; 21 BP.
XX
AC AAQ75765;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KM Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PS (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
PT WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 9; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily.
XX
SQ Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 17.8; DB 1; Length 21;

```


PT map of the human genome.
XX
PS Claim 8, Page 2174, 2745bp; English.
XX
CC AA265654 to AA269578 represent human diallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AA269579 to AA277440 represent amplification
CC primers for the diallelic markers. The diallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID Nos 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention
XX
SQ Sequence 21 BP, 11 A; 2 C; 5 G; 3 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3899 GTTACTTTCATGACATTTTTC 3919
DB 21 GTTCTTTCATGACACTTTTC 1
XX
RESULT 1041
AAFB3810
ID AAFB3810 standard; DNA; 21 BP.
XX
AC AAFB3810;
XX
DT 23-JUL-2001 (first entry)
XX
DE Dengue-3 virus derived primer.
XX
KM Yellow fever virus; prM-E protein; flavivirus; chimeric; medicament;
KM infection; tumor antigen; cytokine; lymphoid; reticuloendothelial;
KM cancer; virucide; vaccine; PCR primer; dengue virus; ss.
XX
OS Dengue virus.
XX
OS WO200139802-A1.
XX
PN 07-JUN-2001.
XX
PD 01-DEC-2000; 2000WO-US032821.
XX
PF 01-DEC-1999; 99US-00452638.
XX
PR (ORAV-) ORAVAX INC.
XX
PA Chambers TJ, Monath TP, Guirakhoo F;
XX
PI WPI; 2001-343953/36.
XX
DR
XX
PT Chimeric live, infectious, attenuated yellow fever viruses used for
PT preventing and treating diseases caused by flaviviruses have prM-E
PT nucleotide sequence from a second, different flavivirus as functional
PT yellow fever prM-E is not expressed.
XX
PS Disclosure; Page 139; 232pp; English.
XX
CC The invention relates to a chimeric live, infectious, attenuated virus
CC comprising a yellow fever virus with the nucleotide sequence encoding a
CC prM-E protein deleted, truncated or mutated so that functional yellow
CC fever virus prM-E protein is not expressed and also integrated into the
CC genome of the yellow fever virus a nucleotide sequence encoding a prM-E

CC protein of a second, different flavivirus so that the prM-E protein of
CC the second flavivirus is expressed. The chimeric live, infectious,
CC attenuated virus is used to prepare medicaments for preventing or
CC treating flavivirus infection in a patient. The yellow fever virus vector
CC produces its gene product (tumor antigen or cytokine) in cells of the
CC lymphoid or reticuloendothelial system or in a precursor of these systems
CC in patients with cancer. Flaviviruses replicate in the cytoplasm of cells
CC so that the virus replication does not involve integration of the viral
CC genome into the host cell. Sequences AAFB3796-819 represent PCR primers
CC derived from dengue virus, used for engineering a yellowfever/dengue-3
CC chimera
XX
SQ Sequence 21 BP; 6 A; 2 C; 9 G; 4 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1100 TGGAGAGTGGACAGACTGTGG 1120
DB 1 TGGATAGTGGACAGACTGTG 21
XX
RESULT 1042
ABK70327
ID ABK70327 standard; DNA; 21 BP.
XX
AC ABK70327;
XX
DT 15-JUL-2002 (first entry)
XX
DE Synthetic antisense IGFBP-2-oligonucleotide (ODN) #15.
XX
KM Hormone-regulated cancer; antisense oligonucleotide; IGFBP-2;
KM insulin-like growth factor binding protein-2; hormone-regulated tumour;
KM breast cancer; prostate cancer; IGF-1-sensitive cancer; apoptosis;
KM hormone-responsive cancer; hormonal withdrawal; oligonucleotide;
KM ODN; endocrine tumour therapy; ss.
XX
OS Synthetic.
XX
OS WO200222642-A1.
XX
PN 21-MAR-2002.
XX
PD 13-SEP-2001; 2001WO-US028748.
XX
PF 14-SEP-2000; 2000US-0232641P.
XX
PR (UYBR-) UNIV BRITISH COLUMBIA.
XX
PA Gleave M, Satoshi K, Nelson C, Rennie PS;
XX
PI WPI; 2002-339861/37.
XX
DR
XX
PT Composition for treating hormone-regulated cancer, particularly of
PT prostate or breast, comprises oligonucleotide antisense to insulin-like
PT growth factor binding protein-2.
XX
PS Claim 3; Page 12; 36pp; English.
XX
CC The present invention relates to a new composition for treating hormone-
CC regulated cancer. The composition comprises an antisense oligonucleotide
CC that inhibits expression of IGFBP-2 (insulin-like growth factor binding
CC protein-2). The molecules of the invention are used to delay progression
CC of hormone-regulated tumours, particularly of breast or prostate, to the
CC hormone-independent state, to delay metastatic progression to the bone of
CC IGF-1-sensitive cancers and to treat hormone-responsive cancers by
CC inducing apoptosis, after hormonal withdrawal. The present nucleic acid
CC sequence represents one of a collection (ABK70313-ABK70375) of antisense
CC IGFBP-2-oligonucleotides (ODN) that were used in the invention for
CC prostate and other endocrine tumour therapy
XX

SQ Sequence 21 BP; 6 A; 6 C; 8 G; 1 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.8; DB 1; Length 21;

Best Local Similarity 90.5%; Pred. No. 7e+02; 2; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7413 CAGCAGCAGCAGCAGCAGCAG 74133

DB 1 CAGTACGACGACGACGACGCG 21

RESULT 1043

AAD33500/c

ID AAD33500 standard; DNA; 21 BP.

XX AAD33500;

DT 01-JUL-2002 (first entry)

DE T7718Apad_p526-21-0003 probe for calibration of molecular array data.

XX Molecular array; probe; ss.

OS Unidentified.

XX EP1186673-A2.

PN 13-MAR-2002.

PD 10-SEP-2001; 2001EP-00307665.

PF 11-SEP-2000; 2000US-00659173.

PR (AGIL-) AGILENT TECHNOLOGIES INC.

PA Wobler PK, Delenstarr GC;

PI WPI; 2002-282886/33.

DR Calibration of molecular array data by employing calibration probes that

PT generate signals proportional to total concentrations of labeled target

PS molecules, and molecular arrays incorporating sets of calibration probes.

XX Disclosure; Page 14; 32pp; English.

CC The invention relates to a method for calibrating data scanned from a

CC molecular array. The method involves employing calibration probes that

CC generate signals proportional to the total concentrations of labeled

CC target molecules to which the molecular array probes are directed over an

CC entire range of sample solutions and molecular arrays incorporating sets

CC of calibration probes. Method is useful for calibrating different types

CC of signals scanned from a molecular array, or calibrating signals scanned

CC from different molecular arrays. The present sequence is poly (A)

CC normalisation probe used in calibration of molecular array data

XX Sequence 21 BP; 16 A; 3 C; 0 G; 2 T; 0 U; 0 Other;

SQ

Query Match 0.2%; Score 17.8; DB 1; Length 21;

Best Local Similarity 90.5%; Pred. No. 7e+02; 2; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4460 GGACCTTTTCTTTTCTTTTCTT 4480

DB 21 GGAGATTTTCTTTTCTTTTCTT 1

RESULT 1044

AAF98936

ID AAF98936 standard; DNA; 22 BP.

XX AAF98936;

DT 12-JUN-2001 (first entry)

XX Immunostimulatory nucleic acid #52.

DE Vaccine; cytostatic; vitruoidal; bactericidal; fungicidal; anti-parasitic;

XX immunostimulatory; tumour; viral infection; bacterial infection;

KW fungal infection; parasitic infection; cancer; asthma;

XX infectious disease; allergy; immune deficiency; phosphorothioate; ss.

OS Synthetic.

XX WO200122972-A2.

PN 05-APR-2001.

PD 25-SEP-2000; 2000WO-US026383.

PF 25-SEP-1999; 99US-0156113P.

PR 27-SEP-1999; 99US-0156113P.

XX 23-AUG-2000; 2000US-0227436P.

PA (IOWA) UNIV IOWA RES FOUND.

XX (COLE-) COLEY PHARM GMBH.

PI Krieg AM, Schetter C, Vollmer J;

XX WPI; 2001-273485/28.

DR Vaccinating against tumors, infectious diseases, allergies and asthma

XX using immunostimulatory Py-rich and TG nucleic acids.

PT Disclosure; Page 39; 338pp; English.

PS The present invention relates to a method for stimulating an immune

CC response. The method comprises administering an immunostimulatory nucleic

CC acid to a non-rodent subject in sufficient quantity to stimulate an

CC immune response. The present sequence is one such immunostimulatory

CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich

CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects

CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae

CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,

CC haemophilus, campylobacter, clostridium, Escherichia coli and/or

CC scaptylococcus), fungal antigens and/or parasitic antigens. The method is

CC also useful for preventing cancer, asthma, infectious disease, allergy or

CC immune deficiency. The present sequence can also be used to redirect a

CC Th2 to a Th1 immune response and to activate immune cells. Note: the

CC present sequence may have a phosphorothioate backbone

XX Sequence 22 BP; 0 A; 0 C; 2 G; 20 T; 0 U; 0 Other;

SQ

Query Match 0.2%; Score 17.8; DB 1; Length 22;

Best Local Similarity 90.5%; Pred. No. 7.5e+02;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4468 TTTTCTTTTCTTTTCTTTCTT 4488

DB 1 TTTTCTTTTCTTTTCTTTCTT 21

RESULT 1045

AB877577

ID AB877577 standard; DNA; 22 BP.

XX AB877577;

DT 13-DEC-2002 (first entry)

XX Angiogenesis inhibitory oligonucleotide #61.

DE Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;

XX tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;

KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;

XX corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;

KW rubeosis; Osler-Weber Syndrome; myocardial angiogenesis;

KM plaque neovascularisation; telangiectasia; haemophiliac joint;
 KM angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
 KM scleroderma; hypertrophic scar.
 OS Synthetic.
 XX
 PN WO200253141-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 14-DEC-2001; 2001WO-US048458.
 XX
 PR 14-DEC-2000; 2000US-0255534P.
 XX
 PA (COLE-) COLEY PHARM GROUP INC.
 XX
 PI Bratzler RL;
 XX
 DR WPI; 2002-566690/60.
 XX
 PT Inhibiting angiogenesis in a subject, involves administering at least one
 PT antiangiogenic nucleic acid molecule to the subject.
 XX
 PS Claim 2; Page 20; 276pp; English.
 XX
 CC The invention relates to inhibiting angiogenesis in a subject, comprising
 CC administering at least one antiangiogenic nucleic acid molecule. Also
 CC included is a kit comprising a first container housing the antiangiogenic
 CC nucleic acids, and instructions for administering them to a subject
 CC having a condition characterised by unwanted angiogenesis. The method is
 CC useful for inhibiting angiogenesis associated with solid tumour growth,
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
 CC rubecosis, Ogler-Webber Syndrome, myocardial angiogenesis, plaque
 CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma, and
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
 CC acid of the invention
 XX
 SQ Sequence 22 BP; 0 A; 0 C; 2 G; 20 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 17.8; DB 1; Length 22;
 Best Local Similarity 90.5%; Pred. No. 7.5e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OS
 QY 4468 TTTTCTTTTCTTCTT 4488
 |||||
 Db 1 TTTTCTTTTCTTCTT 21
 XX
 RESULT 1046
 AAD33501/c
 ID AAD33501 standard; DNA; 22 BP.
 XX
 AC AAD33501;
 XX
 DT 01-JUL-2002 (first entry)
 XX
 DE TTT18pad_P625-22-0003 probe for calibration of molecular array data.
 XX
 KM Molecular array; probe; ss.
 XX
 OS unidentified.
 XX
 PN EP1186673-A2.
 XX
 PD 13-MAR-2002.
 XX
 PF 10-SEP-2001; 2001EP-00307665.
 XX
 PR 11-SEP-2000; 2000US-00659173.
 XX

PA (AGIL-) AGILENT TECHNOLOGIES INC.
 XX
 PI Wobler PK, Delenstarr GC;
 XX
 DR WPI; 2002-282886/33.
 XX
 PT Calibration of molecular array data by employing calibration probes that
 PT generate signals proportional to total concentrations of labeled target
 PT molecules, and molecular arrays incorporating sets of calibration probes.
 XX
 PS Disclosure; Page 14; 32pp; English.
 XX
 CC The invention relates to a method for calibrating data scanned from a
 CC molecular array. The method involves employing calibration probes that
 CC generate signals proportional to the total concentrations of labelled
 CC target molecules to which the molecular array probes are directed over an
 CC entire range of sample solutions and molecular arrays incorporating sets
 CC of calibration probes. Method is useful for calibrating different types
 CC of signals scanned from a molecular array, or calibrating signals scanned
 CC from different molecular arrays. The present sequence is poly (A)
 CC normalisation probe used in calibration of molecular array data
 XX
 SQ Sequence 22 BP; 16 A; 4 C; 0 G; 2 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 17.8; DB 1; Length 22;
 Best Local Similarity 90.5%; Pred. No. 7.5e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OS
 QY 4460 GGACTTTTCTTTTCTT 4480
 |||||
 Db 21 GGAGATTTTCTTTTCTT 1
 XX
 RESULT 1047
 ABV74140
 ID ABV74140 standard; DNA; 22 BP.
 XX
 AC ABV74140;
 XX
 DT 23-JAN-2003 (first entry)
 XX
 DE Oligonucleotide used in cDNA library array.
 XX
 KM G-protein coupled receptor; odourant; receptor; olfaction; array;
 KM microarray; anosmia; attractant; aromatic; pesticide; PCR; primer; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1 /*tag= a
 FT /mod_base= OTHER
 FT /note= "5' polylinker"
 XX
 PN WO200277200-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 26-MAR-2002; 2002WO-US009559.
 XX
 PR 27-MAR-2001; 2001US-0279168P.
 XX
 PR 31-JAN-2002; 2002US-0353392P.
 XX
 PA (INSC-) INSCENT INC.
 XX
 PI Woods D, Dimitracos S;
 XX
 DR WPI; 2003-029930/02.
 XX
 PT Identifying nucleic acid encoding novel sex-linked-tissue-linked
 PT receptors, useful for isolating odourant binding proteins or pesticide
 PT alternatives, by analyzing sequences from a male- and female-specific
 PT nucleic acid library.
 XX

XX Disclosure; Fig 5; 83pp; English.
XX
XX The present sequence is that of an oligonucleotide used in a method
CC designed to rapidly array and normalize a complex cDNA library obtained
CC from a target species. Clones are arrayed into multi-well plates. Each
CC well contains 16 oligonucleotides with a 5' polylinker, a poly-T run
CC capable of binding cDNAs by their poly-A tail and a unique 3' sequence,
CC which allows an anchored oligonucleotide in each well to selectively
CC hybridize only to those cDNA clones with a complementary 5' end. The
CC unique 3' key sequences are designed to give a comprehensive level of
CC degeneracy since they are diverse and numerous enough to ensure that
CC every possible cDNA sequence can be bound by an individual, specific
CC oligonucleotide in a single well. The cDNA library is heated to denature
CC the clones into single stranded DNA, and an aliquot is added to every
CC well. The anchored oligonucleotide serves as the 3' primer in PCR, and
CC the common 5' region present in every cDNA clone serves as the 5' priming
CC site. Denaturing and washing leave anchored cDNA in each well. The
CC library is now arrayed and normalised. The method was used to identify
CC and isolate clones encoding G-protein coupled receptors, especially
CC odourant receptors, and active effectors involved in the olfactory
CC pathway of invertebrates and vertebrates, e.g. odourant binding proteins,
CC or other olfactory or neuronal proteins. The identified receptors and
CC proteins are useful for identifying compounds that reduce a target
CC animal's sensitivity to odours, for manufacturing compounds or devices
CC that mask odours, or trapping invertebrates with odourants.
CC Semiochemicals (e.g. aromatics or pheromone mimetics) can be developed
CC with desirable effects on specific species, for the development of pest
CC monitoring systems or non-toxic, species-specific pesticide alternatives,
CC for controlling insect feeding and breeding behaviour, detecting the
CC presence of small air-borne molecules, etc
XX
SQ Sequence 22 BP; 2 A; 1 C; 3 G; 16 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.8; DB 1; Length 22;
Best Local Similarity 90.5%; Pred. No. 7.5e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4469 TTTTGTGCTTG 4489
|||||
1 TTTTGTGCTTGACATG 21
Db

RESULT 1048
ACD99369
ID ACD99369 standard; DNA; 22 BP.
XX
AC ACD99369;
XX
DT 25-SEP-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #55.
XX
XX Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW antitumor; gene therapy; vaccine; non-allergic inflammatory disease;
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS Synthetic.
XX
XX US2003050268-A1.
XX
XX 13-MAR-2003.
XX
XX 29-MAR-2002; 2002US-00112653.
XX
XX 29-MAR-2001; 2001US-0279642P.
XX
XX (KRIE/) KRIEG A M.
XX (BERG/) BERG D J.
XX
XX Krieg AM, Berg DJ;
XX

DR WPI; 2003-521815/49.
XX
XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT disease by administering an immunostimulatory nucleic acid.
XX
XX Disclosure; Page 10; 22pp; English.
XX
XX The invention describes a method of treating non-allergic inflammatory
CC disease comprising administering to a subject having or at risk of
CC developing a non-allergic inflammatory disease an immunostimulatory
CC nucleic acid for prevention or treatment of the disease. The method is
CC useful for treating non-allergic inflammatory diseases, such as
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC This sequence represents an immunostimulatory nucleic acid
XX
SQ Sequence 22 BP; 0 A; 0 C; 2 G; 20 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.8; DB 1; Length 22;
Best Local Similarity 90.5%; Pred. No. 7.5e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4468 TTTTGTGCTTGCTT 4488
|||||
1 TTTTGTGCTTTTGTGTTT 21
Db

RESULT 1049
ADB36438
ID ADB36438 standard; DNA; 22 BP.
XX
AC ADB36438;
XX
DT 04-DEC-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #52.
XX
XX ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW hypo-responsive subject; immunostimulatory.
XX
OS Synthetic.
XX
XX US2003087848-A1.
XX
XX 08-MAY-2003.
XX
XX 02-FEB-2001; 2001US-00776479.
XX
XX 03-FEB-2000; 2000US-0179991P.
XX
XX (BRAT/) BRATZLER R L.
XX (PETE/) PETERSEN D M.
XX (FOUR/) FOURON Y.
XX
XX Bratzler RL, Petersen DM, Fouron Y;
XX
XX WPI; 2003-657977/62.
XX
XX Treating and/or preventing allergy or asthma using an immunostimulatory
PT nucleic acid alone or in combination with an asthma/allergy medicament.
XX
XX Claim 10; Page 6; 22pp; English.
XX
XX The invention relates to a method of treating or preventing allergy or
CC asthma which comprises administering to a subject a poly-G nucleic acid
CC in an aerosol formulation. The methods and compositions of the present
CC invention are useful for diagnosing and/or treating asthma and allergy
CC especially in a hypo-responsive subject. The present sequence represents
CC an immunostimulatory nucleic acid of the invention.
XX
SQ Sequence 22 BP; 0 A; 0 C; 2 G; 20 T; 0 U; 0 Other;

Query Match	0.2%	Score 17.8	DB 1	Length 22
Best Local Similarity	90.5%	Pred. No. 7.5e+02		
Matches 19	Conservative 0	Mismatches 2	Indels 0	Gaps 0
QY	4468	TTTTTTTTTTTTTTTTTGCTT	4468	
DB	1	TTTTTTTGTGTTTTGTTTT	21	
RESULT 1050				
AAT33703				
ID	AAT33703	standard; DNA; 23 BP.		
AC				
XX	AAT33703;			
XX				
DT	19-MAY-1997	(first entry)		
XX				
DE	Primer #3 for tissue or cell derived RNA.			
XX				
KW	PCR; polymerase chain reaction; primer; amplify; reverse-transcription;			
KW	molecular indexing; class IIS restriction enzyme; cancer; causative gene;			
KW	viral infection; hereditary disease; agricultural gene; ss.			
XX				
OS	Synthetic.			
XX				
FA	Key	Location/Qualifiers		
FT	misc_feature	1		
FT		/*tag= a		
FT		/note= "hydroxylated"		
XX				
PN	EP735144-A1.			
XX				
PD	02-OCT-1996.			
XX				
PF	26-MAR-1996;	96EP-00104817.		
XX				
PR	28-MAR-1995;	95JP-00069695.		
PR	20-JUL-1995;	95JP-00184006.		
PR	12-SEP-1995;	95JP-00234122.		
XX				
PA	(SHKJ) RES DEV CORP JAPAN.			
XX				
P1	Kato K;			
XX				
DR	WPI; 1996-435619/44.			
XX				
PT	Molecular indexing of DNA - using restriction enzymes, PCR amplification			
PT	and electrophoresis to analyse DNA fragments.			
XX				
PS	Claim 3; Page 14; 20pp; English.			
XX				
CC	AAT33701-733703 represent amplification primers used in the reverse-			
CC	transcription of tissue or cell derived mRNA, in the method of the			
CC	invention. The method of the invention is a molecular indexing method,			
CC	and comprises digesting the cDNA amplified by these sequences with a			
CC	class IIS restriction enzyme. Each resultant cDNA fragment is then			
CC	ligated to a biotinylated adaptor (selected from a pool of 64 adaptors			
CC	composive to all possible overhangs), and digesting the products with two			
CC	further class IIS restriction enzymes. These steps are repeated (but the			
CC	enzyme used for the first step is different in each) to produce two			
CC	further cDNA samples. The ligation samples are then recovered using			
CC	streptavidin-coated paramagnetic beads, removing the strand complementary			
CC	to an adaptor-primer. The adaptor primer and an anchored oligo-dT primer			
CC	(such as this sequence) are then used to amplify the cDNA samples. The			
CC	amplified products are separated, and the sizes of the fragments obtained			
CC	is recorded. The method can be used for the analysis and diagnosis or			
CC	diseases such as cancers or viral infections, for the search and			
CC	isolation of the genes of physiologically active substances that are			
CC	potential pharmaceuticals, or causative genes of hereditary diseases, as			
CC	well as for the isolation of genes for improving agricultural products.			
CC	Using this method, it is possible to classify (index) DNA into groups in			
XX	a short period of time without duplication			

```

SQ Sequence 23 BP; 1 A; 2 C; 3 G; 17 T; 0 U; 0 Other;
  Query Match          0.2%; Score 17.8; DB 1; Length 23;
  Best Local Similarity 90.5%; Pred. No. 7.9e+02;
  Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4459 TGCACCTTTTCTTTTCTTTT 4479
  ||| ||||| ||||| |||||
DB 2 TCGAGTTTCTTTTCTTTTCTTTT 22

RESULT 1051
AAV61556
ID AAV61556 standard; DNA; 23 BP.
XX
XX AAV61556;
XX AC
XX
XX DT 08-DEC-1998 (first entry)
XX
XX Double-anchored oligo-dT primer, used to synthesise apolipoprotein cDNA.
DE
XX
XX Primer; PCR; amplification; RT-PCR; quantitate; amount ratio; liver;
XX kidney; apolipoprotein; ATAC-PCR; adaptor-tagged Competitive PCR;
XX gene expression; internal standard; calibration curve; ss.
XX
XX Synthetic.
OS
XX Mus sp.
XX
XX EP670842-A2.
XX
XX PN 14-OCT-1998.
XX
XX PD 07-APR-1998; 98EP-003022726.
XX
XX PF 07-APR-1997; 97JP-00088495.
XX
XX PR 07-APR-1997; 97JP-00088495.
XX
XX PA (NISC-) JAPAN SCT & TECHNOLOGY CORP.
XX
XX PI Kato K;
XX
XX DR WPI; 1998-523164/45.
XX
XX Determination of gene expression levels - using combinations of different
PT cDNA samples tagged with different PCR adaptors.
PS
XX Example 2; Page 9; 22pp; English.
XX
XX The present sequence represents a primer which was used to synthesise
CC Apolipoprotein cDNA in a RT-PCR reaction. This primer as well as primers
CC AAV61554 and AAV61555 were added to both mouse liver-derived and mouse
CC kidney-derived total RNA to generate single-stranded cDNA. These primers
CC were used in the method of the invention to determine the amount ratio
CC between a cDNA coding for mouse liver-derived Apolipoprotein and a cDNA
CC that codes for the mouse kidney-derived Apolipoprotein by using Adaptor-
CC tagged Competitive PCR (ATAC-PCR). This method allows gene expression to
CC be quantitatively determined, and because internal standards are not
CC required to prepare a calibration curve, it is a quicker and less
CC laborious process
XX
XX Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 U; 0 Other;
SQ
  Query Match          0.2%; Score 17.8; DB 1; Length 23;
  Best Local Similarity 90.5%; Pred. No. 7.9e+02;
  Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4459 TGCACCTTTTCTTTTCTTTT 4479
  ||| ||||| ||||| |||||
DB 2 TCGAGTTTCTTTTCTTTTCTTTT 22

RESULT 1052
AAA08409
ID AAA08409 standard; DNA; 23 BP.

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XX AC AAA08409;
XX XX
XX DT 13-JUL-2000 (first entry)
XX DE Oligonucleotide primer SEQ ID NO:3.
XX KM Detection; primer; adapter; probe; hybridisation; gene cluster;
XX KM fractionation; ss.
XX OS Synthetic.
XX PN JP2000055914-A.
XX PD 25-FEB-2000.
XX PF 13-AUG-1998; 98JP-00228944.
XX PR 13-AUG-1998; 98JP-00228944.
XX PA (TAISHO PHARM CO LTD.
XX DR WPI; 2000-36873/32.
XX PT Gene detection method involves hybridizing probe opposite to objective
XX PT gene out of fractional gene cluster.
XX PS Example 1; Page 9; 11pp; Japanese.
XX CC The present invention describes a gene detection method which comprises
XX CC fractionating using a probe opposite to the objective gene which is
XX CC hybridised out of fractioned gene cluster. The objective gene detected
XX CC belongs to the group of objective genes contained in the sample. The
XX CC method is used for gene detection by fractionation of cDNA by molecular
XX CC index method using specific primer. It provides high detection
XX CC sensitivity of objective gene. AAA08407 to AAA08414 represent
XX CC oligonucleotides used in the exemplification of the present invention
XX SQ Sequence 23 BP; 1 A; 2 C; 3 G; 17 T; 0 U; 0 Other;
OY Query Match 0.2%; Score 17.8; DB 1; Length 23;
Best Local Similarity 90.5%; Pred. No. 7.9e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 4459 TGGACTTTTTTTTTTTTTTTT 4479
2 TCGAGTTTTTTTTTTTTTTTTT 22
RESULT 1053
AAD33502/c
ID AAD33502 standard; DNA; 23 BP.
XX AC AAD33502;
XX DT 01-JUL-2002 (first entry)
XX DE T7T18Apad_PS24-23-0003 probe for calibration of molecular array data.
XX KM Molecular array; probe; ss.
XX OS Unidentified.
XX PN EP1186673-A2.
XX PD 13-MAR-2002.
XX PF 10-SEP-2001; 2001EP-00307665.
XX PR 11-SEP-2000; 2000US-00659173.
XX PA (AGIL-) AGILENT TECHNOLOGIES INC.
XX XX

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PI Wobler PK, Delenstarr GC;
XX DR WPI; 2002-282866/33.
XX PT Calibration of molecular array data by employing calibration probes that
XX PT generate signals proportional to total concentrations of labeled target
XX PT molecules, and molecular arrays incorporating sets of calibration probes.
XX PS Disclosure; Page 14; 32pp; English.
XX CC The invention relates to a method for calibrating data scanned from a
XX CC molecular array. The method involves employing calibration probes that
XX CC generate signals proportional to the total concentrations of labelled
XX CC target molecules to which the molecular array probes are directed over an
XX CC entire range of sample solutions and molecular arrays incorporating sets
XX CC of calibration probes. Method is useful for calibrating different types
XX CC of signals scanned from a molecular array, or calibrating signals scanned
XX CC from different molecular arrays. The present sequence is poly (A)
XX CC normalisation probe used in calibration of molecular array data
XX SQ Sequence 23 BP; 17 A; 4 C; 0 G; 2 T; 0 U; 0 Other;
OY Query Match 0.2%; Score 17.8; DB 1; Length 23;
Best Local Similarity 90.5%; Pred. No. 7.9e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 4460 GGACTTTTTTTTTTTTTTTT 4480
21 GGAGATTTTTTTTTTTTTTT 1
RESULT 1054
ABV74138/c
ID ABV74138 standard; DNA; 23 BP.
XX AC ABV74138;
XX DT 23-JAN-2003 (first entry)
XX DE 5' End of cDNA library clone.
XX KM G-protein coupled receptor; odourant; receptor; olfaction; array;
XX KM microarray; anosmia; attractant; aromatic; pesticide; mosquito; ss.
XX OS Aedes aegypti.
XX PN WO200277200-A2.
XX PD 03-OCT-2002.
XX PF 26-MAR-2002; 2002WO-US009559.
XX PR 27-MAR-2001; 2001US-0279168P.
XX PR 31-JAN-2002; 2002US-035392P.
XX PA (INSC-) INSCENT INC.
XX PI Woods D, Dimitratos S;
XX DR WPI; 2003-029930/02.
XX PT Identifying nucleic acid encoding novel sex-linked-cisue-linked
XX PT receptors, useful for isolating odorant binding proteins or pesticide
XX PT alternatives, by analyzing sequences from a male- and female-specific
XX PT nucleic acid library.
XX PS Disclosure; Fig 5; 83pp; English.
XX CC The present sequence is that of the 5' end of a cDNA clone isolated from
XX CC a mosquito antenna cDNA library. The clone was isolated using a method
XX CC designed to rapidly array and normalize a complex cDNA library obtained
XX CC from a target species. Clones are arrayed into multi-well plates. Each
XX CC well contains 16 oligonucleotides (see ABV74137) with a 5' polylinker, a

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CC poly-T run capable of binding cDNAs by their poly-A tail and a unique 3' sequence, which allows an anchored oligonucleotide in each well to CC selectively hybridise only to those cDNA clones with a complementary 5' CC end. The unique 3' key sequences are designed to give a comprehensive CC level of degeneracy since they are diverse and numerous enough to ensure CC that every possible cDNA sequence can be bound by an individual, specific CC oligonucleotide in a single well. The cDNA library is heated to denature CC the clones into single stranded DNA, and an aliquot is added to every CC well. The anchored oligonucleotide serves as the 3' primer in PCR, and CC the common 5' region present in every cDNA clone serves as the 5' priming CC site. Denaturing and washing leave anchored cDNA in each well. The CC library is now arrayed and normalised. The method was used to identify CC and isolate clones encoding G-protein coupled receptors, especially CC odourant receptors, and active effectors involved in the olfactory CC pathway of invertebrates and vertebrates, e.g. odourant binding proteins, CC or other olfactory or neuronal proteins. The identified receptors and CC proteins are useful for identifying compounds that reduce a target CC animal's sensitivity to odours, for manufacturing compounds or devices CC that mask odours, or trapping invertebrates with odourants. CC Semiochemicals (e.g. aromatics or pheromone mimetics) can be developed CC with desirable effects on specific species, for the development of pest CC monitoring systems or non-toxic, species-specific pesticide alternatives, CC for controlling insect feeding and breeding behaviour, detecting the CC presence of small air-borne molecules, etc

SO Sequence 23 BP; 16 A; 3 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.8; DB 1; Length 23;
Best Local Similarity 90.5%; Pred. No. 7.9e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4469 TTTT TTTT TTTT TTTT GCTTG 4489
DB 23 TTTT TTTT TTTT TGACATG 3

RESULT 1055
ABV74139
ID ABV74139 standard; DNA; 23 BP.
XX
AC ABV74139;
XX
DT 23-JAN-2003 (first entry)
XX
DE Oligonucleotide used in cDNA library array.
XX
KW G-protein coupled receptor; odourant; receptor; olfaction; array;
KM microarray; anosmia; attractant; aromatic; pesticide; PCR; primer; ss.
XX
OS Synthetic.
FH
FH Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /mod_base= OTHER
FT /note= "5' polylinker"
XX
XX MO200277200-A2.
XX
XX
XX 03-OCT-2002.
XX
XX
XX 26-MAR-2002; 2002MO-US009559.
XX
XX
XX 27-MAR-2001; 2001US-0279168P.
XX
XX 31-JAN-2002; 2002US-0353392P.
XX
XX (INSC-) INSCENT INC.
XX
XX Woods D, Dimitratos S,
XX
XX WPI; 2003-029930/02.
XX
XX
XX Identifying nucleic acid encoding novel sex-linked-tissue-linked
PT

PT receptors, useful for isolating odourant binding proteins or pesticide
PT alternatives, by analyzing sequences from a male- and female-specific
PT nucleic acid library.

PS Disclosure; Fig 5; 83pp; English.

XX
XX
XX The present sequence is that of an oligonucleotide used in a method
CC designed to rapidly array and normalize a complex cDNA library obtained
CC from a target species. Clones are arrayed into multi-well plates. Each
CC well contains 16 oligonucleotides with a 5' polylinker, a poly-T run
CC capable of binding cDNAs by their poly-A tail and a unique 3' sequence,
CC which allows an anchored oligonucleotide in each well to selectively
CC hybridise only to those cDNA clones with a complementary 5' end. The
CC unique 3' key sequences are designed to give a comprehensive level of
CC degeneracy since they are diverse and numerous enough to ensure that
CC every possible cDNA sequence can be bound by an individual, specific
CC oligonucleotide in a single well. The cDNA library is heated to denature
CC the clones into single stranded DNA, and an aliquot is added to every
CC well. The anchored oligonucleotide serves as the 3' primer in PCR, and
CC the common 5' region present in every cDNA clone serves as the 5' priming
CC site. Denaturing and washing leave anchored cDNA in each well. The
CC library is now arrayed and normalised. The method was used to identify
CC and isolate clones encoding G-protein coupled receptors, especially
CC odourant receptors, and active effectors involved in the olfactory
CC pathway of invertebrates and vertebrates, e.g. odourant binding proteins,
CC or other olfactory or neuronal proteins. The identified receptors and
CC proteins are useful for identifying compounds that reduce a target
CC animal's sensitivity to odours, for manufacturing compounds or devices
CC that mask odours, or trapping invertebrates with odourants. CC
CC Semiochemicals (e.g. aromatics or pheromone mimetics) can be developed
CC with desirable effects on specific species, for the development of pest
CC monitoring systems or non-toxic, species-specific pesticide alternatives,
CC for controlling insect feeding and breeding behaviour, detecting the
CC presence of small air-borne molecules, etc

SO Sequence 23 BP; 2 A; 2 C; 3 G; 16 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.8; DB 1; Length 23;
Best Local Similarity 90.5%; Pred. No. 7.9e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4469 TTTT TTTT TTTT TTTT GCTTG 4489
DB 1 TTTT TTTT TTTT TGACATG 21

RESULT 1056
AAA07321/C
ID AAA07321 standard; DNA; 24 BP.
XX
XX AAA07321;
XX
XX
XX 27-JUN-2000 (first entry)
XX
XX
XX PCR primer for PST phosphatase interacting protein coding sequence.
XX
XX PST phosphatase interacting protein; PSTPIP; tumour therapy;
XX
XX protein tyrosine phosphatase; PCR primer; ss.
XX
XX Mammalia.
XX
XX
XX US6040437-A.
XX
XX
XX 21-MAR-2000.
XX
XX
XX 29-SEP-1997; 97US-00938830.
XX
XX
XX 17-APR-1997; 97US-0104590P.
XX
XX (GETH) GENENTECH INC.
XX
XX
XX Dowbenko DJ, Laaky LA;
XX
XX

DR WPI; 2000-282393/24.
 XX Novel genes encoding protein tyrosine phosphatase binding proteins useful
 PT for isolating homologous genes, e.g. in tumor cells, which provide more
 XX specific targets for tumor therapy.
 PS Example 7; Col 45-46; 65pp; English.
 CC This sequence represents a PCR primer used to isolate the PST phosphatase
 CC interacting protein (PSTPIP) coding sequence of the invention. The
 CC protein is a protein tyrosine phosphatase that possesses a non-catalytic
 CC domain comprising a proline, serine and threonine rich region and a C-
 CC terminal segment of 20 amino acid (aa's) rich in proline, and defines an
 CC SH3 binding domain. Nucleic acids encoding native PSTPIP molecules can be
 CC used to isolate homologous genes specifically expressed in tumour cells,
 CC which might provide more specific targets for tumour therapy. The DNA is
 CC also useful for the preparation of PSTPIP polypeptides by recombinant
 CC techniques and as hybridisation probes for searching cDNA and genomic
 CC libraries for the coding sequence of other PSTPIP polypeptide analogues
 CC in other species
 SQ Sequence 24 BP; 4 A; 9 C; 3 G; 8 T; 0 U; 0 Other;
 Query Match 0.2%; Score 17.8; DB 1; Length 24;
 Best Local Similarity 90.5%; Pred. No. 8.4e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1631 GGAAAGTTTCAGAGATGCGG 1651
 DB 22 GGAAAGATGTCAGAGATGTGG 2
 RESULT 1057
 ID AA236136/c standard; DNA; 24 BP.
 AC AA236136;
 XX 11-FEB-2000 (first entry)
 DT Nucleotide sequence of the CTS region of EIAV.
 DE
 XX Cis-acting central initiation region; cPPT; cis-acting terminator; CTS;
 KM EIAV; retrovirus; reverse transcription regulator; expression regulator;
 KM packaging regulator; genetic immunization; Duchenne muscular dystrophy;
 KM cystic fibrosis; neurodegeneration; cancer; immunotherapy; HIV infection;
 KM ss.
 OS Equine infectious anemia virus.
 XX
 XX WO955892-A1.
 PN 04-NOV-1999.
 PD 23-APR-1999; 99WO-FR000974.
 PF 24-APR-1998; 98FR-00005197.
 PR (INSP) INST PASTEUR.
 PA
 PI Charneau P, Zennou V, Firat H;
 XX WPI; 2000-013440/01.
 DR Recombinant vector containing triplex-forming region of retrovirus that
 PT facilitates import of nucleic acid into nuclei, useful for gene
 PT therapy and preparation of transgenic organisms.
 XX
 PS Disclosure; Page 12; 99pp; French.
 CC AA236135-36 represent the cis-acting central initiation region (cPPT;
 CC polypurine track) and the cis-acting terminator (CTS) region of Equine
 CC infectious anemia virus (EIAV), respectively. The sequences are used to

CC produce the recombinant vectors of the invention. These vectors comprise
 CC a polynucleotide that includes cPPT and a CTS, both of retroviral or
 CC retroviral-like origin. It also includes a selected nucleotide sequence,
 CC i.e. a transgene or gene of interest, and retroviral (or retroviral-like)
 CC regulators of reverse transcription (RT), expression and packaging. The
 CC vectors, and related viral particles, are used for transfection and
 CC transduction of eukaryotic cells, in vivo or ex vivo. The vectors are
 CC particularly useful in gene therapy or genetic immunization, e.g. for
 CC treating Duchenne muscular dystrophy, cystic fibrosis, neurodegeneration,
 CC cancer etc. They may also be used in immunotherapy to stimulate responses
 CC to e.g. cancer, HIV infections or to reduce response to autoantigens, or
 CC to create transgenic animals, plants or cell lines
 SQ Sequence 24 BP; 11 A; 2 C; 1 G; 10 T; 0 U; 0 Other;
 Query Match 0.2%; Score 17.8; DB 1; Length 24;
 Best Local Similarity 90.5%; Pred. No. 8.4e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 5476 TTTTGTAAGATATTTT 5496
 DB 22 TTTTGTAAGATATTTT 2
 RESULT 1058
 ID AA165187 standard; DNA; 24 BP.
 AC AA165187;
 XX 12-DEC-2001 (first entry)
 DT Human gap connexin 10 PCR primer #1.
 DE
 XX Human; gap connexin 10; cytosolic; virucidal; immunomodulatory;
 KM antiinflammatory; haemostatic; gene therapy; malignant tumour;
 KM PCR primer; haemopathy; HIV infection; immunological disease;
 KM inflammation; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200172818-A1.
 PN 04-OCT-2001.
 PD 26-MAR-2001; 2001WO-CN000511.
 PF 29-MAR-2000; 2000CN-00115275.
 PR (BIOW-) BIOWINDOW GENE DEV INC.
 PA
 PI Mao Y, Xie Y;
 XX WPI; 2001-602853/68.
 DR Human gap connexin 10 polynucleotide and polypeptide, useful in diagnosis
 PT and treatment of malignant tumor, hemopathy, HIV infection, immunological
 PT diseases and various inflammatory diseases.
 XX
 PS Example 2; Page 12; 36pp; Chinese.
 CC The present invention relates to human gap connexin 10 (see AA165186 and
 CC AG678856). The protein and its coding sequence are useful in the
 CC diagnosis and treatment of malignant tumours, haemopathy, HIV infection,
 CC immunological diseases and various inflammations. The present sequence is
 CC a PCR primer which was used in an example from the present invention
 XX
 SQ Sequence 24 BP; 2 A; 0 C; 3 G; 19 T; 0 U; 0 Other;
 Query Match 0.2%; Score 17.8; DB 1; Length 24;
 Best Local Similarity 90.5%; Pred. No. 8.4e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX	Insulin-like growth factor binding protein 16.17 and encoding
PT	polynucleotide, used in diagnosis and treatment of cancer.
XX	
PS	Example 2; Page 12; 37pp; Chinese.
XX	
CC	The present invention relates to insulin-like growth factor binding
CC	protein 16.17 (see AAm4365). The binding protein and its coding sequence
CC	are useful for the diagnosis and treatment of cancer. The present
CC	sequence is a PCR primer, which was used in an example from the invention
XX	
XX	Sequence 24 BP; 1 A; 3 C; 1 G; 19 T; 0 U; 0 Other;
XX	
XX	Query Match 0.2%; Score 17.8; DB 1; Length 24;
XX	Best Local Similarity 90.5%; Pred. No. 8.4e+02;
XX	Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0
OY	4463 CTTTTTTTTTTTTTTTTT 4483
DB	1 CTTTCTTCTTTTTTTTTT 21
XX	
XX	RESULT 1062
XX	AA066315/c
ID	AA066315 standard; DNA; 25 BP.
XX	
AC	AA066315;
XX	
DT	25-MAR-2003 (revised)
DT	07-FEB-1995 (first entry)
XX	
DE	Deep Vent reverse primer (CIVP53/Cys).
XX	
KW	Target protein; controllable intervening protein sequence; CIVP5;
KW	Vent IVPS; Deep Vent IVPS; Thermococcus litoralis; Pyrococcus sp;
KW	external protein sequence; EPS; amplification; primer;
KW	polymerase chain reaction; PCR; ss.
XX	
OS	Synthetic.
XX	
PN	EP602899-A2.
XX	
PD	22-JUN-1994.
XX	
XX	09-DEC-1993; 93EP-00309920.
PF	
PR	09-DEC-1992; 92US-0004139.
PR	03-NOV-1993; 93US-00146885.
XX	
PA	(NEW) NEW ENGLAND BIOLABS INC.
XX	
PI	Comb DG, Perlner FB, Jack WE, Hodges RA, Xu M, Noren CJ;
XX	
DR	WPI; 1994-193433/24.
XX	
PT	Modified proteins - comprising target protein and controllable
PT	intervening protein sequence.
XX	
PS	Example 8; Page 21; 73pp; English.
XX	
CC	New modified proteins comprise a target protein and a controllable
CC	intervening protein sequence (CIVP5), the CIVP5 being capable of excision
CC	or cleavage under predetermined conditions. Pref. CIVP5s include CIVP51
CC	and 2 from T.litoralis (=vent IVPS1 and 2 or IVS1 and 2) and CIVP5 3 from
CC	Pyrococcus sp. (=deep vent IVPS1 or IVS1). These CIVP5s are capable of
CC	excision, i.e. removal via protein splicing, from modified proteins upon
CC	an increase in temp. This can be used to inactivate protein activity and
CC	also to restore the activity of an inactivated protein. Example 8
CC	describes the in-frame insertion of modified IVPS into a target gene and
CC	thermal control of peptide bond cleavage. Pyrococcus sp. (or Deep Vent)
CC	IVS1 (CIVP53) can be modified by substitution or deletion in-frame into the
CC	native downstream residue (ser), which is then inserted in-frame into the
CC	ECOFV site of the E.coli lacZ gene. Primers given in AA066297 (Deep Vent

CC	IVPS1 forward, 1839-1862) and one of the four reverse primers given in
CC	AA066314-16 and AA066228 (Deep Vent IVPS1/Ser reverse, 3428-3452) were
CC	used to synthesize the cassettes from pNBB#720. (Updated on 25-MAR-2003
CC	to correct FN field.)
XX	
SQ	Sequence 25 BP; 8 A; 3 C; 7 G; 7 T; 0 U; 0 Other;
OY	Query Match 0.2%; Score 17.8; DB 1; Length 25; Best Local Similarity 90.5%; Pred. NO. 8.9e+02; Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0
Dn	4222 TTCCCTGTGCGAGATTAATACC 4242 21 TTCCCTGTGCGAGATTAATACC 1
RESULT 1063	
ID	AAT70828/C
AC	AAT70828 standard; DNA; 25 BP.
XX	AAT70828;
DT	02-SEP-1997 (first entry)
XX	
DE	Deep Vent DV IVPS1 reverse primer.
KM	DNA polymerase; Vent; controllable intervening protein sequence; CIVP33;
KW	DV IVPS1; Pyrococcus; polymerase chain reaction; PCR; primer; ss.
OS	Synthetic.
XX	
PN	WO9701642-A1.
PD	16-JAN-1997.
XX	
PF	19-JUN-1996; 96WO-US010545.
XX	
PR	28-JUN-1995; 95US-00496227.
PR	29-DEC-1995; 95US-00580555.
PA	(NEW) NEW ENGLAND BIOLABS INC.
XX	
PI	Comb DG, Perler FB, Jack WE, Xu M, Hodges RA, Noren CJ;
XX	Chong SSC;
DR	WP1; 1997-100213/09.
PT	Modified protein comprising target protein and controllable intervening
PT	protein - that can be removed by excision or cleavage under specific
PT	conditions, useful for prepn. and purificn. of recombinant proteins that
PT	are normally toxic to cells.
PS	
XX	Example 8; Page 53; 161pp; English.
CC	A reverse primer (AAT70827) (3428-3452) was used with primer DV IVPS1
CC	forward (AAT70816) to synthesize Deep Vent IVPS1 (see also AAT70813)
CC	cassette CIVP33/Ser (1614 bp) contg. an additional C-terminal serine
CC	codon. This modified IVPS (intervening protein sequence) cassette was
CC	designed for in-frame insertion into blunt sites between target gene
CC	codons, such as the E. coli lacZ gene. Modified proteins that include the
CC	IVS inserted into the target gene can be used for the prodn. and
CC	purification of recombinant target proteins
SQ	Sequence 25 BP; 8 A; 3 C; 7 G; 7 T; 0 U; 0 Other;
OY	Query Match 0.2%; Score 17.8; DB 1; Length 25; Best Local Similarity 90.5%; Pred. NO. 8.9e+02; Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0
Dn	4222 TTCCCTGTGCGAGATTAATACC 4242 21 TTCCCTGTGCGAGATTAATACC 1

RESULT 1064
AAV68170/c
ID AAV68170 standard; DNA; 25 BP.
XX
AC AAV68170;
XX
DT 14-JUN-1999 (first entry)
XX
DE Nucleotide sequence of the specification.
XX
KM Intervening protein sequence; IVPS; protein splicing; protein production;
KM Vent DNA polymerase; ss.
XX
OS Synthetic.
XX
PN US5834247-A.
XX
PD 10-NOV-1998.
XX
PF 05-MAR-1997; 97US-00811492.
XX
PR 09-DEC-1992; 92US-00004139.
PR 03-NOV-1993; 93US-00146885.
PR 28-JUN-1995; 95US-00496247.
PR 29-DEC-1995; 95US-00580555.
XX
PA (NEWB) NEW ENGLAND BIOLABS INC.
PI Hodges RA, Perler FB, Comb DG, Southworth M, Adam E, Noren CJ;
PI Xu M, Chong SSC, Jack WS;
XX
DR WPI; 1999-008713/01.
XX
PT New modified target proteins - which have controllable intervening
PT protein sequence which can facilitate production, purification, labelling
PT or isolation of target proteins.
XX
PS Disclosure; Col 119-120; 123pp; English.
XX
CC The present sequence appears in the specification, which describes IVPS
CC fragments of the Vent and Deep Vent DNA polymerase. IVPS (intervening
CC protein sequence) regions encode peptides which are removed via protein
CC splicing to form the native protein. The specification describes a
CC modified protein comprising a target protein or portion, fused either
CC internally or terminally, to a IVPS, or to an amino- or carboxyl-terminal
CC element of a IVPS. The IVPS are capable of excision from or cleavage of
CC the modified protein upon predetermined conditions, in cis or trans, e.g.
CC temperature increase, deglycosylation, unblocking of amino acid residues,
CC treatment with chemical reagents. The methods can be used for modifying,
CC producing, purifying, labelling or isolating target proteins such as
CC enzymes, toxins, cytokines, glycoproteins and growth factors
XX
SQ Sequence 25 BP; 8 A; 3 C; 7 G; 7 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 8.9e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 4222 TTCCTGTGTCAGTATACC 4242
DB 21 TTCCTGTGTCAGTATACC 1
XX
RESULT 1065
AAC95984
ID AAC95984 standard; DNA; 25 BP.
XX
AC AAC95984;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA HLA-B gene PCR primer #95.

XX
KM DNA sequence analysis; sequencing; protein sequence; protein structure;
KM gene typing; organ donation; bacteria identification; 16S rRNA; HLA;
KM human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN W0200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP03636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 43; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16S rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 3 A; 3 C; 4 G; 15 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 8.9e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 4470 TTTTGTGTCGTA 4490
DB 1 TTTTGTGTCGTA 21
XX
RESULT 1066
AAF99738
ID AAF99738 standard; DNA; 25 BP.
XX
AC AAF99738;
XX
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #854.
XX
KM Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KM immunostimulatory; tumour; viral infection; bacterial infection;
KM fungal infection; parasitic infection; cancer; asthma;
KM infectious disease; allergy; immune deficiency; phosphorochiote; ss.
XX
OS Synthetic.
XX
PN W0200122972-A2.
XX
PD 05-APR-2001.
XX
PF 25-SEP-2000; 2000WO-US026383.
XX
PR 25-SEP-1999; 99US-0156113P.
PR 27-SEP-1999; 99US-0156135P.
PR 23-AUG-2000; 2000US-0227436P.

XX (IOWA) UNIV IOWA RES FOUND.
 PA (COLE-) COLEY PHARM GMBH.
 XX Krieger AM, Schetter C, Vollmer J;
 PI WPI; 2001-273485/28.
 DR WPI; 2001-273485/28.
 XX
 PT Vaccinating against tumors, infectious diseases, allergies and asthma
 PT using immunostimulatory Py-rich and TG nucleic acids.
 XX
 XX Claim 101; Page 56; 338pp; English.
 CC The present invention relates to a method for stimulating an immune
 CC response. The method comprises administering an immunostimulatory nucleic
 CC acid to a non-todent subject in sufficient quantity to stimulate an
 CC immune response. The present sequence is one such immunostimulatory
 CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
 CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
 CC against tumor antigens, viral antigens (e.g. herpesviridae, retroviridae
 CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
 CC haemophilus, campylobacter, clostridium, escherichia coli and/or
 CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
 CC also useful for preventing cancer, asthma, infectious disease, allergy or
 CC immune deficiency. The present sequence can also be used to redirect a
 CC Th2 to a Th1 immune response and to activate immune cells. Note: the
 CC present sequence may have a phosphorothioate backbone
 XX
 SQ Sequence 25 BP; 0 A; 0 C; 6 G; 19 T; 0 U; 0 Other;
 Query Match 0.2%; Score 17.8; DB 1; Length 25;
 Best Local Similarity 90.5%; Pred. No. 8.9e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4460 GGACCTTTTCTTTTCTTTTCTTTT 4480
 Db 5 GGGGTTTTTTTTTTTTTTTTT 25
 RESULT 1067
 AAH38315
 ID AAH38315 standard; DNA; 25 BP.
 XX
 AC AAH38315;
 XX
 DT 14-AUG-2001 (first entry)
 XX
 DE SNP specific SNPE primer SEQ ID 1111.
 XX
 KW Single nucleotide polymorphism; SNP; single nucleotide primer extension;
 KW SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;
 KW Leisch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolemia;
 KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
 KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
 KW inflammation; forensic investigation; paternity analysis; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200129262-A2.
 XX
 PD 26-APR-2001.
 XX
 PF 13-OCT-2000; 2000MO-US028436.
 XX
 PR 15-OCT-1999; 99US-0160096P.
 XX
 PA (ORCH-) ORCHID BIOSCIENCES INC.
 XX
 PI Plcoult-Newburg L, Pohl M;
 XX
 DR WPI; 2001-290930/30.
 XX
 PT New genotyping oligonucleotide, useful for detecting the presence,

PT absence or identity of single polynucleotide polymorphism in a nucleic
 PT acid sample.
 XX
 PS Claim 1; Page 55; 83pp; English.
 XX
 CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
 CC primer extension (SNPE) primers, and the sequences of regions flanking
 CC sites of single nucleotide polymorphisms SNPs. The present invention
 CC includes kits for determining the presence or absence of a SNP, using the
 CC oligonucleotides of the invention. The PCR primers are used to amplify a
 CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
 CC The oligonucleotides are useful for genotyping a nucleic acid sample by
 CC performing a single-nucleotide primer extension reaction. The
 CC oligonucleotides are useful for determining the presence, absence or
 CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
 CC assess by association analysis the genotype of an individual or group of
 CC individuals, having a pathological phenotypic trait suspected of being
 CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
 CC agammaglobulinemia, diabetes insipidus, Leisch-Nyhan syndrome, muscular
 CC dystrophy, familial hypercholesterolemia, polycystic kidney disease,
 CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
 CC traits also include symptoms of or susceptibility to multifactorial
 CC disease of which a component is or may be genetic such as autoimmune
 CC diseases, including, rheumatoid arthritis, multiple sclerosis,
 CC inflammation, cancer, nervous system diseases and infection by pathogenic
 CC microorganism. The method is also useful in forensic investigations and
 CC paternity analysis. The present sequence represents a single nucleotide
 CC primer extension (SNPE) primer specific for a human SNP containing DNA
 CC sequence
 XX
 SQ Sequence 25 BP; 2 A; 2 C; 2 G; 19 T; 0 U; 0 Other;
 Query Match 0.2%; Score 17.8; DB 1; Length 25;
 Best Local Similarity 90.5%; Pred. No. 8.9e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4462 ACTTTTCTTTTCTTTTCTTTT 4482
 Db 5 AGTTTTTTTTTTTGTTTTTT 25
 RESULT 1068
 AAH91320/c
 ID AAH91320 standard; DNA; 25 BP.
 XX
 AC AAH91320;
 XX
 DT 09-OCT-2001 (first entry)
 XX
 DE Human inflammatory bowel disease associated polymorphic site #395.
 XX
 KW Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
 KW chromosome 5q31-33; forensic test; gene therapy; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT msc_feature 14
 FT /tag= a
 FT /note= "SNP, optionally insertion or deletion at this
 FT position"
 XX
 PN WO200142511-A2.
 XX
 PD 14-JUN-2001.
 XX
 PF 11-DEC-2000; 2000MO-US033632.
 XX
 PR 10-DEC-1999; 99US-0170257P.
 XX
 PR 10-APR-2000; 2000US-0196046P.
 XX
 PA (WHED) WHITEHEAD INST BIOMEDICAL RES.

PA (ELLI-) ELIIPSIS BIOTHERAPEUTICS CORP.
XX
XX Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;
XX
XX WPI; 2001-367874/38.
XX
PT Testing for the presence of polymorphisms associated with inflammatory
PT bowel disease, using a hybridization assay.
XX
XX Claim 1; Page 55; 463pp; English.
XX
XX The present invention describes a method for detecting the presence of
CC polymorphisms associated with inflammatory bowel diseases such as
CC ulcerative colitis and Crohn's disease. The methods can be used to detect
CC the presence of genetic polymorphisms associated with inflammatory bowel
CC disease and correlating their occurrence with disease states. They may be
CC used in this way for phenotypic correlations, forensics, paternity
CC testing, medicine and genetic analysis. The present sequence is a
CC polymorphic site described in the exemplification of the invention
XX
XX Sequence 25 BP; 14 A; 4 C; 6 G; 0 T; 0 U; 1 Other;
SQ
Query Match 0.2%; Score 17.8; DB 1; Length 25;
Best Local Similarity 86.4%; Pred. No. 8.9e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4456 GCATGACCTTTTCTTTTCTTTT 4477
DB 22 GCCTGGCCCTTTTCTTTTCTTTT 1
RESULT 1069
ABST8459
ID ABST8459 standard; DNA; 25 BP.
XX
XX ABST8459;
XX
XX 13-DEC-2002 (first entry)
XX
XX Angiogenesis inhibitory oligonucleotide #943.
XX
XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
XX tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
XX diabetic retinopathy; retinopathy of prematurity; macular degeneration;
XX corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
XX rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
XX plaque neovascularisation; telangiectasia; haemophilic joint;
XX angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
XX scleroderma; hypertrophic scar.
XX
XX Synthetic.
XX
XX WO200253141-A2.
XX
XX 11-JUL-2002.
XX
XX 14-DEC-2001; 2001WO-US048458.
XX
XX 14-DEC-2000; 2000US-0255534P.
XX
XX (COLE-) COLEY PHARM GROUP INC.
XX
XX Bratzler RL;
XX
XX WPI; 2002-566690/60.
XX
XX Inhibiting angiogenesis in a subject, involves administering at least one
PT antiangiogenic nucleic acid molecule to the subject.
XX
XX Claim 2; Page 36; 276pp; English.
XX
XX The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule. Also

CC included is a kit comprising a first container housing the antiangiogenic
CC nucleic acids, and instructions for administering them to a subject
CC having a condition characterised by unwanted angiogenesis. The method is
CC useful for inhibiting angiogenesis associated with solid tumour growth,
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC acid of the invention
XX
XX Sequence 25 BP; 0 A; 0 C; 6 G; 19 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 8.9e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4460 GCACCTTTTCTTTTCTTTTCTTTT 4480
DB 5 GCGGCTTTTCTTTTCTTTTCTTTT 25
RESULT 1070
ABN13920
ID ABN13920 standard; DNA; 25 BP.
XX
XX ABN13920;
XX
XX 29-MAY-2002 (first entry)
XX
XX Human GDMPL-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:13912.
XX
XX Human; genome-derived myosin-like protein 1; GDMPL-1; hGDMPL-1; heart;
XX muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
XX skeletal muscle disorder; amplicon; screening; ss.
XX
XX Homo sapiens.
XX
XX WO200192524-A2.
XX
XX 06-DEC-2001.
XX
XX 25-MAY-2001; 2001WO-US016981.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX
XX 21-SEP-2000; 2000US-0234687P.
XX
XX 27-SEP-2000; 2000US-0236359P.
XX
XX 04-OCT-2000; 2000GB-00024263.
XX
XX 30-JAN-2001; 2001WO-US000661.
XX
XX 30-JAN-2001; 2001WO-US000662.
XX
XX 30-JAN-2001; 2001WO-US000663.
XX
XX 30-JAN-2001; 2001WO-US000664.
XX
XX 30-JAN-2001; 2001WO-US000665.
XX
XX 30-JAN-2001; 2001WO-US000666.
XX
XX 30-JAN-2001; 2001WO-US000667.
XX
XX 30-JAN-2001; 2001WO-US000668.
XX
XX 30-JAN-2001; 2001WO-US000669.
XX
XX 30-JAN-2001; 2001WO-US000670.
XX
XX 05-FEB-2001; 2001US-0266860P.
XX
XX (AEON-) AEONICA INC.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
XX WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognize hGDMPL-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMPL-1.
XX
XX Disclosure; SEQ ID NO 13912; 214pp; English.

XX The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
 CC nucleic acids can be used as probes to detect, characterize and quantify
 CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption/ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX
 SQ Sequence 25 BP; 6 A; 3 C; 11 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.8; DB 1; Length 25;
 Best Local Similarity 90.5%; Pred. No. 8.9e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5545 GGTCATGCAGTCGAGAACT 5565
 |||||
 1 GGTCATGCAGCTCGAGAACT 21

RESULT 1071
 ABN13919
 ID ABN13919 standard; DNA; 25 BP.
 XX
 AC ABN13919;
 XX
 DT 29-MAY-2002 (first entry)
 XX
 DE Human GDMLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:13911.
 XX
 KW Human: genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200192524-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 25-MAY-2001; 2001WO-US016981.
 XX
 XX 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 05-FEB-2001; 2001WO-US000670.
 PR
 XX

PA (AECOM-) AECOMICA INC.
 XX
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX
 DR WPI; 2002-179446/23.
 XX
 XX New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption/ionization, comprises human myosin-like protein hGDMLP-1.
 XX
 PS Disclosure; SEQ ID NO 13911; 214pp; English.

XX The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
 CC nucleic acids can be used as probes to detect, characterize and quantify
 CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption/ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX
 SQ Sequence 25 BP; 6 A; 4 C; 11 G; 4 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.8; DB 1; Length 25;
 Best Local Similarity 90.5%; Pred. No. 8.9e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5545 GGTCATGCAGTCGAGAACT 5565
 |||||
 2 GGTCATGCAGCTCGAGAACT 22

RESULT 1072
 AAD33506/C
 ID AAD33506 standard; DNA; 25 BP.
 XX
 AC AAD33506;
 XX
 DT 01-JUL-2002 (first entry)
 XX
 DE T7T18Apad_PS22-25-0003 probe for calibration of molecular array data.
 XX
 KW Molecular array; probe; ss.
 XX
 OS Unidentified.
 XX
 PN EP1186673-A2.
 XX
 PD 13-MAR-2002.
 XX
 PF 10-SEP-2001; 2001EP-00307665.
 XX
 PR 11-SEP-2000; 2000US-00659173.
 XX
 PA (AGILENT-) AGILENT TECHNOLOGIES INC.
 XX
 PI Wobler PK, Delenstarr GC;
 XX
 DR WPI; 2002-282886/33.

XX Calibration of molecular array data by employing calibration probes that
PT generate signals proportional to total concentrations of labeled target
PT molecules, and molecular arrays incorporating sets of calibration probes.
XX
PS Disclosure; Page 14; 32pp; English.
XX
CC The invention relates to a method for calibrating data scanned from a
CC molecular array. The method involves employing calibration probes that
CC generate signals proportional to the total concentrations of labelled
CC target molecules to which the molecular array probes are directed over an
CC entire range of sample solutions and molecular arrays incorporating sets
CC of calibration probes. Method is useful for calibrating different types
CC of signals scanned from a molecular array, or calibrating signals scanned
CC from different molecular arrays. The present sequence is poly (A)
CC normalisation probe used in calibration of molecular array data
CC
SQ Sequence 25 BP; 19 A; 4 C; 0 G; 2 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 8.9e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4460 GGACCTTTTTTTTTTTTTTT 4480
Db 21 GGAGATTTTTTTTTTTTTTTT 1
RESULT 1073
ADB04566
ID ADB04566 standard; DNA; 25 BP.
AC ADB04566;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5552.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KM zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KM chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KM developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
DR WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
XX
PS Example 8; SEQ ID NO 5552; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.

CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 25 BP; 2 A; 2 C; 4 G; 17 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 8.9e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4460 GGACCTTTTTTTTTTTTTTT 4480
Db 5 GGATCTTTTTTTTTTTTTTTT 25
RESULT 1074
ADB04577
ID ADB04577 standard; DNA; 25 BP.
AC ADB04577;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 5563.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KM zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KM chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KM developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
DR WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
XX
PS Example 8; SEQ ID NO 5563; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.

XX Sequence 25 BP; 4 A; 1 C; 4 G; 16 T; 0 U; 0 Other;
SQ Query Match 0.2%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 8.9e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4474 TTTTCTTCTTGAGACA 4494
|||||
1 TTTTCTTCTTGAGACA 21
Db TTTTCTTCTTGAGACA 21

RESULT 1075
ACI80665/c
ID ACI80665 standard; DNA; 25 BP.
XX ACI80665;
AC ACI80665;
XX 14-OCT-2003 (first entry)
DT 14-OCT-2003 (first entry)
XX Human microarray DNA oligonucleotide SEQ ID NO 80656.
DE Human microarray DNA oligonucleotide SEQ ID NO 80656.
XX EST, 89; probe; expressed sequence tag; microarray; gene expression;
KM genetic variation; diallelic marker; polymorphism; human;
KW cross-species comparison.
XX Homo sapiens.
OS Homo sapiens.
XX US2003104410-A1.
PN US2003104410-A1.
XX 05-JUN-2003.
PD 05-JUN-2003.
XX 15-MAR-2002; 2002US-00098263.
PF 15-MAR-2002; 2002US-00098263.
XX 16-MAR-2001; 2001US-0276759P.
PR 16-MAR-2001; 2001US-0276759P.
XX (AFYX-) AFFYMETRIX INC.
PA (AFYX-) AFFYMETRIX INC.
XX Miltmann MP;
PI Miltmann MP;
XX WPI; 2003-567953/53.
DR WPI; 2003-567953/53.
XX New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PR sequence or specific mutations of any gene.
XX
XX Claim 1; SEQ ID NO 80656; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridization to a DNA library,
CC in analysis of genetic variation or in hybridization of tag-labeled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridizing at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridization. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying diallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in situ hybridization, in Southern, Northern or dot-
CC blot hybridization to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 25 BP; 4 A; 8 C; 8 G; 5 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 8.9e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 719 CCATGAGTACACCCCTGTGG 739
|||||
Db 24 CCACGAGGTACACCTGTGG 4
CCACGAGGTACACCTGTGG 4

RESULT 1076
ACH03276
ID ACH03276 standard; DNA; 25 BP.
XX ACH03276;
AC ACH03276;
XX 25-SEP-2003 (first entry)
DT 25-SEP-2003 (first entry)
XX Immunostimulatory nucleic acid #911.
DE Immunostimulatory nucleic acid #911.
XX Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KM anticulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis; ss.
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX Synthetic.
OS Synthetic.
XX US2003050268-A1.
PN US2003050268-A1.
XX 13-MAR-2003.
PD 13-MAR-2003.
XX 29-MAR-2002; 2002US-00112653.
PF 29-MAR-2002; 2002US-00112653.
XX 29-MAR-2001; 2001US-0279642P.
PR 29-MAR-2001; 2001US-0279642P.
XX (KRIE/) KRIEG A M.
PA (KRIE/) KRIEG A M.
XX (BERG/) BERG D J.
PI (BERG/) BERG D J.
XX Kriegl AM, Berg DJ;
PI Kriegl AM, Berg DJ;
XX WPI; 2003-521815/49.
DR WPI; 2003-521815/49.
XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel
PR disease by administering an immunostimulatory nucleic acid.
XX
XX Disclosure; Page 33; 229pp; English.

XX The invention describes a method of treating non-allergic inflammatory
CC disease comprising administering to a subject having or at risk of
CC developing a non-allergic inflammatory disease an immunostimulatory
CC nucleic acid for prevention or treatment of the disease. The method is
CC useful for treating non-allergic inflammatory diseases, such as
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC This sequence represents an immunostimulatory nucleic acid
XX
SQ Sequence 25 BP; 0 A; 0 C; 6 G; 19 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 8.9e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4460 GGACCTTTTCTTCTTCTT 4480
|||||
Db 5 GGCGTTTCTTCTTCTTCTT 25
GGCGTTTCTTCTTCTTCTT 25

RESULT 1077
ADB37240
ID ADB37240 standard; DNA; 25 BP.
XX ADB37240;
AC ADB37240;

XX	04-DEC-2003	(first entry)
XX		
DE	Immunostimulatory nucleic acid #854.	
KW	ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;	
KW	hypo-responsive subject; immunostimulatory.	
XX		
OS	Synthetic.	
XX		
PN	US2003087848-A1.	
XX		
PD	08-MAY-2003.	
XX		
PF	02-FEB-2001; 2001US-00776479.	
XX		
PR	03-FEB-2000; 2000US-0179991P.	
XX		
PA	(BRAT/) BRATZLER R L.	
PA	(PETE/) PETERSEN D M.	
XX	(FOUR/) FOURON Y.	
PI	Bratzler RL, Petersen DM, Fouron Y;	
XX		
DR	WPI: 2003-657977/62.	
XX		
PT	Treating and/or preventing allergy or asthma using an immunostimulatory	
PT	nucleic acid alone or in combination with an asthma/allergy medicament.	
XX		
PS	Disclosure; Page 18; 22ipp; English.	
XX		
CC	The invention relates to a method of treating or preventing allergy or	
CC	asthma which comprises administering to a subject a poly-G nucleic acid	
CC	in an aerosol formulation. The methods and compositions of the present	
CC	invention are useful for diagnosing and/or treating asthma and allergy	
CC	especially in a hypo-responsive subject. The present sequence represents	
CC	an immunostimulatory nucleic acid of the invention.	
XX		
SQ	Sequence 25 BP; 0 A; 0 C; 6 G; 19 T; 0 U; 0 Other;	
XX		
QY	Query Match	0.2%; Score 17.8; DB 1; Length 25;
XX	Best Local Similarity	90.5%; Pred. No. 8.9e+02;
XX	Matches 19; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
DB	4460 GGACTTTTTTTTTTTTTTTT 4480	
	5 GGGGTTTTTTTTTTTTTTTTTT 25	
RESULT 1078		
ABK51820/C		
ID	ABK51820 standard; DNA; 26 BP.	
XX		
NC	ABK51820;	
XX		
DT	30-JUL-2002 (first entry)	
XX		
DE	DNA probe #2 for human UGT1A10 gene.	
XX		
KW	Human; enzyme classification; enzyme quantitative determination;	
KW	glucuronic acid conjugation; UDP-glucuronosyltransferase; UGT1A10; probe;	
XX	88.	
OS	Homo sapiens.	
XX		
PN	JP2002085066-A.	
XX		
PD	26-MAR-2002.	
XX		
PF	07-SEP-2000; 2000JP-00272228.	
XX		
PR	07-SEP-2000; 2000JP-00272228.	
XX		

PA (SAKA) OTSUKA SEIYAKU KOSYO KK.
DR WPI; 2002-378271/41.
PT Determination of enzymes participating in glucuronic acid conjugation in
PT human being, comprises use of oligonucleotide probes.
XX
XX
PS Claim 8; Page 11; 13pp; Japanese.
XX
XX The present invention relates to a method for classification and
CC quantitative determination of enzymes participating in glucuronic acid
CC conjugation. The method involves the use of oligonucleotide probes
CC hybridising to regions of the human UDP-glucuronosyltransferase (UGT)
CC genes (e.g. UGT1, UGT1A9, UGT1A10, UGT2A1, UGT2B7, UGT2B10,
CC UGT2B15, UGT2B17, UGT8), and the DDOST gene. The method and
CC probes are useful for the genetic determination of enzymes participating
CC in glucuronic acid conjugation with catalysed UGT. The method is both
CC rapid and accurate. ABR51813-ABR51836 represent oligonucleotide probes
CC useful for human UGT or DDOST genes
XX
SQ Sequence 26 BP; 11 A; 6 C; 5 G; 4 T; 0 U; 0 Other;
OY Query March 0.2%; Score 17.8; DB 1; Length 26;
Best local Similarity 90.5%; Pred. NO. 9.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
DB 6448 GCAGTGTGTTTGGATACCTTT 6468
26 GCAGTGTGTTTGGATACCTTT 6
RESULT 1079
ABX03814/C
ID ABX03814 standard; cDNA; 27 BP.
AC ABX03814;
XX
DT 09-JAN-2003 (first entry)
XX
DE DNA encoding secreted protein signal peptide sequence #23.
XX
KM Differential display method; leucine-rich motif; transmembrane protein;
KW secreted protein; secreted protein signal peptide; ss.
XX
OS Unidentified.
XX
PM WO200259259-A2.
PD 01-AUG-2002.
XX
PF 23-JAN-2002; 2002WO-IL000071.
XX
PR 23-JAN-2001; 2001US-0263158P.
XX
PA (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
XX
PI Wreschner DH;
XX
DR WPI; 2002-599769/64.
DR P-PSDB; ABR98343.
PT
PT Differential display method for identifying secreted or transmembrane
PT protein, comprises contacting a DNA with a first primer that hybridises
PT to a sequence coding for a leucine-rich motif and with a second
PT oligonucleotide primer.
XX
PS Disclosure; Fig 2; 37pp; English.
XX
XX The invention relates to a differential display comprising contacting
CC cDNA with a first primer that hybridises to an oligonucleic sequence
CC coding for a leucine-rich motif, and with a second oligonucleotide primer
CC to form a cDNA-hybrid molecule. The method comprises obtaining mRNA from
CC at least 2 samples, synthesising cDNA from the RNA of each sample,


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XX WO200226990-A1.
PN
XX
XX 04-APR-2002.
XX
XX 29-JUN-2001; 2001WO-CN001090.
XX
XX 30-JUN-2000; 2000CN-00116964.
XX
XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
XX Mao Y, Xie Y;
XX
XX WPI; 2002-269651/31.
XX
XX Prolyl oligomeric peptidase 13.2 polypeptide for diagnosing and treating
XX angiodysplasia and nervous system retrograde disease.
XX
XX Example 2; Page 17; 35pp; Chinese.
XX
XX PCR primers AB156666-67 were used to amplify cDNA encoding human prolyl
XX oligomeric peptidase 13.2. The polypeptide and polynucleotide are used in
XX diagnosis and treatment of angiodysplasia and nervous system retrograde
XX disease. The polynucleotide may also be used for gene therapy
XX
XX Sequence 24 BP; 18 A; 3 C; 1 G; 2 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 9.1e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4466 TTTTCTTTTCTTTTCTGCTG 4489
Db 24 TTTTCTTTTCTTTTCTGAGATG 1
RESULT 1085
ABL58113
ID ABL58113 standard; DNA; 24 BP.
XX
XX ABL58113;
XX
XX 26-JUL-2002 (first entry)
XX
XX Human serine/threonine protein kinase 15.18 PCR primer #2.
XX
XX Human; cytosolic; serine/threonine protein kinase 15.18; enzyme;
XX embryo development teratogenesis; tumour; PCR; primer; ss.
XX
XX Homo sapiens.
XX
XX CN1331325-A.
XX
XX 16-JAN-2002.
XX
XX 30-JUN-2000; 2000CN-00116980.
XX
XX 30-JUN-2000; 2000CN-00116980.
XX
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
XX Mao Y, Xie Y;
XX
XX WPI; 2002-340671/38.
XX
XX A human serine/threonine protein kinase 15.18 polypeptide, and the
XX polynucleotide encoding it, for treating e.g. embryo development
XX teratogenesis and tumors.
XX
XX Example 2; Page 19 (Disclosure); 34pp; Chinese.
XX
XX The present invention relates to human serine/threonine protein kinase
XX 15.18 (AB176999). The kinase and its coding sequence are useful for

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```

CC treating diseases such as embryo development teratogenesis and tumors.
CC The present sequence is a PCR primer, which was used in an example from
CC the invention
XX
XX Sequence 24 BP; 3 A; 0 C; 5 G; 16 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 9.1e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4471 TTTTCTTTTCTTTTCTGAGACA 4494
Db 1 TTTTCTTTTCTTTTCTGAGATA 24
RESULT 1086
ABK11020
ID ABK11020 standard; DNA; 24 BP.
XX
XX ABK11020;
XX
XX 05-JUN-2002 (first entry)
XX
XX Gamma-COP13 polypeptide, RT-PCR primer #2.
XX
XX Gamma-COP13; cytosolic; haemostatic; vitruide; immunomodulatory;
XX anti-inflammatory; malignant tumour; haemopathy; inflammation;
XX human immunodeficiency virus; HIV; immunological disease;
XX reverse transcriptase PCR; RT-PCR; primer; ss.
XX
XX Unidentified.
XX
XX WO200202616-A1.
XX
XX 10-JAN-2002.
XX
XX 11-JUN-2001; 2001WO-CN000961.
XX
XX 14-JUN-2000; 2000CN-00116482.
XX
XX (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
XX Mao Y, Xie Y;
XX
XX WPI; 2002-090536/12.
XX
XX Gamma-cop 13 polypeptide and encoded polynucleotide, used in diagnosis
XX and treatment of malignant tumors, hemopathy, human immunodeficiency
XX virus infection, immunological diseases and inflammation.
XX
XX Example 2; Page 11; 33pp; Chinese.
XX
XX The invention relates to an isolated polypeptide (I), of gamma-COP13 and
XX the polynucleotide (II) encoding it. (I) and (II) are used in diagnosis
XX and treatment of malignant tumour, haemopathy, human immunodeficiency
XX virus (HIV) infection, immunological diseases and various inflammations.
XX The present sequence represents a reverse transcriptase (RT)-PCR primer
XX used to isolate the coding sequence of gamma-COP13 polypeptide
XX
XX Sequence 24 BP; 3 A; 2 C; 0 G; 19 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 9.1e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4464 TTTTCTTTTCTTTTCTGCT 4487
Db 1 TTTTCTTTTCTTTTCTTATCT 24
RESULT 1087
AB258841
ID AB258841 standard; DNA; 24 BP.

```


XX AC ABZ58841;
 XX DT 28-APR-2003 (first entry)
 XX DE Histidine tag encoding DNA.
 XX KM Genetic information; glyph; molecular biology; histidine tag; ds.
 XX OS Synthetic.
 XX FH Key
 XX FT CDS Location/Qualifiers
 XX FT 1..24
 XX FT /*tag= a
 XX PN WO200282264-A2.
 XX PD 17-OCT-2002.
 XX PF 05-APR-2002; 2002WO-US010825.
 XX PR 06-APR-2001; 2001US-0282022P.
 XX PA (SEED/) SEED B.
 XX PI Seed B;
 XX DR WPI; 2003-058588/05.
 XX DR P-PSDB; ABP71241.
 XX PT Displaying genetic information represented by set of glyphs, by receiving
 XX PT entered command, and displaying identified glyph assigned to the
 XX PT entered command, and displaying identified glyph.
 XX PS Example 3; Page 37; 50pp; English.
 XX CC The invention relates to displaying genetic information represented by a
 XX CC set of glyphs. The method involves receiving an entered command to
 XX CC display one of the set of glyphs, identifying the glyph of the set
 XX CC assigned to the entered command, and displaying the identified glyph,
 XX CC where the glyph is displayed at a location on a display screen with a
 XX CC cursor. Another method for displaying a double-stranded codon and an
 XX CC amino acid encoded by the codon is also provided. The methods provide
 XX CC simple and quick way for displaying and genetic information that has been
 XX CC modified by a standard molecular biology technique. The present sequence
 XX CC represents a DNA fragment encoding a histidine tag
 XX CC
 XX SQ Sequence 24 BP; 8 A; 12 C; 4 G; 0 T; 0 U; 0 Other;
 XX
 XX Query Match 0.2%; Score 17.6; DB 1; Length 24;
 XX Best Local Similarity 83.3%; Pred. No. 9.1e+02;
 XX Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 XX
 XX QY 7410 CATCAGCAGCAGCAGCAGCAG 7433
 XX DB 1 CACCAGCAGCAGCAGCAGCAG 24
 XX
 XX RESULT 1088
 XX AAC66194
 XX ID AAC66194 standard; DNA; 25 BP.
 XX AC AAC66194;
 XX DT 14-FEB-2001 (first entry)
 XX DE PCR primer EcoRI-dt used in trypsin hL identification.
 XX KM Human; trypsin hL; serine protease; lung disease model animal;
 XX KW PCR primer; ss.
 XX OS Synthetic.

PN JP2000253887-A.
 XX DT 19-SEP-2000.
 XX DE 11-MAR-1999; 99JP-00065337.
 XX PR 11-MAR-1999; 99JP-00065337.
 XX PA (TTPH-) TT PHARMA KK.
 XX DR WPI; 2000-658814/64.
 XX PT Novel gene encoding a serine protease and its protein used to screen for
 XX PT serine protease inhibitors and to prepare lung disease animal models.
 XX PS Disclosure; Page 7-8; 17pp; Japanese.
 XX CC Nucleotide sequence AAC66182 encodes human trypsin hL AAB35701, a serine
 XX CC protease. The invention relates to the human hL gene and protein
 XX CC sequences, to a recombinant vector containing the nucleotide sequence,
 XX CC and a host cell containing the vector. Human trypsin hL can be used for
 XX CC screening for serine protease inhibitors, in the preparation of a lung
 XX CC disease model animal, and for the development of an index marker of lung
 XX CC diseases caused by an anti-trypsin hL antibody. The present sequence
 XX CC represents a PCR primer used in the identification of trypsin hL
 XX CC
 XX SQ Sequence 25 BP; 2 A; 2 C; 4 G; 17 T; 0 U; 0 Other;
 XX
 XX Query Match 0.2%; Score 17.6; DB 1; Length 25;
 XX Best Local Similarity 83.3%; Pred. No. 9.6e+02;
 XX Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 XX
 XX QY 4455 GGCATGCACTTTTCTTTTCTTTT 4478
 XX DB 2 GGAATTCGCTTTTCTTTTCTTTT 25
 XX
 XX RESULT 1089
 XX AAC96231
 XX ID AAC96231 standard; DNA; 25 BP.
 XX AC AAC96231;
 XX DT 26-FEB-2001 (first entry)
 XX DE 16S rRNA gene PCR primer #198.
 XX KM DNA sequence analysis; sequencing; protein sequence; protein structure;
 XX KM gene typing; organ donation; bacteria identification; 16S rRNA; HLA;
 XX KW human leukocyte antigen; PCR primer; ss.
 XX OS Homo sapiens.
 XX PN WO200065088-A2.
 XX PD 02-NOV-2000.
 XX PF 20-APR-2000; 2000WO-BE003636.
 XX PR 26-APR-1999; 99EP-00303215.
 XX PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
 XX PI Ulfendahl P, Wong K;
 XX DR WPI; 2000-679677/66.
 XX PT Identifying extendible primers for use in identification, or
 XX PT classification of a nucleic acid of an organism, allele or gene such as
 XX PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
 XX PT specific length.
 XX PS Claim 14; Page 47; 66pp; English.

```

XX CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16S rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 3 A; 3 C; 2 G; 17 T; 0 U; 0 Other;

Query Match      0.2%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 9.6e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4470 TTTTCTTTTGTGCTTGAGACATGG 4493
DB 1 TTTTCTTTTGTGCTTGAGACATGG 24

RESULT 1090
AAC95544 standard; DNA; 25 BP.
XX
AC AAC96544;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA DRB345 gene PCR primer #15.
XX
XX DNA sequence analysis; sequencing; protein sequence; protein structure;
XX gene typing; organ donation; bacteria identification; 16S rRNA; HLA;
XX human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 53; 66pp; English.
XX
XX The present invention provides a method for identifying a set of
XX extendible primers which can be used in the identification, typing and
XX classification of genes. This can then be used to predict protein
XX sequence and structure, in organ donation to match the organ with the
XX receiver, and to identify bacteria in a sample. The method can be used to
XX type the human leukocyte antigen genes (HLA) and 16S rRNA genes in
XX particular
XX
SQ Sequence 25 BP; 6 A; 2 C; 3 G; 14 T; 0 U; 0 Other;

Query Match      0.2%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 9.6e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4474 TTTTCTTTTGTGCTTGAGACATGG 4497
DB 1 TTTTCTTTTGTGCTTGAGACATGG 24

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```

DB 1 TTTTCTTTTGTGCTTGAGACATGG 24

RESULT 1091
AAC95709
ID AAC95709 standard; DNA; 25 BP.
XX
AC AAC95709;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA DQA1 gene PCR primer #6.
XX
XX DNA sequence analysis; sequencing; protein sequence; protein structure;
XX gene typing; organ donation; bacteria identification; 16S rRNA; HLA;
XX human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 38; 66pp; English.
XX
XX The present invention provides a method for identifying a set of
XX extendible primers which can be used in the identification, typing and
XX classification of genes. This can then be used to predict protein
XX sequence and structure, in organ donation to match the organ with the
XX receiver, and to identify bacteria in a sample. The method can be used to
XX type the human leukocyte antigen genes (HLA) and 16S rRNA genes in
XX particular
XX
SQ Sequence 25 BP; 3 A; 2 C; 6 G; 14 T; 0 U; 0 Other;

Query Match      0.2%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 9.6e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4474 TTTTCTTTTGTGCTTGAGACATGG 4497
DB 1 TTTTCTTTTGTGCTTGAGACATGG 24

RESULT 1092
AAC95842
ID AAC95842 standard; DNA; 25 BP.
XX
AC AAC95842;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA HLA-A gene PCR primer #22.
XX
XX DNA sequence analysis; sequencing; protein sequence; protein structure;
XX gene typing; organ donation; bacteria identification; 16S rRNA; HLA;
XX human leukocyte antigen; PCR primer; ss.
XX

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OS	Homo sapiens.
XX	
XX	WO200065088-A2.
XX	
PD	02-NOV-2000.
XX	
PE	20-APR-2000; 2000WO-EP003636.
XX	
PR	26-APR-1999; 99EP-00303215.
XX	
PA	(AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX	
PI	Ulfendahl P, Wong K;
XX	
DR	WPI; 2000-679677/66.
XX	
PT	Identifying extendible primers for use in identification, or
PT	classification of a nucleic acid of an organism, allele or gene such as
PT	class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT	specific length.
XX	
XX	
PS	Claim 14; Page 41; 66pp; English.
XX	
CC	The present invention provides a method for identifying a set of
CC	extendible primers which can be used in the identification, typing and
CC	classification of genes. This can then be used to predict protein
CC	sequence and structure, in organ donation to match the organ with the
CC	recipient, and to identify bacteria in a sample. The method can be used to
CC	type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC	particular
XX	
SQ	Sequence 25 BP; 1 A; 2 C; 6 G; 16 T; 0 U; 0 Other;

```

PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS
XX Claim 14; Page 57; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16S rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 1 A; 2 C; 6 G; 16 T; 0 U; 0 Other;
OY Query Match 0.2%; Score 17.6; DB 1; Length 25;
Best local similarity 83.3%; Pred. No. 9.6e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0.
    4468 TTTTTTTTTTTTGTCTTGAG 4491
        |||||
        1 TTTTTTTTTTATGCGCTTGGG 24

RESULT 1094
AAC96090
ID AAC96090 standard; DNA; 25 BP.
AC AAC96090;
XX
XX DT 26-FEB-2001 (first entry)
```

	Query Match	0.2%	Score 17.6	DB 1	length 25
Best Local Similarity	83.3%		Pred No. 9.6e+02		
Matches	20	Conservative	0	Mismatches 4	Indels 0
					Gaps 0
Oy	4468	TTTTTTTTTTTTTTTTTGTGCTTGAG	4491		
db	1	TTTTTTTTTTTATCGCTTGCGG	24		

DE	16s rRNA gene PCR primer #57.
XX	
KM	DNA sequence analysis; sequencing; protein sequence; protein structure
KM	gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KM	human leukocyte antigen; PCR primer; ss.
XX	
OS	Homo sapiens.

```

RESULT 1093
AAC96778
ID AAC96778 standard; DNA; 25 BP.
XX
XX AAC96778;
AC
XX
XX
DT 26-FEB-2001 (first entry)
XX
XX HLA HLA-A gene PCR primer #155.
DE
XX DNA sequence analysis; sequencing; protein sequence; protein structure;
KV gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
XX WO200065088-A2.
PN
XX
XX 02-NOV-2000.
PD
XX
XX 20-APR-2000; 2000MO-EP003636.
PF
XX
XX 26-APR-1999; 99EP-00303215.
PR
XX
XX (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
PA
XX
XX Ulfendahl P, Wong K;
PI
XX
XX WPI; 2000-679677/66.
DR
XX
XX
PT Identifying extendible primers for use in identification, or

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XX	
PD	02-NOV-2000.
XX	
PF	20-APR-2000; 2000MO-EP003636.
XX	
PR	26-APR-1999; 99EP-00303215.
XX	
PA	(AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX	
PI	Ulfendahl P, Wong K;
XX	
DR	WPI; 2000-679677/66.
XX	
PT	Identifying extendible primers for use in identification, or
PT	classification of a nucleic acid of an organism, allele or gene such as
PT	class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT	specific length.
XX	
PS	Claim 14; Page 45; 66pp; English.
XX	
CC	The present invention provides a method for identifying a set of
CC	extendible primers which can be used in the identification, typing and
CC	classification of genes. This can then be used to predict protein
CC	sequence and structure, in organ donation to match the organ with the
CC	receiver, and to identify bacteria in a sample. The method can be used to
CC	type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC	particular
XX	
SO	Sequence 25 BP; 2 A; 3 C; 4 G; 16 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.6; DB 1; Length 25;

Best Local Similarity 83.3%; Pred. No. 9.6e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4471 TTTTGTCTGTGAGACA 4494
|||||

DB 1 TTTTGTCTGTGAGACA 24
|||||

RESULT 1095

AAC96678
ID AAC96678 standard; DNA; 25 BP.

AC AAC96678;

DT 26-FEB-2001 (first entry)

DE HLA HLA-A gene PCR primer #55.

XX DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16S rRNA; HLA;

KW human leukocyte antigen; PCR primer; ss.

OS Homo sapiens.

PN WO200065088-A2.

PD 02-NOV-2000.

PF 20-APR-2000; 2000WO-EP003636.

PR 26-APR-1999; 99EP-00303215.

PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.

PI Ulfendahl P, Wong K;

DR WPI; 2000-679677/66.

XX Identifying extendible primers for use in identification, or

PT classification of a nucleic acid of an organism, allele or gene such as

PT class 1/2 HLA comprises identifying all possible nucleotide sequences of

PT specific length.

PS Claim 14; Page 55; 66pp; English.

CC The present invention provides a method for identifying a set of

CC extendible primers which can be used in the identification, typing and

CC classification of genes. This can then be used to predict protein

CC sequence and structure, in organ donation to match the organ with the

CC receiver, and to identify bacteria in a sample. The method can be used to

CC type the human leukocyte antigen genes (HLA) and 16S rRNA genes in

CC particular

SO Sequence 25 BP; 3 A; 2 C; 5 G; 15 T; 0 U; 0 Other;

QY Query Match 0.2%; Score 17.6; DB 1; Length 25;

Best Local Similarity 83.3%; Pred. No. 9.6e+02;

Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

DB 4470 TTTTGTCTGTGAGACA 4493
|||||

DB 1 TTTTGTCTGTGAGACA 24
|||||

RESULT 1096

AAC96172
ID AAC96172 standard; DNA; 25 BP.

AC AAC96172;

DT 26-FEB-2001 (first entry)

DE 16S rRNA gene PCR primer #139.

XX DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16S rRNA; HLA;

KW human leukocyte antigen; PCR primer; ss.

OS Homo sapiens.

PN WO200065088-A2.

PD 02-NOV-2000.

PF 20-APR-2000; 2000WO-EP003636.

PR 26-APR-1999; 99EP-00303215.

PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.

PI Ulfendahl P, Wong K;

DR WPI; 2000-679677/66.

XX Identifying extendible primers for use in identification, or

PT classification of a nucleic acid of an organism, allele or gene such as

PT class 1/2 HLA comprises identifying all possible nucleotide sequences of

PT specific length.

PS Claim 14; Page 46; 66pp; English.

CC The present invention provides a method for identifying a set of

CC extendible primers which can be used in the identification, typing and

CC classification of genes. This can then be used to predict protein

CC sequence and structure, in organ donation to match the organ with the

CC receiver, and to identify bacteria in a sample. The method can be used to

CC type the human leukocyte antigen genes (HLA) and 16S rRNA genes in

CC particular

SO Sequence 25 BP; 3 A; 0 C; 4 G; 18 T; 0 U; 0 Other;

QY Query Match 0.2%; Score 17.6; DB 1; Length 25;

Best Local Similarity 83.3%; Pred. No. 9.6e+02;

Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

DB 4473 TTTTGTCTGTGAGACA 4496
|||||

DB 1 TTTTGTCTGTGAGACA 24
|||||

RESULT 1097

AAC96654
ID AAC96654 standard; DNA; 25 BP.

AC AAC96654;

DT 26-FEB-2001 (first entry)

DE HLA HLA-A gene PCR primer #31.

XX DNA sequence analysis; sequencing; protein sequence; protein structure;

KW gene typing; organ donation; bacteria identification; 16S rRNA; HLA;

KW human leukocyte antigen; PCR primer; ss.

OS Homo sapiens.

PN WO200065088-A2.

PD 02-NOV-2000.

PF 20-APR-2000; 2000WO-EP003636.

PR 26-APR-1999; 99EP-00303215.

PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.

PI ulfendahl P, Wong K;
 XX WPI; 2000-679677/66.
 XX
 PT Identifying extendible primers for use in identification, or
 PT classification of a nucleic acid of an organism, allele or gene such as
 PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
 PT specific length.
 XX
 PS Claim 14; Page 55; 66pp; English.
 XX
 CC The present invention provides a method for identifying a set of
 CC extendible primers which can be used in the identification, typing and
 CC classification of genes. This can then be used to predict protein
 CC sequence and structure, in organ donation to match the organ with the
 CC receiver, and to identify bacteria in a sample. The method can be used to
 CC type the human leukocyte antigen genes (HLA) and 16S rRNA genes in
 CC particular
 XX
 SQ Sequence 25 BP; 0 A; 3 C; 5 G; 17 T; 0 U; 0 Other;
 Query Match 0.2%; Score 17.6; DB 1; Length 25;
 Best Local Similarity 83.3%; Pred. No. 9.6e+02;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 4470 TTTTGTGCTTGTGAGAC 4493
 DB 1 TTTTGTGCTTGTGAGAC 24
 RESULT 1098
 AAC96504
 ID AAC96504 standard; DNA; 25 BP.
 XX
 AC AAC96504;
 XX
 DT 26-FEB-2001 (first entry)
 XX
 DE HLA DQB1 gene PCR primer #56.
 XX
 KM DNA sequence analysis; sequencing; protein sequence; protein structure;
 KM gene typing; organ donation; bacteria identification; 16S rRNA; HLA;
 KM human leukocyte antigen; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200065088-A2.
 XX
 PD 02-NOV-2000.
 XX
 PF 20-APR-2000; 2000WO-EP003636.
 XX
 PR 26-APR-1999; 99EP-00303215.
 XX
 PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
 PI ulfendahl P, Wong K;
 XX
 DR WPI; 2000-679677/66.
 XX
 PT Identifying extendible primers for use in identification, or
 PT classification of a nucleic acid of an organism, allele or gene such as
 PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
 PT specific length.
 XX
 PS Claim 14; Page 52; 66pp; English.
 XX
 CC The present invention provides a method for identifying a set of
 CC extendible primers which can be used in the identification, typing and
 CC classification of genes. This can then be used to predict protein
 CC sequence and structure, in organ donation to match the organ with the
 CC receiver, and to identify bacteria in a sample. The method can be used to
 CC type the human leukocyte antigen genes (HLA) and 16S rRNA genes in

CC particular
 XX
 SQ Sequence 25 BP; 5 A; 4 C; 2 G; 14 T; 0 U; 0 Other;
 Query Match 0.2%; Score 17.6; DB 1; Length 25;
 Best Local Similarity 83.3%; Pred. No. 9.6e+02;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 4471 TTTTGTGCTTGTGAGACA 4494
 DB 1 TTTTGTGCTTGTGAGACA 24
 RESULT 1099
 AAC96843
 ID AAC96843 standard; DNA; 25 BP.
 XX
 AC AAC96843;
 XX
 DT 26-FEB-2001 (first entry)
 XX
 DE HLA HLA-C gene PCR primer #48.
 XX
 KM DNA sequence analysis; sequencing; protein sequence; protein structure;
 KM gene typing; organ donation; bacteria identification; 16S rRNA; HLA;
 KM human leukocyte antigen; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200065088-A2.
 XX
 PD 02-NOV-2000.
 XX
 PF 20-APR-2000; 2000WO-EP003636.
 XX
 PR 26-APR-1999; 99EP-00303215.
 XX
 PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
 PI ulfendahl P, Wong K;
 XX
 DR WPI; 2000-679677/66.
 XX
 PT Identifying extendible primers for use in identification, or
 PT classification of a nucleic acid of an organism, allele or gene such as
 PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
 PT specific length.
 XX
 PS Claim 14; Page 58; 66pp; English.
 XX
 CC The present invention provides a method for identifying a set of
 CC extendible primers which can be used in the identification, typing and
 CC classification of genes. This can then be used to predict protein
 CC sequence and structure, in organ donation to match the organ with the
 CC receiver, and to identify bacteria in a sample. The method can be used to
 CC type the human leukocyte antigen genes (HLA) and 16S rRNA genes in
 CC particular
 XX
 SQ Sequence 25 BP; 4 A; 2 C; 4 G; 15 T; 0 U; 0 Other;
 Query Match 0.2%; Score 17.6; DB 1; Length 25;
 Best Local Similarity 83.3%; Pred. No. 9.6e+02;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 4470 TTTTGTGCTTGTGAGAC 4493
 DB 1 TTTTGTGCTTGTGAGAC 24
 RESULT 1100
 AAC95753
 ID AAC95753 standard; DNA; 25 BP.
 XX

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AC AAC95753;
XX
XX 26-FEB-2001 (first entry)
XX
XX HLA DQB1 gene PCR primer #24.
XX
XX DNA sequence analysis; sequencing; protein sequence; protein structure;
XX gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
XX human leukocyte antigen; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200065088-A2.
XX
XX 02-NOV-2000.
XX
XX 20-APR-2000; 2000WO-EP003636.
XX
XX 26-APR-1999; 99EP-00303215.
XX
XX (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
XX Ulfendahl P, Wong K;
XX
XX WPI; 2000-679677/66.
XX
XX Identifying extendible primers for use in identification, or
XX classification of a nucleic acid of an organism, allele or gene such as
XX class 1/2 HLA comprises identifying all possible nucleotide sequences of
XX specific length.
XX
XX Claim 14; Page 39; 66pp; English.
XX
XX The present invention provides a method for identifying a set of
XX extendible primers which can be used in the identification, typing and
XX classification of genes. This can then be used to predict protein
XX sequence and structure, in organ donation to match the organ with the
XX receiver, and to identify bacteria in a sample. The method can be used to
XX type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
XX particular
XX
XX Sequence 25 BP; 5 A; 4 C; 2 G; 14 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 17.6; DB 1; Length 25;
XX Best Local Similarity 83.3%; Pred. No. 9.6e+02;
XX Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 4471 TTTT TTTT TTTT TTTT GCTTGTGACGA 4494
XX 1 TTTT TTTT TTTT TTTT GTTGTGACGACA 24
XX
XX RESULT 1101
XX AAC96256
XX ID AAC96256 standard; DNA; 25 BP.
XX
XX AAC96256;
XX
XX 26-FEB-2001 (first entry)
XX
XX HLA DPA1 gene PCR primer #13.
XX
XX DNA sequence analysis; sequencing; protein sequence; protein structure;
XX gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
XX human leukocyte antigen; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200065088-A2.
XX
XX 02-NOV-2000.
XX
XX 20-APR-2000; 2000WO-EP003636.
XX

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XX
XX 26-APR-1999; 99EP-00303215.
XX
XX (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
XX Ulfendahl P, Wong K;
XX
XX WPI; 2000-679677/66.
XX
XX Identifying extendible primers for use in identification, or
XX classification of a nucleic acid of an organism, allele or gene such as
XX class 1/2 HLA comprises identifying all possible nucleotide sequences of
XX specific length.
XX
XX Claim 14; Page 48; 66pp; English.
XX
XX The present invention provides a method for identifying a set of
XX extendible primers which can be used in the identification, typing and
XX classification of genes. This can then be used to predict protein
XX sequence and structure, in organ donation to match the organ with the
XX receiver, and to identify bacteria in a sample. The method can be used to
XX type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
XX particular
XX
XX Sequence 25 BP; 3 A; 2 C; 3 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 17.6; DB 1; Length 25;
XX Best Local Similarity 83.3%; Pred. No. 9.6e+02;
XX Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 4467 TTTT TTTT TTTT TTTT TTTT GCTTGTGA 4490
XX 1 TTTT TTTT TTTT TTTT GTTGTGACAGA 24
XX
XX RESULT 1102
XX AAH39503/C
XX ID AAH39503 standard; DNA; 25 BP.
XX
XX AAH39503;
XX
XX 14-AUG-2001 (first entry)
XX
XX SNP specific SNPE primer SEQ ID 2699.
XX
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
XX SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;
XX Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
XX polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
XX inflammation; forensic investigation; paternity analysis; primer; ss.
XX
XX Homo sapiens.
XX
XX WO200129262-A2.
XX
XX 26-APR-2001.
XX
XX 13-OCT-2000; 2000WO-US028436.
XX
XX 15-OCT-1999; 99US-0160096P.
XX
XX (ORCH-) ORCHID BIOSCIENCES INC.
XX Picoult-Newburg L, Pohl M;
XX
XX WPI; 2001-290930/30.
XX
XX New genotyping oligonucleotide, useful for detecting the presence,
XX absence or identity of single polynucleotide polymorphism in a nucleic
XX acid sample.
XX
XX Claim 1; Page 63; 83pp; English.
XX

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CC based upon interaction of those clones with an appropriate anti-idiotype.
CC The method is useful for making a single chain antibody directed against
CC an antigen. Control PCR primers ACC70415-16 and probe ACC70417 were used
CC during real time quantitative PCR of murine antibody 8H9 scFv, in the
CC course of the invention
XX.

SQ Sequence 25 BP; 5 A; 9 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 9.6e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 527 CCATTGGCAACGACGGTGCAGT 550
Db 25 CCATTGGCAATGACGGGTCCGCT 2

RESULT 1105
AC196632
ID AC196632 standard; DNA; 25 BP.

XX AC196632;

DT 14-OCT-2003 (first entry)

XX Human microarray DNA oligonucleotide SEQ ID NO 96623.

DE EST; sb; probe; expressed sequence tag; microarray; gene expression;
XX genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.

XX Homo sapiens.

OS US2003104410-A1.

PN 05-JUN-2003.

PD 15-MAR-2002; 2002US-00098263.

PF 16-MAR-2001; 2001US-0276759P.

PR (AFRY-) AFFYMETRIX INC.

PA Miltmann MP;

XX WPI; 2003-567953/53.

PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX

PS Claim 1; SEQ ID NO 96623; 9pp; English.

CC The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridization to a DNA library,
CC in analysis of genetic variation or in hybridization of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridizing at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridization. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridization, in Southern, Northern or dot-
CC blot hybridization to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' terminus of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the

CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html

XX SQ Sequence 25 BP; 7 A; 9 C; 9 G; 0 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 9.6e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7405 AGCAACATCAGCAGCAGCAGCAGC 7428
Db 1 AGCGACAGCAGCAGCAGCAGCGC 24

RESULT 1106
ACK24505
ID ACK24505 standard; DNA; 25 BP.

XX ACK24505;

DT 14-OCT-2003 (first entry)

XX Human microarray DNA oligonucleotide SEQ ID NO 124486.

DE EST; sb; probe; expressed sequence tag; microarray; gene expression;
XX genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.

XX Homo sapiens.

OS US2003104410-A1.

PN 05-JUN-2003.

PD 15-MAR-2002; 2002US-00098263.

PF 16-MAR-2001; 2001US-0276759P.

PR (AFRY-) AFFYMETRIX INC.

PA Miltmann MP;

XX WPI; 2003-567953/53.

PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX

PS Claim 1; SEQ ID NO 124486; 9pp; English.

CC The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridization to a DNA library,
CC in analysis of genetic variation or in hybridization of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridizing at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridization. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridization, in Southern, Northern or dot-
CC blot hybridization to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' terminus of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly

CC from USPRO at segdata.uspto.gov/sequence.html
 XX Sequence 25 BP; 3 A; 7 C; 8 G; 7 T; 0 U; 0 Other;
 SQ Query Match 0.2%; Score 17.6; DB 1; Length 25;
 Best Local Similarity 83.3%; Pred. No. 9.6e+02;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 2595 TGTCTATATCCGACGACTGCTTA 2618
 Db 1 TGTCTCTGTCCAGAGCTGCGTA 24

RESULT 1107
 ACK30483/C
 ID ACK30483 standard; DNA; 25 BP.
 XX ACK30483;
 AC
 XX 14-OCT-2003 (first entry)
 DT
 XX Human microarray DNA oligonucleotide SEQ ID NO 130464.
 DE
 XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
 KM genetic variation; diallelic marker; polymorphism; human;
 KM cross-species comparison.
 OS Homo sapiens.
 XX
 XX US2003104410-A1.
 PN
 XX 05-JUN-2003.
 PD
 XX 15-MAR-2002; 2002US-00098263.
 PF
 XX 16-MAR-2001; 2001US-0276759P.
 PR
 XX (AFY-) AFFYMETRIX INC.
 PA
 XX Miltmann MP;
 PI
 XX MPI; 2003-567953/53.
 DR
 XX New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.
 XX
 XX Claim 1; SEQ ID NO 130464; 9pp; English.

CC The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridization to a DNA library,
 CC in analysis of genetic variation or in hybridization of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridizing at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridization. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying diallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in situ hybridization, in Southern, Northern or dot-
 CC blot hybridization to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPRO at segdata.uspto.gov/sequence.html
 XX

SQ Sequence 25 BP; 9 A; 4 C; 9 G; 3 T; 0 U; 0 Other;
 XX Query Match 0.2%; Score 17.6; DB 1; Length 25;
 Best Local Similarity 83.3%; Pred. No. 9.6e+02;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 6597 AAGGTTGACGTTCTTCCCATC 6620
 Db 25 AAGGTCGACGTTCTTCTCTCC 2

RESULT 1108
 ACK13866
 ID ACK13866 standard; DNA; 25 BP.
 XX ACK13866;
 AC
 XX 14-OCT-2003 (first entry)
 DT
 XX Human microarray DNA oligonucleotide SEQ ID NO 113847.
 DE
 XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
 KM genetic variation; diallelic marker; polymorphism; human;
 KM cross-species comparison.
 OS Homo sapiens.
 XX
 XX US2003104410-A1.
 PN
 XX 05-JUN-2003.
 PD
 XX 15-MAR-2002; 2002US-00098263.
 PF
 XX 16-MAR-2001; 2001US-0276759P.
 PR
 XX (AFY-) AFFYMETRIX INC.
 PA
 XX Miltmann MP;
 PI
 XX MPI; 2003-567953/53.
 DR
 XX New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.
 XX
 XX Claim 1; SEQ ID NO 113847; 9pp; English.

CC The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridization to a DNA library,
 CC in analysis of genetic variation or in hybridization of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridizing at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridization. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying diallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in situ hybridization, in Southern, Northern or dot-
 CC blot hybridization to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPRO at segdata.uspto.gov/sequence.html
 XX
 XX Sequence 25 BP; 6 A; 9 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.6; DB 1; Length 25;
 Best Local Similarity 83.3%; Pred. No. 9.6e+02;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2193 CCGCATCATCTTCTACCGAGATCG 2216
 |||||
 Db 2 CCGTATCTCTCTTACCAGATGG 25

RESULT 1109
 ADC26866/c
 ID ADC26866 standard; DNA; 25 BP.
 AC ADC26866;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Forward PCR primer used to mutate DbpA Lys50, #1.
 XX
 KW Decorin binding protein A; DbpA; immune response; bacterial infection;
 KW decorin; colonisation; spirochete; adhesion; collagen fibre;
 KW dermatan sulphate proteoglycan; DbpB; lipoprotein; vaccine;
 KW delayed type hypersensitivity; DTH; Lyme disease; LD;
 KW multisystemic disorder; Lyme arthritis; antibacterial; PCR; primer; ss;
 KW mutant.
 XX
 OS Synthetic.
 OS Borrelia burgdorferi.
 XX
 PN US6517838-B1.
 XX
 PD 11-FEB-2003.
 XX
 PF 16-JUN-2000; 2000US-00596120.
 XX
 PR 16-JUN-2000; 2000US-00596120.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 PI Hoeek MA, Brown EL;
 XX
 DR WPI; 2003-634321/60.
 XX
 PT Generating immune response against Borrelia bacteria, for treating Lyme
 PT disease, by administering decorin binding protein A-derived peptide or a
 PT combination of decorin binding protein A-derived peptides to mammal.
 XX
 PS Disclosure; Col 28; 33pp; English.
 XX
 CC The invention discloses a method for generating an immune response
 CC against Borrelia bacteria infection which involves administering a
 CC decorin binding protein A (DbpA)-derived peptide or a combination of two
 CC or more DbpA-derived peptides, where the peptides span critical binding
 CC regions required for DbpA/decorin adhesion. Colonisation of the
 CC spirochetes occurs by adhesion of B. burgdorferi to collagen fibres,
 CC particularly to decorin, a dermatan sulphate proteoglycan. DbpA and B are
 CC expressed at the surface of the spirochetes as lipoproteins and act as
 CC adhering, binding to the decorin. Also disclosed are antisera and
 CC antibodies generated against the decorin binding proteins, vaccines
 CC comprising decorin binding peptides, antisera and antibodies raised
 CC against the decorin binding proteins, diagnostic kits comprising the
 CC decorin binding peptides, or antibodies or antisera raised against them,
 CC pharmaceutical compositions comprising the decorin binding peptides, or
 CC antibodies or antisera raised against them, inhibiting decorin binding
 CC protein from binding decorin in a blood sample by contacting the blood
 CC sample with DbpA-derived peptide fragment, identifying a candidate
 CC substance that alters the binding of DbpA-derived protein fragment or
 CC related peptide to decorin, a modulator of DbpA-derived protein or
 CC peptide fragment binding to decorin, modulating DbpA-derived protein or
 CC peptide fragment binding to decorin, identifying a candidate DbpA-derived
 CC peptide fragment with improved decorin binding and use of decorin binding
 CC peptides, or antibodies or antisera raised against them for the
 CC treatment, prevention and diagnosis of Borrelia burgdorferi infections

CC and for coating medical devices or polymeric biomaterials in vitro and in
 CC vivo. The peptides are administered by topical, oral, anal, vaginal,
 CC intravenous, intraperitoneal, intramuscular, subcutaneous, intranasal or
 CC intradermal route. The method is useful (e.g. as a vaccine) for
 CC generating an immune response against Borrelia bacteria or preventing
 CC Borrelia infection in a mammal and as a delayed type hypersensitivity
 CC (DTH) response inducer. Preferably, the method is useful for treating
 CC Lyme disease (LD), which can lead to multisystemic disorders that may
 CC affect the joints (Lyme arthritis), skin, heart and central nervous
 CC system. The sequence presented is a PCR primer which was used to mutate
 CC the B. burgdorferi DbpA gene at one of the critical lysine residues.
 XX
 SQ Sequence 25 BP; 10 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.6; DB 1; Length 25;
 Best Local Similarity 83.3%; Pred. No. 9.6e+02;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4280 GCACCTCTTCTTGCAAGTCATCT 4303
 |||||
 Db 24 GCAGCCTTTTTCATTCATTCATCT 1

RESULT 1110
 ADC26867
 ID ADC26867 standard; DNA; 25 BP.
 AC ADC26867;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Reverse PCR primer used to mutate DbpA Lys50, #1.
 XX
 KW Decorin binding protein A; DbpA; immune response; bacterial infection;
 KW decorin; colonisation; spirochete; adhesion; collagen fibre;
 KW dermatan sulphate proteoglycan; DbpB; lipoprotein; vaccine;
 KW delayed type hypersensitivity; DTH; Lyme disease; LD;
 KW multisystemic disorder; Lyme arthritis; antibacterial; PCR; primer; ss;
 KW mutant.
 XX
 OS Synthetic.
 OS Borrelia burgdorferi.
 XX
 PN US6517838-B1.
 XX
 PD 11-FEB-2003.
 XX
 PF 16-JUN-2000; 2000US-00596120.
 XX
 PR 16-JUN-2000; 2000US-00596120.
 XX
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 XX
 PI Hoeek MA, Brown EL;
 XX
 DR WPI; 2003-634321/60.
 XX
 PT Generating immune response against Borrelia bacteria, for treating Lyme
 PT disease, by administering decorin binding protein A-derived peptide or a
 PT combination of decorin binding protein A-derived peptides to mammal.
 XX
 PS Disclosure; Col 28; 33pp; English.
 XX
 CC The invention discloses a method for generating an immune response
 CC against Borrelia bacteria infection which involves administering a
 CC decorin binding protein A (DbpA)-derived peptide or a combination of two
 CC or more DbpA-derived peptides, where the peptides span critical binding
 CC regions required for DbpA/decorin adhesion. Colonisation of the
 CC spirochetes occurs by adhesion of B. burgdorferi to collagen fibres,
 CC particularly to decorin, a dermatan sulphate proteoglycan. DbpA and B are
 CC expressed at the surface of the spirochetes as lipoproteins and act as
 CC adhering, binding to the decorin. Also disclosed are antisera and
 CC antibodies generated against the decorin binding proteins, vaccines

CC comprising decorin binding peptides, antisera and antibodies raised
 CC against the decorin binding proteins, diagnostic kits comprising the
 CC decorin binding peptides, or antibodies or antisera raised against them,
 CC pharmaceutical compositions comprising the decorin binding peptides, or
 CC antibodies or antisera raised against them, inhibiting decorin binding
 CC protein from binding decorin in a blood sample by contacting the blood
 CC sample with Dbpa-derived peptide fragment, identifying a candidate
 CC substance that alters the binding of Dbpa-derived protein fragment or
 CC related peptide to decorin, a modulator of Dbpa-derived protein or
 CC peptide fragment binding to decorin, modulating Dbpa-derived protein or
 CC peptide fragment binding to decorin, identifying a candidate Dbpa-derived
 CC peptide fragment with improved decorin binding and use of decorin binding
 CC peptides, or antibodies or antisera raised against them for the
 CC treatment, prevention and diagnosis of Borrelia burgdorferi infections
 CC and for coating medical devices or polymeric biomaterials in vitro and in
 CC vivo. The peptides are administered by topical, oral, anal, vaginal,
 CC intravenous, intraperitoneal, intramuscular, subcutaneous, intranasal or
 CC intradermal route. The method is useful (e.g. as a vaccine) for
 CC generating an immune response against Borrelia bacteria or preventing
 CC Borrelia infection in a mammal and as a delayed type hypersensitivity
 CC (DTH) response inducer. Preferably, the method is useful for treating
 CC Lyme disease (LD), which can lead to multisystemic disorders that may
 CC affect the joints (Lyme arthritis), skin, heart and central nervous
 CC system. The sequence presented is a PCR primer which was used to mutate
 CC the B. burgdorferi Dbpa gene at one of the critical lysine residues.

XX
 SQ Sequence 25 BP; 5 A; 6 C; 4 G; 10 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.6; DB 1; Length 25;
 Best Local Similarity 83.3%; Pred. No. 9.6e+02;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4280 GCACCTCTTCTTCGACGTCATCT 4303
 Db 2 GCAGCCTTTTTCGATTGCATCT 25

RESULT 1111
 AAQ93051 standard; DNA; 26 BP.

XX
 AC AAQ93051;
 XX
 DT 22-MAR-1996 (first entry)
 XX
 DB IFN-gamma mediated MHC-I induction inhibiting peptide VI.
 XX
 KM Transplantation antigen; transplantation antigen-depleted cell;
 KM interferon-gamma; IFN-gamma; human; cervical carcinoma cell line; Hela;
 KM K562 cell; fibroblast; keratinocyte; monocyte; transplantation; graft;
 KM autoimmune disorder; ss.
 XX
 OS Synthetic.
 XX
 FT Key Location/Qualifiers
 FT modified_base 1..26
 FT /*tag= a
 FT /note= "Joined by phosphorothioate linkages"
 FT modified_base 26
 FT /*tag= b
 FT /note= "T-RNH2, where R = -CH2CH(OH)CH2-"
 XX
 FT W09520317-A1.
 XX
 PD 03-AUG-1995.
 XX
 PD 26-JUN-1995; 95WO-US001198.
 XX
 PR 28-JAN-1994; 94US-00188435.
 PR 04-MAR-1994; 94US-00206131.
 PR 12-SEP-1994; 94US-00305467.
 XX
 PA (REGC) UNIV CALIFORNIA.

XX Garovoy MR, Huey B, Tam S, Tam RC, Ramanathan M, Macgregor RD;
 PI Hunt CA, Lantz M;
 XX
 DR WPI; 1995-275249/36.
 XX
 PT Preparation of transplantation antigen-depleted cell and universal donor
 PT organs - by exposure of target cells to oligonucleotide(s) capable of
 PT binding to the antigen sequence, or inhibiting IFN-gamma induction of
 PT cell surface expression.
 XX
 PS Claim 3; Page 88; 134pp; English.

CC The sequences given in AAQ93046-51 represent oligonucleotides which are
 CC capable of binding to a transplantation antigen nucleotide sequence.
 CC These oligonucleotides, when present in sufficient amounts, make a target
 CC cell a transplantation antigen-depleted cell. These oligonucleotides
 CC inhibit interferon-gamma (IFN-gamma) in e.g. human cervical carcinoma
 CC cell line (Hela), K562 cells, fibroblasts, keratinocytes and human
 CC monocytes. These oligonucleotides may be used in the production of
 CC transplantation antigen depleted/reduced cells and organs. These may be
 CC used in transplantation and will be more easily tolerated by the host.
 CC This will result in improved graft survival rates and the requirement of
 CC lower levels of immunosuppressant drugs to be administered. The cells may
 CC also be used in the treatment of autoimmune disorders. The 3'
 CC modification causes retention binding ability and the modification of the
 CC linkages imparts extended and increased biological activity

XX
 SQ Sequence 26 BP; 0 A; 0 C; 22 G; 4 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.6; DB 1; Length 26;
 Best Local Similarity 83.3%; Pred. No. 1e+03;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3614 TGGGGAATGGGCGTGGGCGTGGAG 3637
 Db 3 TGGGGGTGGGCGTGGGCGTGGGCGG 26

RESULT 1112
 AAT13051
 ID AAT13051 standard; DNA; 26 BP.

XX
 AC AAT13051;
 XX
 DT 25-MAR-2003 (revised)
 DT 27-MAY-1996 (first entry)
 XX
 DB cDNA primer.
 XX
 KM Cotton; fibre; promoter; transgenic plant; crop improvement; primer;
 KM Gossypium; ss.
 XX
 OS Synthetic.
 XX
 FT US5495070-A.
 FT 27-FEB-1996.
 XX
 PD 18-MAY-1992; 92US-00885970.
 XX
 PR 04-OCT-1988; 88US-00253243.
 PR 21-NOV-1990; 90US-00617239.
 XX
 PA (CETU) AGRACETUS INC.
 XX
 PI John M;
 XX
 DR WPI; 1996-139095/14.
 XX
 PT New isolated fibre-specific promoters - used for introducing altered-
 PT fibre specific characteristics into plants, partic. cotton.

```

PS      Example 1; Col 8; 48bp; English.
XX
XX      cDNA was prep'd. from cotton fibre cell RNA using the primer given in
CC      AAT13051. cDNA libraries were produced and screened for fibre-specific
CC      clones (see AAT13033-50) and these were in turn used to screen genomic
CC      libraries to identify fibre-specific promoter sequences (see AAT13025-32
CC      and AAT13052-53). (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ      Sequence 26 BP; 2 A; 3 C; 3 G; 18 T; 0 U; 0 Other;
      Query Match          0.2%; Score 17.6; DB 1; Length 26;
      Best Local Similarity 83.3%; Pred. No. 1e+03;
      Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0
      QY      4456 GCATGACCTTTTTTTTTTTTTT 4479
      DB      3 GCTGGACCTTTTTTTTTTTTTT 26
      RESULT 1113
      AAT39393
      ID      AAT39393 standard; DNA; 26 BP.
      XX      AAT39393;
      XX      25-MAR-2003 (revised)
      DT      16-DEC-1996 (first entry)
      XX      Cotton fibre cDNA first strand synthesis primer.
      DE      Cotton fibre; promoter; differential screening; leaf; ovule; root;
      KW      flower; PCR; polymerase chain reaction; homology; transgenic plant; ds.
      XX      Synthetic.
      OS      US5521078-A.
      XX      PM
      XX      28-MAY-1996.
      PD      19-OCT-1994; 94US-00298687.
      PF      04-OCT-1988; 88US-00253243.
      PR      21-NOV-1990; 90US-00617239.
      PR      18-MAY-1992; 92US-00885970.
      XX      (CETU ) AGRACETUS INC.
      PA      John M;
      PI      WPI, 1996-267794/27.
      DR      Isolation of fibre-specific cotton promoter sequences - using selected
      PT      DNA probes to screen genomic DNA fragments, for production of cotton
      PR      fibres with improved characteristics.
      XX      Example; Col 23; 46pp; English.
      PS      Cotton fibre cell-specific promoter sequences were isolated by
      CC      differential screening of a cotton plant cDNA library. Of 4788 clones
      CC      from a 10 day cell library screened with leaf cDNAs, 800 clones not
      CC      present in the leaf were isolated. These were screened with cDNAs from
      CC      ovule, root and flower mRNAs and resulted in 79 clones isolated. PCR
      CC      analysis was then used to remove cross-hybridising clones. This resulted
      CC      in the isolation of 18 cDNA clones specifically expressed in cotton fibre
      CC      cells (AAT30242-4 and AAT30253-67). These cDNAs were then used to screen
      CC      for homologous genomic sequences (AAT30245-53 and AAT30268) in order to
      CC      obtain the corresp. promoter sequences. This primer was used to generate
      CC      the first cDNA strand from mRNA isolated from the cotton fibre cells. The
      CC      promoters isolated from the fibre cell-specific clones can be used to
      CC      generate transgenic cotton plants and lines producing fibres having
      CC      altered quantity and quality. (Updated on 25-MAR-2003 to correct PF
      CC      field.)
      XX

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```

SQ      Sequence 26 BP; 2 A; 3 C; 3 G; 18 T; 0 U; 0 Other;

Query Match          0.2%; Score 17.6; DB 1; Length 26;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches    20; Conservative   0; Mismatches     4; Indels       0; Gaps      0;

OY      4456 GCATGCACTTTTTTTTTTTTTTTT 4479
        ||| ||||| ||||| ||||| |||||
DB      3 GCTGTACCTTTTTTTTTTTTTTTT 26

RESULT 1114
ID      AAT43363 standard; DNA; 26 BP.
XX
XX      AAT43363;
AC
DT      11-MAR-1997 (first entry)
XX
DE      Cotton fibre first strand cDNA primer.
XX
KW      Fblate; promoter; fibre; transgenic plant; cotton; Gossypium hirsutum;
KM      primer; ss.
KK
OS      Synthetic.
XX
PN      MO9639021-A1.
XX
PD      12-DEC-1996.
XX
PF      06-JUN-1996; 96WO-US009449.
XX
PR      06-JUN-1995; 95US-00467504.
XX
PA      (MONS ) MONSANTO CO.
XX
PI      John ME;
XX
DR      WPI; 1997-042726/04.
PT      Plant fibre-specific, developmentally regulated Fblate promoter - useful
PT      for producing transgenic plants, esp. cotton, with altered fibre
PT      properties.
XX
PS      Example 2; Page 15; 79pp; English.
XX
CC      A primer (AAT43363) was used for first strand cDNA synthesis from RNA
CC      obd. From fibre cells of 23 day-old Coker 312 or 10 day-old Sea Island
CC      cotton bolls. The cDNA was used to construct a cDNA library from which
CC      cDNA clones (see also AAT43361-62) were isolated that corresponded to RNA
CC      prevalent in later fibre development. These clones were used to identify
CC      the Fblate promoter (AAT43360)
CC      CC
CC      XX
SQ      Sequence 26 BP; 2 A; 3 C; 3 G; 18 T; 0 U; 0 Other;

Query Match          0.2%; Score 17.6; DB 1; Length 26;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches    20; Conservative   0; Mismatches     4; Indels       0; Gaps      0;

OY      4456 GCATGCACTTTTTTTTTTTTTTTT 4479
        ||| ||||| ||||| ||||| |||||
DB      3 GCTGTACCTTTTTTTTTTTTTTTT 26

RESULT 1115
ID      AAT62627
XX
XX      AAT62627 standard; cDNA to mRNA; 26 BP.
AC      AAT62627;
XX
XX      25-MAR-2003 (revised)
DT      14-MAY-1997 (first entry)
XX
```

DE Primer for cotton fibre-specific cDNA amplification.
 XX cotton; fibre-specific; strength; transgenic plant; anthesis;
 KW developmentally regulated; E6; H6; antisense; sense; primer; PCR; ss.
 XX Synthetic.
 PN US5597718-A.
 XX
 PD 28-JAN-1997.
 XX
 PF 20-SEP-1995; 95US-00530797.
 XX
 PR 04-OCT-1988; 88US-00253243.
 PR 21-NOV-1990; 90US-00617239.
 PR 18-OCT-1993; 93US-00138814.
 XX
 PA (CETU) AGRACETUS.
 XX
 PI Bill WJ, Umbeck PF, John ME;
 XX
 DR WPI; 1997-108326/10.
 XX
 PT Produ. of transgenic cotton plants - by transformation with the H6 coding
 PT sequence or E6 anti-sense sequence, produces fibre of altered strength.
 XX
 PS Example 1; Col 6; 33pp; English.
 XX
 CC AAT62627 is a primer used for first strand cDNA synthesis from mRNA
 CC isolated from cotton fibre cells at different stages of development.
 CC Cotton fibre-specific cDNA clones (AAT62609-24) can be used to identify
 CC genomic clones by differential cDNA library screenings. Coding sequences
 CC from these isolated genes are used in sense or antisense orientation to
 CC alter the fibre characteristics, e.g. strength, of transgenic fibre-
 CC producing plants. (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 26 BP; 2 A; 3 C; 3 G; 18 T; 0 U; 0 Other;
 XX
 QY Query Match 0.2%; Score 17.6; DB 1; Length 26;
 Best Local Similarity 83.3%; Pred. No. 1e+03;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 DB 4456 GCATGACCTTTTCTTTTCTTTT 4479
 3 GCTGTACTCTTTTCTTTTCTTTT 26
 RESULT 1116
 AAT63663
 ID AAT63663 standard; DNA; 26 BP.
 XX
 AC AAT63663;
 XX
 DT 25-MAR-2003 (revised)
 DT 11-JUN-1997 (first entry)
 XX
 DE Primer for cotton fibre-specific cDNA synthesis.
 XX
 KW primer; PCR; polymerase chain reaction; cotton fibre; seed floss fibre;
 KW promoter; peroxidase; production; fibre strength; Sea Island;
 KW Gossypium sp; Coker; Kapok; G. barbadense; ss.
 XX
 OS Synthetic.
 OS
 PN US5608148-A.
 XX
 PD 04-MAR-1997.
 XX
 PF 25-JAN-1995; 95US-00378588.
 XX
 PR 30-SEP-1993; 93US-00130086.
 XX
 PA (CETU) AGRACETUS INC.

XX John ME;
 PI
 XX WPI; 1997-164559/15.
 DR
 XX Transgenic cotton plants with increased fibre strength - are transformed
 PT with construct containing peroxidase gene.
 XX
 PS Disclosure; Col 31; 43pp; English.
 XX
 CC This primer sequence was used for first strand cDNA synthesis of mRNA
 CC from cotton fibre-specific library. Cotton plants whose genome contains
 CC heterologous genetic construct comprising a seed floss fibre (SFF) -
 CC specific promoter isolated from cotton plants and a coding sequence
 CC encoding a peroxidase are useful for production of cotton with increased
 CC fibre strength. The peroxidase genes are over-expressed in fibre and not
 CC in other plant tissues where it would be harmful to the plant. (Updated
 CC on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 26 BP; 2 A; 3 C; 3 G; 18 T; 0 U; 0 Other;
 XX
 QY Query Match 0.2%; Score 17.6; DB 1; Length 26;
 Best Local Similarity 83.3%; Pred. No. 1e+03;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 DB 4456 GCATGACCTTTTCTTTTCTTTT 4479
 3 GCTGTACTCTTTTCTTTTCTTTT 26
 RESULT 1117
 AAT70058
 ID AAT70058 standard; cDNA; 26 BP.
 XX
 AC AAT70058;
 XX
 DT 25-MAR-2003 (revised)
 DT 20-AUG-1997 (first entry)
 XX
 DE Primer for cotton fibre specific cDNA amplification.
 XX
 KW cotton; E6; fibre; promoter; transgenic plant; truncated;
 KW heterologous gene expression; primer; PCR; ss.
 XX
 OS Synthetic.
 OS
 PN US5620882-A.
 XX
 PD 15-APR-1997.
 XX
 PF 19-OCT-1994; 94US-00298829.
 XX
 PR 04-OCT-1988; 88US-00253243.
 PR 21-NOV-1990; 90US-00617239.
 PR 18-MAY-1992; 92US-00865970.
 XX
 PA (CETU) AGRACETUS INC.
 XX
 PI John M;
 XX
 DR WPI; 1997-235185/21.
 XX
 PT DNA constructs contg. truncated promoter sequence - for fibre-specific
 PT gene expression in cotton plants.
 XX
 PS Example 1; Col 8; 48pp; English.
 XX
 CC AAT70058 is a primer used to synthesize first strand cDNA from mRNA
 CC isolated from cotton fibre cells at different stages of development.
 CC Claimed DNA constructs comprise a truncated promoter sequence (from one
 CC of AAT70031-38) that promotes preferential gene expression in plant fibre
 CC cells, a protein coding sequence not naturally associated with the
 CC promoter sequence and a 3' termination sequence. The DNA constructs are

CC useful for expressing foreign genes in fibre-producing plants, esp. to
 CC produce transgenic cotton plants with varied cotton fibre characteristics
 CC and quality. (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 26 BP; 2 A; 3 C; 3 G; 18 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.6; DB 1; Length 26;
 Best Local Similarity 83.3%; Pred. No. 1e+03;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4456 GCATGACCTTTTCTTTTCTTTT 4479
 DB 3 GCTGTACCTTTTCTTTTCTTTT 26

RESULT 1118
 AA208243
 ID AA208243 standard; DNA; 26 BP.

XX AA208243;

XX 25-JAN-2000 (first entry)

DE PCR primer-1 for identifying *P. vulgaris* zeatin O-xylosyltransferase DNA.

KW PCR primer; zeatin O-glucosyltransferase; inverse PCR; identify; homolog;
 zeatin O-xylosyltransferase; lima bean; ss.

OS Phaseolus lunatus.
 OS Synthetic.

XX WO951758-A1.

XX 14-OCT-1999;

XX 24-DEC-1998; 98WO-US027759.

XX 06-APR-1998; 98US-0080852P.

XX (UYOR-) UNTV OREGON STATE.

XX Mok DWS, Mok MC, Martin RC;

XX WPI; 1999-620210/53.

PT New purified zeatin-O-glucosyltransferase or -O-xylosyltransferase, used
 for regulating zeatin content.

XX Disclosure; Page 15; 64pp; English.

CC The present sequence is a PCR primer derived from *P. lunatus* zeatin O-
 CC glucosyltransferase cDNA. It can be used in inverse PCR to identify a
 CC homolog, zeatin O-xylosyltransferase gene from *P. vulgaris*

XX Sequence 26 BP; 5 A; 5 C; 7 G; 9 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.6; DB 1; Length 26;
 Best Local Similarity 83.3%; Pred. No. 1e+03;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6039 CTTGAGCTGTTCTTCATTCG 6062
 DB 1 CATGGAGATGGTTCTTCATTCG 24

RESULT 1119
 ABK90122
 ID ABK90122 standard; DNA; 26 BP.

XX ABK90122;

XX 21-OCT-2002 (first entry)

DE PCR primer GRV3HTFOR used to amplify groundnut rosette virus (GRV) ORF3.
 XX Gene silencing; cysteine-rich plant virus protein; suppressing function;
 KW non-plant; human gene therapy; groundnut rosette virus; GRV; ORF3; PCR;
 KW primer; ss.

OS Groundnut rosette virus.

XX WO200257301-A2.

XX 25-JUL-2002.

XX 21-JAN-2002; 2002WO-GB000234.

XX 19-JAN-2001; 2001GB-00001513.

XX (SCCR-) SCOTTISH CROP RES INST.

XX Talianekl ME, Riabov EV, Reavy B, Macfarlane SA;

XX WPI; 2002-590715/63.

PT Suppressing or inhibiting the gene silencing mechanism in a non-plant
 PT host cell, useful in many therapeutic implications, uses a cysteine-
 PT rich plant virus protein with post-transcriptional gene silencing
 PT suppressing functions.

PS Example 3; Page 39; 71pp; English.

CC The present invention relates to a new method of suppressing or
 CC inhibiting one or more gene silencing mechanisms in a non-plant host cell
 CC through the use of a cysteine-rich plant virus protein exhibiting post-
 CC transcriptional gene silencing suppressing functions. The method, which
 CC employs cysteine-rich plant virus protein, is useful in suppressing or
 CC inhibiting gene silencing mechanisms in a non-plant host cell. The
 CC suppression or inhibition of these gene silencing mechanisms may have
 CC many therapeutic implications, especially in gene therapy for humans,
 CC when a foreign gene expressing e.g. a therapeutic substance, needs to be
 CC introduced and expressed in a host cell. The present nucleic acid
 CC sequence represents a PCR primer that was used in the methods of the
 CC invention to amplify groundnut rosette virus (GRV) ORF3

XX Sequence 26 BP; 8 A; 10 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.6; DB 1; Length 26;
 Best Local Similarity 83.3%; Pred. No. 1e+03;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2401 GCTGGACCCACAGTGACACCAAC 2424

DB 2 GATGGTACCAATGACACCAAC 25

RESULT 1120
 ABK90743
 ID ABK90743 standard; DNA; 26 BP.

XX ABK90743;

XX 05-NOV-2002 (first entry)

DE Post-transcriptional gene silencing protection related primer #11.

KW Post-transcriptional gene silencing; transgene; unbraviral protein; ORF3;
 KW PTGS; PCR; primer; ss; groundnut rosette virus; GRV.

XX Synthetic.

XX WO200257467-A2.

XX 25-JUL-2002.

XX 21-JAN-2002; 2002WO-GB000252.

XX 19-JAN-2001; 2001GB-00001505.
PR (SCCR-) SCOTTISH CROP RES INST.
XX Reavy B, Macfarlane SA, Tilianski ME, Ribov EV;
XX WPI; 2002-590748/63.
DR
XX
XX use of umbravirus or an umbraviral protein for increasing expression of
PT heterologous protein or for protecting against post-transcriptional gene
XX silencing effected by a host cell.
XX
PS Example 5; Page 31, 49pp; English.
XX
XX The invention describes a method of increasing the expression of a
CC heterologous protein encoded by a virus vector or a transgene in a host
CC cell, or protecting a heterologous protein encoded by a virus vector or
CC transgene from post-transcriptional gene silencing effected by a host
CC cell. The method comprises causing the expression of an umbraviral
CC protein in the host cell and is useful for increasing the expression of
CC or protecting the heterologous protein encoded by a virus vector or a
CC transgene in a host cell. The ORF3 from an umbravirus is useful for
CC protecting RNA molecules from post-translational gene silencing (PTGS)
CC and PTGS-like responses. This sequence represents a PCR primer used in
CC the creation of a vector encoding groundnut rosette virus (GRV) ORF3 that
CC can suppress RNA interference in drosophila cells
XX
SQ Sequence 26 BP; 8 A; 10 C; 5 G; 3 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 17.6; DB 1; Length 26;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
QY 2401 GCTGGAGCCAGTGGACCAAC 2424
DB 2 GATGTAACCAATGACACACC 25
XX
RESULT 1121
ID ACC78121/c
XX ACC78121 standard; DNA; 26 BP.
XX
AC ACC78121;
XX
DT 18-AUG-2003 (first entry)
XX
DE Human group IIF sPLA2 cDNA amplifying RT-PCR antisense primer.
XX
XX Group IIF secreted phospholipase A2; sPLA2; phosphatidylglycerol; human;
KM phosphatidylcholine; antibacterial; virucide; cytosolic; vasotropic;
KM antiinflammatory; vulnery; cardiant; chromosome 1p35; transgenic; RT-;
KM primer; ss.
XX
OS Homo sapiens.
XX
XX WO2003033689-A1.
XX
XX 24-APR-2003.
XX
XX 12-OCT-2001; 2001WO-1B002407.
XX
XX 12-OCT-2001; 2001WO-1B002407.
XX
XX (CNRS) CNRS CENT NAT RECH SCI.
XX
XX Lazdunski M, Lambeau G, Valentin E;
XX
XX WPI; 2003-403216/38.
XX
XX Novel mammalian secreted group IIF secreted phospholipase A2, useful for
PT preventing and treating bacterial and viral infections, and cancers.
XX

PS Disclosure; Page 10; 33pp; English.
XX
XX The invention relates to a mammalian secreted group IIF secreted
CC phospholipase A2 (sPLA2) (I), where the enzyme is Ca2+ dependent.
CC maximally active at pH 7-8 and hydrolyzes phosphatidylglycerol versus
CC phosphatidylcholine with a 15-fold preference. A pharmaceutical
CC composition comprising (I) is useful for treating or preventing viral and
CC bacterial infections, and cancers. A pharmaceutical composition
CC containing compounds capable of inhibiting catalytic activity of (I),
CC biologically active compounds that bind sPLA2 receptors, or a compound
CC that modulates cell proliferation, cell migration, cell contraction or
CC apoptosis is useful for treating disease states or disorders involving
CC group IIF sPLA2, such as inflammatory disease, cancers, cardiac and brain
CC ischaemia, acute lung injury, acute respiratory distress syndrome or
CC Crohn's disease. Specific antibodies are useful for searching new
CC secreted mammalian group IIF sPLA2 or the homologues of the enzyme in
CC other mammals. The encoding polynucleotides and vectors are useful for
CC transforming animals and establishing a line of transgenic animals. The
CC present sequence represents a RT-PCR primer for amplifying the human
CC secreted group IIF sPLA2 enzyme encoding cDNA
XX
SQ Sequence 26 BP; 4 A; 14 C; 1 G; 7 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 17.6; DB 1; Length 26;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
QY 3209 TTGAGAAAGTGGTGGAGAGAGG 3232
DB 25 TTGAGAGAGAGAGCGGAGAGAGG 2
XX
RESULT 1122
ID ACD27980/c
XX ACD27980 standard; DNA; 26 BP.
XX
AC ACD27980;
XX
DT 25-SEP-2003 (first entry)
XX
DE Human group IIF secreted phospholipase A2 PCR primer #2.
XX
XX Human; group IIF secreted phospholipase A2; virucide; antibacterial;
KM cytosolic; antiinflammatory; vasotropic; cerebroprotective; sPLA2;
KM phosphatidylglycerol hydrolysis; phosphatidylcholine hydrolysis;
KM viral infection; bacterial infection; cancer; inflammatory disease;
KM cardiac ischaemia; brain ischaemia; acute lung injury;
KM acute respiratory distress syndrome; Crohn's disease; PCR; primer; ss.
XX
OS Homo sapiens.
XX
XX US2003073087-A1.
XX
XX 17-APR-2003.
XX
XX 11-OCT-2001; 2001US-00975456.
XX
XX 11-OCT-2000; 2000US-0239491P.
XX
XX (LAZD/) LAZDUNSKI M.
XX (LAMBE/) LAMBEAU G.
XX (VALE/) VALENTIN E.
XX
XX Lazdunski M, Lambeau G, Valentin E;
XX
XX WPI; 2003-567302/53.
XX
XX New mammalian secreted group IIF phospholipase A2 or nucleic acid, useful
PT for treating or preventing viral or bacterial infections, or cancers, or
PT screening inhibitors of the enzyme for treating e.g. inflammatory
XX diseases or ischaemia.
XX
XX Disclosure; Page 3; 16pp; English.
PS

SQ Sequence 27 BP; 8 A; 6 C; 7 G; 0 T; 5 U; 1 Other;

Dy 1345 AGTCGCTGATGAAGATGCCACT 1369
 |||::|||::|||:
Db 3 AGUGCCUAGANAGAACCACUCU 27

RESULT 1124
AAAX70934/C
ID AAAX70934 standard; RNA; 27 BP.
XX
AC AAAX70934;
DX
DT 28-JUL-1999 (first entry)
XX
DE Human KDR VEGF receptor hamsterhead ribozyme #606.

KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hamsterhead ribozyme; hairpin ribozyme; cleavage;
KM tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KM fms-like tyrosine kinase 1; kinase insert domain containing receptor;
 foetal liver kinase I; ss.

OS Synthetic.
SS Homo sapiens.

XN NO97J15662-AZ.
PD 01-MAY-1997.
XX
PF 25-OCT-1996; 96WO-US017480.
XX
PR 26-OCT-1995; 9SUS-0005974P.
PR 11-JUN-1996; 9BUS-00584040.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (CHIR) CHIRON CORP.
XX
PI Pavco P, Mcswigen J, Stinchcomb D, Escobedo J,
PT WPI; 1997-259017/23.

PX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PY stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.

PX Claim 9, Page 115, 218pp: English.

CC The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and Rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAK67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
CX
SQ Sequence 27 BP; 8 A; 8 C; 5 G; 0 T; 5 U; 1 Other;

Query Match 0.2%; Score 17.6; DB 1; Length 27;
Best Local Similarity 80.0%; Pred.No. 1.1e+03;
Matches 20;/Conservative 0;/Mismatches 5;/Indels 0;/Gaps 0

QY 4627 GGGAGTTGCACTTCAGTGGCAAT 4651
 |||||
 Db 25 GGGAGTTTCATCATGATGGCAT 1
 |||||

RESULT 1125

AA93814
 ID AAT93814 standard; DNA; 27 BP.

XX AAT93814;
 XX

DT 25-MAR-2003 (revised)
 DT 24-FEB-1998 (first entry)

XX Antitumoral phosphodiester oligonucleotide 4 with cytotoxic activity.
 XX

KM Phosphodiester; selective binding; cell viability; growth;
 KM tumoural cell line; cytotoxic activity; tumour cell; lymphoma;
 KM lymphoblastic tumour; ss.

XX Synthetic.
 XX

OS Key Location/Qualifiers
 FH modified_base 1..27
 FT /tag= a
 FT /note= "phosphodiester oligonucleotide"

XX MO9720924-A1.
 XX

PD 12-JUN-1997.
 PD

XX 04-DEC-1996; 96MO-EP005388.
 XX

XX 04-DEC-1995; 95IT-MI002539.
 XX

XX (SAIC-) SAICOM SRL.
 XX

PI Scaggiante B, Quadrifoglio F;
 PI

XX WPI; 1997-319771/29.
 XX

PT New phosphodiesteric oligonucleotide(s) - which exert a specific and
 PT selective cytotoxic effect on tumour cells, for treating both solid and
 PT liquid tumours.
 PT

XX Claim 10; Page 5; 38pp; English.
 XX

CC Novel phosphodiesteric oligonucleotides AAT93811-27 are based on the
 CC generic formula, in the 3'-5' or 5'-3' direction: (Gata')a''-(Gbtb')b''-
 CC (Gerc')c''-(Gdtd')d''-(Gerte')e''-(Gtrf')f''-(G-grg')g''-N', where: N and
 CC N' = T or G, equal or different from each other; x = 0-8, equal or
 CC different from each other; a', b', c', d', e', f', and g' = 0-10, equal or
 CC different from each other; a'', b'', c'', d'', e'', f'', and g'' = 0-30, equal
 CC or different from each other; a''', b''', c''', d''', e''', f''', and g''' = 1-
 CC 16, equal or different from each other. The oligonucleotides are believed
 CC to selectively bind and sequester some proteins which are essential to
 CC the viability and growth of tumoural cell line. They have specific and
 CC selective cytotoxic activity against tumour cells, and can be used for
 CC treating tumours of the liquid type, in particular of lymphoblastic
 CC origin, and of solid type, in particular lymphomas. The present
 CC phosphodiester oligonucleotide, at a concentration of 15 micromolar,
 CC reduced growth of CCRF-CEM tumoural cells by 79%, which is detectable 48
 CC hours after administration. (Updated on 25-MAR-2003 to correct PR field.)
 CC

XX Sequence 27 BP; 0 A; 0 C; 5 G; 22 T; 0 U; 0 Other;
 XX

Query Match 0.2%; Score 17.6; DB 1; Length 27;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;

Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4465 TTTTGTGTTTGTGTTGCTT 4488
 |||||

Db 1 TGTGTTTGTGTTTGTGTTT 24
 |||||

RESULT 1126

AA98219
 ID AAV98219 standard; RNA; 27 BP.
 XX

XX AAV98219;
 XX

DT 17-MAR-1999 (first entry)
 DT

XX Human EGF-R hammerhead ribozyme nucleotide position 1461.
 XX

KM Human; epidermal growth factor receptor; EGFR; EGF-R; target sequence;
 KM hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation;
 KM cancer; genetic drift; detection; mutation; ss.
 KM

XX Synthetic.
 XX

OS Homo sapiens.
 OS

XX WO9833893-A2.
 XX

PD 06-AUG-1998.
 PD

XX 14-JAN-1998; 98MO-US000730.
 XX

XX 31-JAN-1997; 97US-0036476P.
 XX

XX 04-DEC-1997; 97US-00985162.
 XX

XX (RIBO-) RIBOZYME PHARM INC.
 XX

PA (UYAS-) UNIV ASTON.
 PA

PI Akhtar S, Fell P, Mcswigen JA;
 PI

XX WPI; 1998-437449/37.
 XX

PT Enzymatic nucleic acids - which cleave RNA derived from an epidermal
 PT growth factor receptor, useful for inhibiting cell proliferation and for
 PT treating cancers.
 PT

XX Claim 8; Page 71; 109pp; English.
 XX

CC The present invention describes enzymatic nucleic acid molecules (NAMS)
 CC which specifically cleave RNA derived from an epidermal growth factor
 CC receptor (EGF-R) gene. AAV97221 to AAV98043 and AAV98979 to AAV99090
 CC represent specifically claimed target sequence from human EGF-R. AAV98044
 CC to AAV98866 and AAV98867 to V9878 represent hammerhead ribozymes and
 CC hairpin ribozymes respectively for human EGF-R. The NAMS are useful for
 CC cleaving EGF-R RNA in the treatment of a condition associated with EGFR
 CC expression levels e.g. to inhibit cell proliferation in the prevention or
 CC treatment of cancers. The NAMS can also be used as diagnostic tools to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of EGF-R RNA in a cell
 CC

XX Sequence 27 BP; 7 A; 5 C; 6 G; 0 T; 8 U; 1 Other;
 XX

Query Match 0.2%; Score 17.6; DB 1; Length 27;
 Best Local Similarity 52.0%; Pred. No. 1.1e+03;

Matches 13; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 5812 CTGCGTATGAGTGAATGCT 5836
 |||||

Db 1 CCGCGUACUGAGUAGAAUUUCU 25
 |||||

RESULT 1127

AA59569
 ID AA59569 standard; DNA; 27 BP.

XX AA59569;
 XX

DT 14-NOV-2000 (first entry)
 DT

DE PCR primer used to amplify a human mGluR6 gene fragment.
 XX
 XX Human; metabotropic glutamate receptor; mGluR6; central nervous system;
 KW presynaptic release; glutamate; post synaptic sensitivity; neuronal cell;
 KW glutamate excitation; neurodegenerative condition; antipsychotic;
 KW anticonvulsant; analgesic; anxiolytic; antidepressant; antiemetic;
 KW PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 XX US6103524-A.
 XX
 XX 15-AUG-2000.
 XX
 XX 30-AUG-1998; 98US-00126280.
 XX
 XX 30-AUG-1998; 98US-00126280.
 XX
 XX (ELIL) LILLY & CO ELI.
 XX
 XX Belagaje RM, Wu S;
 XX
 XX WPI; 2000-531979/48.
 XX
 XX Novel nucleic acid encoding a human metabotropic glutamate receptor,
 PT useful for treating neurodegenerative disorders and for modulating
 PT presynaptic release of glutamate.
 XX
 XX Example 2; Col 20; 25pp; English.
 XX
 XX PCR primers AAA59568-69 were used to amplify a human metabotropic
 CC glutamate receptor (designated mGluR6) gene fragment. The receptor is
 CC believed to potentiate central nervous system responses. The polypeptide
 CC is useful to modulate the presynaptic release of glutamate and post
 CC synaptic sensitivity of neuronal cell to glutamate excitation. Agonists
 CC and antagonists of mGluR6 are useful for treating acute and chronic
 CC neurodegenerative conditions, and are used as antipsychotic,
 CC anticonvulsant, analgesic, anxiolytic, antidepressant, antiemetic agents
 CC
 SQ Sequence 27 BP; 4 A; 7 C; 10 G; 6 T; 0 U; 0 Other;
 Query Match 0.2%; Score 17.6; DB 1; Length 27;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 364 GACGTGACCACTACGAGTGAGC 387
 DB 4 GACGGGTACCGCTTCCAGGTGAGC 27
 RESULT 1128
 AAS98280
 ID AAS98280 standard; DNA; 27 BP.
 XX
 XX AAS98280;
 AC
 XX
 XX 12-MAR-2002 (first entry)
 DT
 XX
 XX Human plakoglobin interacting protein PLA_2H12 PCR primer #76.
 DE
 XX
 XX Human; plakoglobin; cytosolic; osteopathic; dermatological; cardiac;
 KW plakoglobin related disease; skin carcinoma; acantholytic disease;
 KW basal cell carcinoma; squamous cell carcinoma; Naxos disease; PCR primer;
 KW extramammary Paget's disease; heart disease; skin blistering;
 KW subcorneal acantholysis; Grover's disease; Halley-Halley's disease;
 KW Darier's disease; ectodermal dysplasia; skin fragility syndrome; ss.
 KW
 XX
 OS Homo sapiens.
 XX
 XX WO200185933-A2.
 XX
 XX 15-NOV-2001.
 PD
 XX

PF 02-MAY-2001; 2001WO-EP004872.
 XX
 XX
 PR 09-MAY-2000; 2000EP-00201668.
 XX
 XX (VLA-) VLAAMS INTERNUNIVERSITAIR INST BIOTECNOG.
 XX
 XX Van Roy F, Bonne S, Vanlandeschot A;
 PI
 XX
 XX WPI; 2002-062246/08.
 DR
 XX
 PT New polypeptide, useful for treating skin carcinoma or acantholytic
 PT disease such as Grover's and Darier's disease, comprises a protein
 PT interacting with human plakoglobin and involved in transduction of
 PT plakoglobin related signal to nucleus.
 XX
 XX
 PS Disclosure; Page 29; 98pp; English.
 XX
 XX The invention relates to an isolated plakoglobin interacting polypeptide
 CC (1). (1) is useful as a medicament and in the manufacture of a medicament
 CC for treating plakoglobin related diseases, such as skin carcinoma or an
 CC acantholytic disease, and to screen compounds that interfere with the
 CC interaction of the polypeptide with plakoglobin The plakoglobin related
 CC diseases include basal cell carcinoma; squamous cell carcinoma;
 CC extramammary Paget's disease; Naxos disease; heart diseases; skin
 CC blistering and acantholytic diseases such as subcorneal acantholysis,
 CC Grover's disease, Halley-Halley's disease or Darier's disease, and
 CC ectodermal dysplasia/skin fragility syndrome. AAS98201- AAS98288
 CC represent novel human plakoglobin interacting protein coding sequences
 CC and PCR primers of the invention
 XX
 SQ Sequence 27 BP; 8 A; 10 C; 6 G; 3 T; 0 U; 0 Other;
 Query Match 0.2%; Score 17.6; DB 1; Length 27;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 4988 GCACAAGCCGACTGAGAAGAGA 5011
 DB 4 GCACCTCCCACTGAGAAGAGA 27
 RESULT 1129
 ABZ58842
 ID ABZ58842 standard; DNA; 27 BP.
 XX
 XX ABZ58842;
 AC
 XX
 XX 28-APR-2003 (first entry)
 DT
 XX
 XX Histidine tag encoding DNA.
 DE
 XX
 KW Genetic information; glyph; molecular biology; histidine tag; ds.
 KW
 XX
 OS Synthetic.
 XX
 XX
 FH Key Location/Qualifiers
 FT CDS 1..27
 FT /*tag= a
 XX
 XX WO200282264-A2.
 XX
 XX 17-OCT-2002.
 PD
 XX
 PF 05-APR-2002; 2002WO-US010825.
 XX
 XX 06-APR-2001; 2001US-0282022P.
 PR
 XX
 XX (SEED/) SEED B.
 PA
 XX
 XX Seed B;
 PI
 XX
 XX WPI; 2003-058588/05.
 DR
 XX P-PSDB; ABB71241.

XX displaying genetic information represented by set of glyphs, by receiving
PT entered command to display glyphs, identifying glyph assigned to the
PT entered command, and displaying identified glyph.
XX
XX Example 3; Page 37; 50pp; English.
XX
CC The invention relates to displaying genetic information represented by a
CC set of glyphs. The method involves receiving an entered command to
CC display one of the set of glyphs, identifying the glyph of the set
CC assigned to the entered command, and displaying the identified glyph,
CC where the glyph is displayed at a location on a display screen with a
CC cursor. Another method for displaying a double-stranded codon and an
CC amino acid encoded by the codon is also provided. The methods provide
CC simple and quick way for displaying and genetic information that has been
CC modified by a standard molecular biology technique. The present sequence
CC represents a DNA fragment encoding a histidine tag
XX
SQ Sequence 27 BP; 9 A; 12 C; 5 G; 1 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 17.6; DB 1; Length 27;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
QY 7410 CATCAGCAGCAGCAGCAGCAGCAG 7433
DB 1 CACCAGCAGCAGCAGCAGCAGCAG 24
XX
RESULT 1130
AAH20344/C
XX AAH20344 standard; DNA; 40 BP.
XX
AC AAH20344;
XX
DT 01-AUG-2001 (first entry)
XX
XX HHV6 virus p41 gene specific primer p41FH373 SEQ ID 25.
DB
XX
XX Primer; solid phase amplification of DNA template; SPADT; detection; RGP;
XX genomic scanning; bacterial diagnostic; p41; HHV6; ss.
XX
OS Human herpesvirus 6.
XX
XX Synthetic.
XX
XX US6221635-B1.
XX
XX 24-APR-2001.
XX
XX 06-MAY-1999; 99US-00306290.
XX
XX 06-MAY-1999; 99US-00306290.
XX
XX (WIST-) WISTAR INSR.
XX
XX
XX Rovera G, Mukhopadhyay S;
XX
XX MPI; 2001-315577/33.
XX
XX
PT Detecting the presence of a specific nucleic acid in a sample containing
PT DNA, useful in scanning large genomic fragments for the presence of genes
PT or gene families, comprises performing solid phase amplification of DNA
PT template.
XX
XX Example 2; Col 28; 49pp; English.
XX
XX This invention relates to a method for detecting the presence of a
XX specific nucleic acid in a sample containing DNA. The method comprises
XX performing solid phase amplification of DNA template (SPADT). 5' and 3'
XX primers are irreversibly bound to a solid support, and the DNA from a
XX sample is absorbed and reversibly bound, incubated under amplification
XX reaction conditions and the presence of the specific target DNA is
XX detected. The method is useful for detecting the presence of a specific

CC nucleic acid (e.g. bacterial, viral or parasitic DNA) in a sample or in a
CC cell. SPADT may be used for scanning large genomic fragments for the
CC presence of genes or gene families; or for bacterial diagnostics by
CC examining the ribosomal RNA genes; or for viral diagnostics by scanning
CC for the presence of viral nucleic acid sequences in a sample. SPADT may
CC also be used in forensic medicine by detecting and identifying species
CC specific sequences or for the presence of major histocompatibility
CC complex. The present sequence represents a primer specific for the human
CC herpesvirus 6 (HHV6) p41 gene. The primer is used in an example
XX illustrating the method of the invention
XX
SQ Sequence 40 BP; 4 A; 2 C; 6 G; 28 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 17.6; DB 1; Length 40;
Best Local Similarity 65.0%; Pred. No. 1.6e+03;
Matches 26; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
XX
QY 3992 AACAAATACTTGTCTAAATGAGAAAGAGAGA 4031
DB 40 ACCAAACCTCTGTATGTAGAAAAA 1
XX
RESULT 1131
AAT78911/C
XX AAT78911 standard; cDNA; 42 BP.
XX
AC AAT78911;
XX
DT 09-FEB-1998 (first entry)
XX
XX
DE Poly-glutamine repeat region coding sequence from clone AAD20.
XX
XX Monoclonal antibody; neurodegenerative disease; polyglutamine; TBP;
XX repeat region; affinity; TARA binding protein; Kennedy disease;
XX transcription initiation factor; lymphoblastic cell line; schizophrenia;
XX Huntington's disease; dominant autosomal spinocerebellar ataxia;
XX X-linked spinobulbar muscular atrophy; familial spastic paraplegia;
XX dentroribial-pallidolusial atrophy; bipolar affective disorder;
XX manic depressive psychosis; ss.
XX
XX Homo sapiens.
XX
XX WO9717445-A1.
XX
XX 15-MAY-1997.
XX
XX 08-NOV-1996; 96WO-FR001773.
XX
XX 10-NOV-1995; 95FR-00013576.
XX
XX (CNRS) CNRS CENT NAT RECH SCI.
XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX
XX Tora L, Lutz Y, Trotter Y, Mandel J;
XX
XX MPI; 1997-281034/25.
XX
XX
PT Antibody 1C2 used for treating or preventing neuro-degenerative diseases
PT - associated with proteins containing long poly-glutamine repeats, e.g.
PT Huntington's disease.
XX
XX Claim 21; Page 44; 69pp; French.
XX
XX The invention relates to a monoclonal antibody (Mab) 1C2 for the
XX treatment of neurodegenerative diseases associated with the presence of
XX polyglutamine repeat regions. This Mab is already known for its affinity
XX to the TARA binding protein (TBP) transcription initiation factor,
XX especially at the amino acid sequence LEEQQRQQRQQRQ found at the N-
XX terminus of TBP. Mab 1C2 has been shown to have a high affinity for
XX polyglutamine repeats with a proportional affinity to the number of
XX glutamine repeats. This affinity has been used to identify genes encoding
XX proteins containing long polyglutamine repeats which are implicated in
XX neurodegenerative diseases. A screen of an expression library, generated

CC from a lymphoblastic cell line from a patient suffering from
CC spinocerebellar ataxia (SCA), with Mab 1C2 isolated 6 new sequences
CC (AA178966-178911) encoding polyglutamine repeats. This sequence is
CC derived from clone MAD20 isolated from a patient suffering from SCA2. Mab
CC 1C2, active fragment of it or nucleic acids encoding it are specifically
CC used to treat Huntington's disease, SCA types 1-5 or 7, X-linked spino-
CC bulbar muscular atrophy (Kennedy disease), dentatorubral-pallidoluysial
CC atrophy, dominant autosomal spinocerebellar ataxia, familial spastic
CC paraplegia, bipolar affective disorder, manic depressive psychoses and
CC schizophrenia
XX
SQ Sequence 42 BP, 14 A, 14 C, 14 G, 0 T, 0 U, 0 Other;
XX
Query Match 0.2%; Score 17.6; DB 1; Length 42;
Best Local Similarity 65.0%; Pred. No. 1.7e+03;
Matches 26; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 32 GCTGCTGCAGGCTCCGCGCGGCGGCAACGAGGCTGCGG 71
DB 40 GCTGCTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1
RESULT 1132
AA513782/C
ID AA513782 standard; DNA; 42 BP.
XX
AC AA513782;
XX
DT 08-MAY-2002 (first entry)
XX
DE Simple sequence repeat, SSR, #53.
XX
KM Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat;
XX cereal profiling; grass profiling; seed batch purity testing.
XX
OS Synthetic.
XX
PN NZ509193-A.
XX
PD 25-MAY-2001.
XX
PF 03-JAN-2001; 2001NZ-00509193.
XX
PR 24-DEC-1999; 99AU-00004906.
XX
PR 04-MAY-2000; 2000AU-00007310.
XX
PA (SAUS-) STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R.
XX (UYSC-) UNIT SOUTHERN CROSS.
XX (VIC-) STATE VICTORIA DEPT NATURAL RES & ENVIRO.
XX (UYAD-) UNIT ADELAIDE.
XX (ITMA-) INT MAIZE & WHEAT IMPROVEMENT CENT.
XX
PI Forster JW, Jones ES;
XX
XX WPI; 2001-512563/56.
XX
PT New simple sequence repeats having 2 or more tandemly repeated nucleotide
PT core elements isolated from ryegrass and fescue, useful for selecting of
PT genes in grass or cereal breeding or profiling grass or cereal species
PT varieties.
XX
PS Claim 13; Page 53; 72pp; English.
XX
XX The invention relates to a substantially purified or isolated nucleic
XX acid (I) from ryegrass or fescue species including a simple sequence
XX repeat (SSR), having 2 or more tandemly repeated nucleotide core elements
XX 2-6 nucleotides in length. Also included are a nucleic acid primer
XX suitable for amplifying an SSR, identifying (MI) an SSR by preparing a
XX library of ryegrass or fescue genomic DNA enriched for SSRs and
XX identifying clones in the library containing SSRs, a library of ryegrass
XX or fescue genomic DNA enriched for SSRs prepared by the MI, selecting for
XX a gene in grass or cereal breeding by identifying an SSR that is closely
XX associated with the gene such that the SSR and the gene are

CC preferentially co-inherited, and selecting for the SSR in the breeding, a
CC method for DNA profiling grass or cereal species varieties by assessing
CC variation between SSR varieties and testing the purity of grass or cereal
CC seed batches by assessing variation within seed batch of an SSR. The SSRs
CC may be used in the selection of genes in grass or cereal breeding, for
CC profiling grass or cereal species varieties, for testing the purity of
CC grass or cereal seed batches, and for DNA profiling to establish the
CC distinct identity, uniformity and/or stability of a cultivar. The present
CC sequence is a ryegrass or fescue SSR
XX
SQ Sequence 42 BP, 14 A, 14 C, 14 G, 0 T, 0 U, 0 Other;
XX
Query Match 0.2%; Score 17.6; DB 1; Length 42;
Best Local Similarity 65.0%; Pred. No. 1.7e+03;
Matches 26; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 32 GCTGCTGCAGGCTCCGCGCGGCGGCAACGAGGCTGCGG 71
DB 42 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3
RESULT 1133
AAQ75553
ID AAQ75553 standard; DNA; 19 BP.
XX
AC AAQ75553;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KM Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENSEQ files AAQ75547-075798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c) the
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 19 BP, 1 A, 0 C, 0 G, 18 T, 0 U, 0 Other;
XX
Query Match 0.2%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 7.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4482
DB 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 19

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RESULT 1134
AAQ75551
ID AAQ75551 standard; DNA; 19 BP.
XX
XX AAQ75551;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 19 BP; 1 A; 0 C; 1 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 17.4; DB 1; Length 19;
XX Best Local Similarity 94.7%; Pred. No. 7.1e+02;
XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 4466 TTTTTTTTTTTTTTTG 4484
XX 1 TTTTTTTTTTTTTTTAG 19
XX
XX RESULT 1135
XX AAQ75555
XX ID AAQ75555 standard; DNA; 19 BP.
XX
XX AAQ75555;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX

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PR 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 19 BP; 0 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 17.4; DB 1; Length 19;
XX Best Local Similarity 94.7%; Pred. No. 7.1e+02;
XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 4466 TTTTTTTTTTTTTTTG 4484
XX 1 TTTTTTTTTTTTTTTTCG 19
XX
XX RESULT 1136
XX AAQ75557
XX ID AAQ75557 standard; DNA; 19 BP.
XX
XX AAQ75557;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 19 BP; 0 A; 1 C; 0 G; 18 T; 0 U; 0 Other;
XX

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XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESBQ files AAQ75547-075798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily.
XX
XX Sequence 20 BP; 0 A; 2 C; 1 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 17.4; DB 1; Length 20;
XX Best Local Similarity 94.7%; Pred. No. 7.6e+02;
XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 4466 TTTT TTTT TTTT TTTT TTTT G 4484
XX | | | | | | | | | | | | | | | | | |
XX 1 TTTT TTTT TTTT TTTT TTTT CG 19
XX
XX RESULT 1143
XX AAQ75600
XX ID AAQ75600 standard; DNA; 20 BP.
XX
XX AAQ75600;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESBQ files AAQ75547-075798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily.
XX
XX Sequence 20 BP; 0 A; 2 C; 1 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 17.4; DB 1; Length 20;
XX Best Local Similarity 94.7%; Pred. No. 7.6e+02;
XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 4466 TTTT TTTT TTTT TTTT TTTT G 4484
XX | | | | | | | | | | | | | | | | | |
XX 1 TTTT TTTT TTTT TTTT TTTT CG 19
XX
XX RESULT 1145
XX AAQ75592
XX ID AAQ75592 standard; DNA; 20 BP.
XX
XX

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CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily.
XX
XX Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 17.4; DB 1; Length 20;
XX Best Local Similarity 94.7%; Pred. No. 7.6e+02;
XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 4464 TTTT TTTT TTTT TTTT TTTT T 4482
XX | | | | | | | | | | | | | | | | | |
XX 1 TTTT TTTT TTTT TTTT TTTT CT 19
XX
XX RESULT 1144
XX AAQ75578
XX ID AAQ75578 standard; DNA; 20 BP.
XX
XX AAQ75578;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESBQ files AAQ75547-075798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily.
XX
XX Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 17.4; DB 1; Length 20;
XX Best Local Similarity 94.7%; Pred. No. 7.6e+02;
XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 4466 TTTT TTTT TTTT TTTT TTTT G 4484
XX | | | | | | | | | | | | | | | | | |
XX 1 TTTT TTTT TTTT TTTT TTTT TG 19
XX
XX RESULT 1145
XX AAQ75592
XX ID AAQ75592 standard; DNA; 20 BP.
XX
XX

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AC AAQ75592;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX
XX Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
SO
XX
XX Query Match 0.2%; Score 17.4; DB 1; Length 20;
XX Best Local Similarity 94.7%; Pred. No. 7.6e+02;
XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4466 TTTT TTTT TTTT TTTT TTTT G 4484
XX 1 TTTT TTTT TTTT TTTT TTTT G 19
DB
XX
XX RESULT 1146
XX AAQ75576
XX ID AAQ75576 standard; DNA; 20 BP.
XX
XX AAQ75576;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX

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DR WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX
XX Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 U; 0 Other;
SO
XX
XX Query Match 0.2%; Score 17.4; DB 1; Length 20;
XX Best Local Similarity 94.7%; Pred. No. 7.6e+02;
XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4466 TTTT TTTT TTTT TTTT TTTT G 4484
XX 1 TTTT TTTT TTTT TTTT TTTT G 19
DB
XX
XX RESULT 1147
XX AAV52665
XX ID AAV52665 standard; DNA; 20 BP.
XX
XX AAV52665;
XX
XX 21-DEC-1998 (first entry)
XX
XX Hepatocyte nuclear factor 4 alpha gene exon 1 forward PCR primer.
DE
XX
XX Hepatocyte nuclear factor 4 alpha; HNF-4 alpha; MODY1; human;
KM transcription factor; maturity onset diabetes of the young; TCF14;
KM diabetes; NIDDM; diagnosis; therapy; PCR; primer; ss.
XX
XX Synthetic.
XX
XX Homo sapiens.
OS
XX
XX WO9811254-A1.
XX
XX 19-MAR-1998.
XX
XX 10-SEP-1997; 97WO-US016037.
XX
XX 10-SEP-1996; 96US-0025719P.
XX
XX 02-OCT-1996; 96US-0028056P.
XX
XX 30-OCT-1996; 96US-0029679P.
XX
XX (ARCH-) ARCH DEV CORP.
XX
XX Bell GI, Yamagata K, Oda N, Kaisaki PJ, Furuta H, Menzel S;
PI Horikawa Y;
XX
XX WPI; 1998-271667/24.
XX
XX Isolated nucleic acid encoding hepatocyte nuclear factor 1-alpha and 1-
PT beta - useful for detecting susceptibility for non-insulin dependent
XX diabetes, especially maturity-onset diabetes of the young.
XX
XX Example 3; Page 112; 363pp; English.
XX
XX This is a forward PCR primer designed for use with a reverse primer (see
CC AAV52665) in the PCR amplification of exon 1 and the flanking introns
CC (see AAV52654) of the human hepatocyte nuclear factor-4 alpha (HNF-4
CC alpha) gene (see AAV52687). Mutations of the HNF-4 alpha gene have been
CC identified by amplifying (see AAV52665-86) and sequencing the appropriate
CC exon. The invention concerns the identification of genes responsible for

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CC non-insulin dependent diabetes mellitus (NIDDM) for use in diagnostics
 CC and therapeutics. It demonstrates that the MODY1 (maturity-onset diabetes
 CC of the young) locus is the HNF-4 alpha gene. Analysis of mutations in the
 CC HNF-4 alpha gene can be diagnostic for diabetes

CC Sequence 20 BP; 4 A; 3 C; 11 G; 2 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.4; DB 1; Length 20;
 Best Local Similarity 94.7%; Pred. No. 7.6e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5017 GGGCTCTGGAGAGGAGCAG 5035

DB 1 GGGCACTGGAGAGGAGCAG 19

RESULT 1148
 AAA55807/C
 ID AAA55807 standard; DNA; 20 BP.

AC AAA55807;

DT 01-SEP-2000 (first entry)

DE Human histone deacetylase HD2 antisense oligonucleotide SEQ ID NO:52.

DE Human; DNA methyltransferase; DNA Methylase; antisense oligonucleotide;
 KM modulation; inhibition; gene expression; combination therapy; p16;
 KM histone deacetylase; HDAC; thymidylate synthase; tumour suppressor;
 KM methylation; gene therapy; cyclostatic; antiasthmatic;
 KM antiinflammatory; inflammation; asthma; ss.

OS Homo sapiens.

PN WO200023112-A1.

PD 27-APR-2000.

PF 19-OCT-1999; 99WO-US024278.

PR 19-OCT-1998; 98US-0104804P.

PA (METH-) METHYLGENE INC.

PI Besterman JM, Macleod AR, Siders WM;

DR WPI; 2000-339532/29.

PT Inhibiting gene expression e.g. DNA methyltransferase, by treating cells
 PT with a synergistic amount of antisense oligonucleotide and protein
 PT effectors e.g. 5-aza-cytidine of gene products, useful for gene therapy
 PT of e.g. tumors.

PS Disclosure; Page 29; 99pp; English.

CC The present invention describes a method for inhibiting the expression of
 CC a gene in a cell comprising contacting the cell with an effective
 CC synergistic amount of an antisense oligonucleotide which inhibits
 CC expression of the gene, and an effective synergistic amount of a protein
 CC effector of a product of the gene. Also described are: (1) a method for
 CC treating a disease responsive to inhibition of a gene in a mammal; (2) a
 CC method for inhibiting tumour growth in mammal; (3) an inhibitor of a gene
 CC comprising an antisense oligonucleotide which inhibits expression of the
 CC gene in operable association with a protein effector of a gene product;
 CC and (4) a pharmaceutical composition comprising the inhibitor of (3). The
 CC methods and compositions are useful as analytical tools for transgenic
 CC studies and as therapeutic tools, e.g. as gene therapy tools for human
 CC diseases including benign and malignant tumors, inflammation or asthma.
 CC The methods, inhibitors and compositions of the invention that inhibit
 CC expression or activity of a gene or gene product may be used to treat
 CC patients having, or predisposed to developing, a disease responsive to
 CC inhibition of the gene. These may also be used to activate silenced genes
 CC to provide missing gene functions and improve a given condition.

CC Furthermore, the methods and compositions are useful as probes of the
 CC physiological function of a gene product in an experimental cell culture
 CC or animal system; and to evaluate the effect of inhibiting gene activity
 CC or expression. AAA5558 to AAA55842 represent oligonucleotide sequences
 CC which are used in the exemplification of the present invention

CC Sequence 20 BP; 0 A; 9 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.4; DB 1; Length 20;
 Best Local Similarity 94.7%; Pred. No. 7.6e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7415 GCAGCAGCAGCAGCAGCAG 7433

DB 20 GCAGCAGCAGCAGCAGCAG 2

RESULT 1149
 AAH43117/C
 ID AAH43117 standard; DNA; 20 BP.

AC AAH43117;

DT 19-SEP-2001 (first entry)

DE Antisense oligo, target HDAC-2 132-152.

DE Antisense; histone deacetylase; HDAC-1; HDAC-2; HDAC-4; inhibitor;
 KM cell proliferation; cancer; restenosis; psoriasis; protozoal infection;
 KM fungal infections; ss.

OS Synthetic.

PN WO200138322-A1.

PD 31-MAY-2001.

PF 22-NOV-2000; 2000WO-IB001881.

PR 23-NOV-1999; 99US-0167035P.

PA (METH-) METHYLGENE INC.

PI Delorme D, Ruel R, Lavoie R, Thibault C, Abou-Khalil E;

DR WPI; 2001-432601/46.

PT New inhibitors of histone deacetylase e.g. N-hydroxy-5-(4-
 PT (benzenesulfonylamino)-phenyl)-4-yn-2-pentanamide for treating cancer,
 PT restenosis or fungal infections.

PS Disclosure; Page 40; 147pp; English.

CC The sequences given in AAH43115-21 are oligonucleotides which are
 CC antisense to the histone deacetylase gene, HDAC-2. These oligonucleotides
 CC may be used in combination with an inhibitor of histone deacetylase
 CC enzyme function, to given an improved inhibitory effect, thereby reducing
 CC the amount of inhibitor required to obtain a given inhibitory effect.
 CC Compounds containing these oligonucleotides may be used to treat cell
 CC proliferation conditions such as cancer, restenosis or psoriasis. They
 CC can also be used to treat protozoal and fungal infections

CC Sequence 20 BP; 0 A; 9 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.4; DB 1; Length 20;
 Best Local Similarity 94.7%; Pred. No. 7.6e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7415 GCAGCAGCAGCAGCAGCAG 7433

DB 20 GCAGCAGCAGCAGCAGCAG 2

```

RESULT 1150
AAC89537/C
ID AAC89537 standard; DNA; 20 BP.
XX
AC AAC89537;
XX
DT 08-MAR-2001 (first entry)
XX
DE Human HDAC-2 PCR primer SEQ ID NO: 7.
XX
KM Histone deacetylase; HDAC-1; HDAC-2; HDAC-3; HDAC-4; HDAC-5; HDAC-C;
KM HDAC-D; cell cycle; tumorigenesis; cancer; inhibitor; antisense;
KM gene therapy; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200071703-A2.
XX
PD 30-NOV-2000.
XX
PF 03-MAY-2000; 2000WO-IB001252.
XX
PR 03-MAY-1999; 99US-0132287P.
XX
PA (METH-) METHYLGENE INC.
XX
PI Macleod AR, Li Z, Besterman JM;
XX
DR WPI; 2001-016407/02.
XX
PT Antisense oligonucleotide that inhibits expression of a histone
PT deacetylase, useful for treating and/or alleviating the symptoms of
PT neoplasia, or for inhibiting neoplastic cell growth in an animal.
XX
PS Disclosure; Page 12; 125pp; English.
XX
CC The present invention provides inhibitors of histone deacetylase enzymes
CC such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-C and HDAC-D. These
CC inhibitors may be antisense strands or they may be compounds identified
CC by contacting the enzyme with the compound and measuring the resulting
CC enzyme activity. These inhibitors are useful for treating cancers and for
CC identifying which histone deacetylase is involved in a neoplasia
XX
SQ Sequence 20 BP; 0 A; 9 C; 5 G; 6 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 7.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7415 GCAGCAGCAGCAGCAGCAG 7433
DB 20 GCAGCAGCAGCAGCAGCAG 2

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XX
PF 03-MAY-2000; 2000WO-IB001252.
XX
PR 03-MAY-1999; 99US-0132287P.
XX
PA (METH-) METHYLGENE INC.
XX
PI Macleod AR, Li Z, Besterman JM;
XX
DR WPI; 2001-016407/02.
XX
PT Antisense oligonucleotide that inhibits expression of a histone
PT deacetylase, useful for treating and/or alleviating the symptoms of
PT neoplasia, or for inhibiting neoplastic cell growth in an animal.
XX
PS Example 1; Page 24; 125pp; English.
XX
CC The present invention provides inhibitors of histone deacetylase enzymes
CC such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-C and HDAC-D. These
CC inhibitors may be antisense strands or they may be compounds identified
CC by contacting the enzyme with the compound and measuring the resulting
CC enzyme activity. These inhibitors are useful for treating cancers and for
CC identifying which histone deacetylase is involved in a neoplasia
XX
SQ Sequence 20 BP; 0 A; 9 C; 5 G; 4 T; 2 U; 0 Other;
XX
Query Match 0.2%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 7.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7415 GCAGCAGCAGCAGCAGCAG 7433
DB 20 GCAGCAGCAGCAGCAGCAG 2

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RESULT 1152
AAF83959
ID AAF83959 standard; DNA; 20 BP.
XX
AC AAF83959;
XX
DT 06-AUG-2001 (first entry)
XX
DE BAP28 gene fragment amplifying primer BAP28polyTCout.
XX
KM BAP28; prostate; tumour; cancer; diagnostic; genetic analysis; PCTA-1;
KM PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200100669-A2.
XX
PD 04-JAN-2001.
XX
PF 23-JUN-2000; 2000WO-IB001183.
XX
PR 25-JUN-1999; 99US-0141323P.
XX
PR 18-JAN-2000; 2000US-0176880P.
XX
PA (GEST ) GENSET.
XX
PI Barry C, Bougueleret L, Chumakov I, Cohen-Akenine A;
XX
DR WPI; 2001-367032/38.
XX
PT New BAP28 polynucleotides and polypeptides overexpressed in prostate
PT cancer cells for diagnosing prostate tumors, e.g. by hybridization or
PT polymerase chain reaction assays.
XX
PS Example; Page 347; 349pp; English.
XX
CC The invention is directed to BAP28 polypeptides, BAP28 polynucleotide
CC sequences and regulatory region located at the 3' and 5' ends of the

```

CC BAP28 coding region. The BAP28 polypeptides can be expressed by standard
 CC recombinant methodology. BAP28 polynucleotides and polypeptides have been
 CC found to be over expressed in prostate tumour cells, therefore levels of
 CC BAP28 expression and/or activity may be assayed (e.g. by polymerase chain
 CC reaction (PCR)) to diagnose patient suffering from or susceptible to
 CC prostate cancer. Antibodies specific for the BAP28 polypeptides are
 CC useful as diagnostic reagents. Biallelic markers of the BAP28 gene are
 CC useful in genetic analysis. Sequences AAF83934-963 represent primers for
 CC the BAP28 gene and PCTA-1 gene (the coding strand of PCTA-1 gene is on
 CC the opposite of the coding strand of BAP28)

XX Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

QY Query Match 0.2%; Score 17.4; DB 1; Length 20;
 Db Best Local Similarity 94.7%; Pred. No. 7.6e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4469 TTTTGTGCT 4487
 Db 1 TTTTGTGCTAT 19

RESULT 1153

ABQ79871
 ID ABQ79871 standard; DNA; 20 BP.

XX
 AC ABQ79871;

DT 23-DEC-2002 (first entry)

XX Nucleotide sequence of a PCR primer #1.

XX Polymerase chain reaction; thermal cycle; immobilisation;

XX genetic engineering; PCR; primer; ss.

XX Synthetic.

XX JP2002191369-A.

XX 09-JUL-2002;

XX 27-DEC-2000; 2000JP-00399573.

XX 27-DEC-2000; 2000JP-00399573.

XX (TOYO) TOYO KOHAN CO LTD.

XX (TAKA/) TAKAHASHI K.

XX WPI; 2002-630904/68.

XX Carrying out a thermal cycle of polymerase chain reaction (PCR) by using
 PT a substrate on which a DNA is immobilized used in medical, biochemical,
 PT molecular biological and gene engineering fields.

XX Example; Page 9; 13pp; Japanese.

XX The invention relates to performing a thermal cycle of PCR by using a
 CC substrate on which a deoxyribonucleic acid (DNA) is immobilized. The
 CC method is useful in the medical, biochemical, molecular biological and
 CC genetic engineering fields. Sequences ABQ79871-881 represent PCR primers
 CC used in the method of the invention

XX Sequence 20 BP; 3 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

QY Query Match 0.2%; Score 17.4; DB 1; Length 20;
 Db Best Local Similarity 94.7%; Pred. No. 7.6e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4462 ACTTTTTTTTTT 4480
 Db 2 AATTTTTTTTTT 20

RESULT 1154

ABZ86068/c
 ID ABZ86068 standard; DNA; 20 BP.

XX
 AC ABZ86068;

DT 17-OCT-2003 (first entry)

XX Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;

XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;

XX antiasthmatic; hypotensive; immunosuppressive; cycostatic; gene therapy;

XX antisense gene therapy; respiratory; lung; adenosine sensitivity;

XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;

XX lung inflammation; respiratory disease; ds.

XX Homo sapiens.

XX WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIC-) EPICGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasegara A, Katz E, Pabalan J, Aguilar D,

XX Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired

XX respiration, has oligo(e) antisense to specific gene(s) or its

XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or

XX ubiquinone.

XX Claim 15; SEQ ID NO 1310; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a

XX first active agent comprising an oligonucleotide antisense to the

XX initiation codon, coding region, 5' or 3' end genomic flanking regions,

XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

XX junctions of genes encoding a polypeptide associated with lung and/or

XX nasal airway dysfunction and a second active agent comprising an

XX antiinflammatory steroid and ubiquinone. A composition of the invention

XX has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

XX immunosuppressive, and cycostatic activity. The composition may have a

XX use in antisense gene therapy. The composition is useful for treating or

XX preventing a respiratory, lung or malignant disease or condition, also

XX for enhancing the prophylactic or therapeutic respiratory effect of an

XX antiinflammatory steroid in a subject, for reducing or depleting levels

XX of, or reducing sensitivity to adenosine, reducing levels of adenosine

XX receptor, producing bronchodilation, increasing levels of ubiquinone or

XX lung surfactant in a subject's tissue, or treating bronchoconstriction,

XX lung inflammation, lung allergies, or a respiratory disease or condition.

XX Note: The sequence data for this patent is not represented in the printed

XX specification, but was obtained in electronic format directly from WIPO

XX at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 20 BP; 0 A; 8 C; 7 G; 5 T; 0 U; 0 Other;

QY Query Match 0.2%; Score 17.4; DB 1; Length 20;
 Db Best Local Similarity 94.7%; Pred. No. 7.6e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7413 CAGCAGCAGCAGCAGC 7431
 Db 20 CGCAGCAGCAGCAGCAGC 2

RESULT 1155
 AB288266/c
 ID AB288266 standard, DNA; 20 BP.
 XX
 AC AB288266;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE Human oligonucleotide sequence.
 XX
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antisthmatic; hypotensive; immunosuppressive; cyostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200285308-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 23-APR-2002; 2002WO-US013135.
 XX
 PR 24-APR-2001; 2001US-0286137P.
 XX
 PA (EPIG-) EPIGENESIS PHARM INC.
 PI NYCE JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 DR WPI; 2003-229219/22.
 XX
 PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX
 PS Disclosure; SEQ ID NO 3508; 872pp; English.
 XX
 CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antisthmatic, hypotensive,
 CC immunosuppressive, and cyostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 17 A; 1 C; 1 G; 1 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 17.4; DB 1; Length 20;
 Best Local Similarity 94.7%; Pred. No. 7.6e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4466 TTTTGTGTTTGTG 4484
 DB 20 TTTTGTGTTTGTG 2

RESULT 1156
 AB289487/c
 ID AB289487 standard, DNA; 20 BP.
 XX
 AC AB289487;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE Human oligonucleotide sequence.
 XX
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antisthmatic; hypotensive; immunosuppressive; cyostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200285308-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 23-APR-2002; 2002WO-US013135.
 XX
 PR 24-APR-2001; 2001US-0286137P.
 XX
 PA (EPIG-) EPIGENESIS PHARM INC.
 PI NYCE JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 DR WPI; 2003-229219/22.
 XX
 PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX
 PS Disclosure; SEQ ID NO 4729; 872pp; English.
 XX
 CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antisthmatic, hypotensive,
 CC immunosuppressive, and cyostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 18 A; 2 C; 0 G; 0 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 17.4; DB 1; Length 20;
 Best Local Similarity 94.7%; Pred. No. 7.6e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4467 TTTTGTGTTTGTG 4485
 DB 20 TTTTGTGTTTGTG 2

```
RESULT 1157
AB286071/c
ID AB286071 standard; DNA; 20 BP.
XX
AC AB286071;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antilasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIC-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandasaagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR MPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Claim 15; SEQ ID NO 1313; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antilasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 0 A; 8 C; 7 G; 5 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 7.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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RESULT 1158
AB286075/c
ID AB286075 standard; DNA; 20 BP.
XX
AC AB286075;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antilasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIC-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandasaagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR MPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Claim 15; SEQ ID NO 1317; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antilasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 0 A; 8 C; 7 G; 5 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 7.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

RESULT 1159
 AB289719
 ID AB289719 standard; DNA; 20 BP.
 AC
 XX AB289719;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE Human oligonucleotide sequence.
 XX
 KM Human; antisense; lung dysfunction; nasal airway dysfunction;
 KM antiinflammatory steroid; ubiqunone; antiinflammatory; antiallergic;
 KM antisthmatic; hypotensive; immunosuppressive; cyostatic; gene therapy;
 KM antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KM adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KM lung inflammation; respiratory disease; ds.
 XX
 OS Homo sapiens.
 XX
 PN W0200285308-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 23-APR-2002; 2002MO-US013135.
 XX
 PR 24-APR-2001; 2001US-0286137P.
 XX
 PA (EPIC-) EPIGENESIS PHARM INC.
 XX
 PI NYCE JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX
 DR WPI; 2003-229219/22.
 XX
 PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiqunone.
 XX
 PS Disclosure; SEQ ID NO 4961; 872pp; English.
 XX
 CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiqunone. A composition of the invention
 CC has antiinflammatory, antiallergic, antisthmatic, hypotensive,
 CC immunosuppressive, and cyostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiqunone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 17.4; DB 1; Length 20;
 Best Local Similarity 94.7%; Pred. No. 7.6e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4462 ACTTTTCTTTTCTTTTCTTTT 4480
 DB 1 AATTTTCTTTTCTTTTCTTTT 19

RESULT 1160
 AAQ75735
 ID AAQ75735 standard; DNA; 21 BP.
 AC
 XX AAQ75735;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KM Analysis; gene expression; reverse transcription; primer; cDNA;
 KM aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 8; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENBSEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c) the
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 21 BP; 0 A; 1 C; 3 G; 17 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 17.4; DB 1; Length 21;
 Best Local Similarity 94.7%; Pred. No. 8.2e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4466 TTTTCTTTTCTTTTCTTTTCTTTG 4484
 DB 1 TTTTCTTTTCTTTTCTTTTCTTTG 19
 XX
 RESULT 1161
 AAQ75748
 ID AAQ75748 standard; DNA; 21 BP.
 AC
 XX AAQ75748;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KM Analysis; gene expression; reverse transcription; primer; cDNA;
 KM aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX

```
PR 16-APR-1993; 93JP-00112515.
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 8; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESQ files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 8.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4466 TTTTTTTTTTTTTTTG 4484
Db 1 TTTTTTTTTTTTTTCG 19

RESULT 1162
AAQ75676
ID AAQ75676 standard; DNA; 21 BP.
XX
XX AAQ75676;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESQ files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX SQ Sequence 21 BP; 3 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
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```
Query Match 0.2%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 8.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4464 TTTTTTTTTTTTTTTT 4482
Db 1 TTTTTTTTTTTTTTAT 19

RESULT 1163
AAQ75736
ID AAQ75736 standard; DNA; 21 BP.
XX
XX AAQ75736;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 8; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESQ files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 8.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4466 TTTTTTTTTTTTTTTG 4484
Db 1 TTTTTTTTTTTTTTCG 19

RESULT 1164
AAQ75739
ID AAQ75739 standard; DNA; 21 BP.
XX
XX AAQ75739;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX
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KM aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX JP6303997-A.
XX
XX 01-NOV-1994.
XX
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX
XX
XX Disclosure; Page 8; 11pp; Japanese.
XX
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESQ files AAQ75547-075798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX
XX
SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;
XX
XX
Query Match 0.2%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 8.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 4466 TTTT TTTT TTTT TTTT TTTT G 4484
Db 1 TTTT TTTT TTTT TTTT TTTT CG 19
XX
RESULT 1165
AAQ75741
ID AAQ75741 standard; DNA; 21 BP.
XX
XX AAQ75741;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX KM aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX JP6303997-A.
XX
XX 01-NOV-1994.
XX
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX
XX
XX Disclosure; Page 8; 11pp; Japanese.
XX

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC CC 'labelled reverse transcription primers (GENESQ files AAQ75547-075798)
CC CC and using the aggregate of mRNAs as the template for each reverse
CC CC transcription primer; (b) digesting each of the prepared aggregates of
CC CC the double-stranded cDNAs with restriction enzyme and; (c)
CC CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC CC method can be used to analyse gene expression rapidly and easily
XX
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
XX
XX
Query Match 0.2%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 8.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 4466 TTTT TTTT TTTT TTTT TTTT G 4484
Db 1 TTTT TTTT TTTT TTTT TTTT CG 19
XX
RESULT 1166
AAQ75678
ID AAQ75678 standard; DNA; 21 BP.
XX
XX AAQ75678;
XX
XX 04-AUG-1995 (first entry)
XX
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX KM aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX JP6303997-A.
XX
XX 01-NOV-1994.
XX
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESQ files AAQ75547-075798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX
XX
SQ Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;
XX
XX
Query Match 0.2%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 8.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 4464 TTTT TTTT TTTT TTTT TTTT T 4482
Db 1 TTTT TTTT TTTT TTTT TTTT TAT 19
XX
RESULT 1167

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AAQ75747
ID AAQ75747 standard; DNA; 21 BP.
XX
AC AAQ75747;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KM Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PS (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENBSEQ files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 8.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4466 TTTT TTTT TTTT TTTT TTTT G 4484
DB 1 TTTT TTTT TTTT TTTT TTTT G 19

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XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENBSEQ files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 8.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4466 TTTT TTTT TTTT TTTT TTTT G 4484
DB 1 TTTT TTTT TTTT TTTT TTTT G 19

```


CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENSEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

XX
 SQ Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.4; DB 1; Length 21;

Best Local Similarity 94.7%; Pred. No. 8.2e+02; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4466 TTTT TTTT TTTT TTTT TTTT G 4484
 1 TTTT TTTT TTTT TTTT TTTT AG 19

RESULT 1173
 AAQ75708
 ID AAQ75708 standard; DNA; 21 BP.

XX AC AAQ75708;

XX DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

KW Analysis; gene expression; reverse transcription; primer; cDNA;

KW aggregate; restriction enzyme; ss.

OS Synthetic.

PN JP06303997-A.

XX 01-NOV-1994.

PF 16-APR-1993; 93JP-00112515.

PR 16-APR-1993; 93JP-00112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

DR WPI; 1995-018287/03.

PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.

XX PS Disclosure; Page 7; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENSEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

XX SQ Sequence 21 BP; 3 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.4; DB 1; Length 21;

Best Local Similarity 94.7%; Pred. No. 8.2e+02; Indels 0; Gaps 0;

QY 4466 TTTT TTTT TTTT TTTT TTTT G 4484
 1 TTTT TTTT TTTT TTTT TTTT AG 19

Db 1 TTTT TTTT TTTT TTTT TTTT AG 19

RESULT 1174
 AAQ75707

ID AAQ75707 standard; DNA; 21 BP.

XX AC AAQ75707;

XX DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

KW Analysis; gene expression; reverse transcription; primer; cDNA;

KW aggregate; restriction enzyme; ss.

OS Synthetic.

PN JP06303997-A.

XX 01-NOV-1994.

PF 16-APR-1993; 93JP-00112515.

PR 16-APR-1993; 93JP-00112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

DR WPI; 1995-018287/03.

PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.

XX PS Disclosure; Page 7; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENSEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

XX SQ Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.4; DB 1; Length 21;

Best Local Similarity 94.7%; Pred. No. 8.2e+02; Indels 0; Gaps 0;

QY 4466 TTTT TTTT TTTT TTTT TTTT G 4484
 1 TTTT TTTT TTTT TTTT TTTT AG 19

Db 1 TTTT TTTT TTTT TTTT TTTT AG 19

RESULT 1175

AAQ75774
 ID AAQ75774 standard; DNA; 21 BP.

XX AC AAQ75774;

XX DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

KW Analysis; gene expression; reverse transcription; primer; cDNA;

KW aggregate; restriction enzyme; ss.

OS Synthetic.

PN JP06303997-A.

XX 01-NOV-1994.

PF 16-APR-1993; 93JP-00112515.

PR 16-APR-1993; 93JP-00112515.

XX

KM aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
 KM cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
 KM epoxide hydrolase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
 KM glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
 KM HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
 KM NADPH quinone oxidoreductase 2; NQO2; sulfoxidoreductase; thermolabile; STM;
 KM UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
 KM UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;
 KM multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
 KM multidrug resistance associated protein 3; cancer; prostate; CHMR3;
 KM acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
 KM altered drug metabolism; cardiovascular function; colorectal tumour;
 KM central nervous system; pulmonary; immunological; SNP;
 KM single nucleotide polymorphism.
 OS Homo sapiens.
 XX WO200257410-A2.
 XX PD 25-JUL-2002.
 XX 28-NOV-2001; 2001WO-US044838.
 XX 28-NOV-2000; 2000US-00724389.
 XX (DNAS-) DNA SCI LAB INC.
 XX Guida M, Hall J;
 XX WPI; 2002-698522/75.
 XX
 XX Isolated nucleic acid molecules having polymorphisms in known human genes
 PT e.g. cytochrome P450 and cathepsin S useful as genetic linkage markers
 PT for locating, identifying and characterizing the genes responsible for
 PT disorder-related traits.
 XX
 XX Example 24; Page 153; 714pp; English.
 XX
 XX This invention relates to the sequence of an isolated nucleic acid
 CC molecule comprising at least one base variation from that of a known
 CC human cytochrome P450 A1 (CYP450A1), cytochrome P450 A2 (CYP450A2),
 CC cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADBR1),
 CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
 CC (ARNT), cathepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding
 CC inhibitor (DBI), epoxide hydrolase 2 (EPHX2), 5-lipoxygenase activating
 CC protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl
 CC transferase (HNMT), (kallikrein 2) KLK2, nicotinamide-N-methyl
 CC transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),
 CC sulfoxidoreductase thermolabile (STM), UDP-glucuronosyl transferase 2B4
 CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl
 CC transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1
 CC (MDR1), lactotransferrin (LTP), multidrug resistance associated protein 3
 CC (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic
 CC receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
 CC The polymorphisms in the human genes cited in the invention are useful as
 CC genetic linkage markers for locating and characterizing the genes that
 CC are responsible for specific traits within the genome and eventually
 CC identifying the genes responsible for a variety of disorder-related
 CC traits as a result of their e.g., overexpression, constitutive
 CC expression, mutation or underexpression, which may be used in diagnosing
 CC and/or treating the disorders. The nucleic acid molecules comprising the
 CC polymorphic sequences contained in CYP450A1, CYP450A2, CYP4502E1,
 CC ARNT, EPHX2, GST12, NNMT, NQO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
 CC MDR1 and/or MDR3 are useful for screening individuals for altered drug
 CC metabolism. The polymorphic sequences contained in CYP450A1, CYP450A2,
 CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for
 CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
 CC used to screen for altered cardiovascular function, in COX2 for altered
 CC susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
 CC nervous system function, in FLAP and HNMT for altered pulmonary,
 CC immunological or haematological function, in KLK2 for altered serine
 CC protease activity in the prostate, in LTP for altered immunological or
 CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and

CC peripheral nervous system function. The present sequence represents a
 CC polymorphic DNA sequence of the invention
 XX
 XX Sequence 21 BP; 4 A; 7 C; 5 G; 5 T; 0 U; 0 Other;
 SQ
 Query Match 0.2%; Score 17.4; DB 1; Length 21;
 Best Local Similarity 94.7%; Pred. No. 8.2e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY
 268 CAGGCTCCAGGCACCTC 286
 |||||
 3 CAGGCTCCAGGCACCTC 21
 DB
 RESULT 1179
 AAT33702
 ID AAT33702 standard; DNA; 23 BP.
 XX
 XX AAT33702;
 XX
 XX 19-MAY-1997 (first entry)
 XX
 XX DT
 XX
 XX DE Primer #2 for tissue or cell derived RNA.
 XX
 XX PCR; polymerase chain reaction; primer; amplify; reverse-transcription;
 KM molecular indexing; class IIS restriction enzyme; cancer; causative gene;
 KM viral infection; hereditary disease; agricultural gene; ss.
 XX
 XX OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH misc_feature 1
 FT /tag= a
 FT /note= "hydroxylated"
 XX
 XX EP75144-A1.
 XX
 XX 02-OCT-1996.
 XX
 XX PD
 XX 26-MAR-1996; 96EP-00104817.
 XX
 XX PR 28-MAR-1995; 95JP-00069695.
 XX 20-JUL-1995; 95JP-00184006.
 XX 12-SEP-1995; 95JP-00234122.
 XX
 XX (SHKJ) RES DEV CORP JAPAN.
 XX
 XX Kato K;
 PI
 WPI; 1996-435619/44.
 DR
 PT Molecular indexing of DNA - using restriction enzymes, PCR amplification
 PT and electrophoresis to analyse DNA fragments.
 XX
 XX Claim 3; Page 14; 20pp; English.
 PS
 AAT33701-T33703 represent amplification primers used in the reverse-
 CC transcription of tissue or cell derived mRNA, in the method of the
 CC invention. The method of the invention is a molecular indexing method,
 CC and comprises digesting the cDNA amplified by these sequences with a
 CC class IIS restriction enzyme. Each resultant cDNA fragment is then
 CC ligated to a biotinylated adaptor (selected from a pool of 64 adaptors
 CC cohesive to all possible overhangs), and digesting the products with two
 CC further class IIS restriction enzymes. These steps are repeated (but the
 CC enzyme used for the first step is different in each) to produce two
 CC further cDNA samples. The ligation samples are then recovered using
 CC streptavidin-coated paramagnetic beads, removing the strand complementary
 CC to an adaptor-primer. The adaptor primer and an anchored oligo-dT primer
 CC (such as this sequence) are then used to amplify the cDNA samples. The
 CC amplified products are separated, and the sizes of the fragments obtained
 CC is recorded. The method can be used for the analysis and diagnosis or
 CC diseases such as cancers or viral infections, for the search and
 CC isolation of the genes of physiologically active substances that are


```

XX 20-APR-2000; 2000WO-EP003636.
PF 26-APR-1999; 99EP-00303215.
PR (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
PA Ulfendahl P, Wong K;
PI WPI; 2000-679677/66.
DR
XX Identifying extendible primers for use in identification, or
XX classification of a nucleic acid of an organism, allele or gene such as
XX class 1/2 HLA comprises identifying all possible nucleotide sequences of
XX specific length.
XX
XX Claim 14; Page 53; 66pp; English.
XX
XX The present invention provides a method for identifying a set of
XX extendible primers which can be used in the identification, typing and
XX classification of genes. This can then be used to predict protein
XX sequence and structure, in organ donation to match the organ with the
XX receiver, and to identify bacteria in a sample. The method can be used to
XX type the human leukocyte antigen genes (HLA) and 16S rRNA genes in
XX particular
XX
XX Sequence 25 BP; 1 A; 2 C; 4 G; 18 T; 0 U; 0 Other;
SQ
XX
XX Query Match 0.2%; Score 17.4; DB 1; Length 25;
XX Best Local Similarity 94.7%; Pred. No. 1e+03;
XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 4466 TTTTCTTTTCTTTCTT 4484
DB 1 TTTTCTTTTCTTTCTT 19

```

RESULT 1183
AAC96550
ID AAC96550 standard; DNA; 25 BP.
AC AAC96550;
AT 26-FEB-2001 (first entry)
DT
XX HLA DRB345 gene PCR primer #21.
XX
XX DNA sequence analysis; sequencing; protein structure;
XX gene typing; organ donation; bacteria identification; 16S rRNA; HLA;
XX human leukocyte antigen; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200065088-A2.
XX
XX 02-NOV-2000.
XX
XX 20-APR-2000; 2000WO-EP003636.
XX
XX 26-APR-1999; 99EP-00303215.
XX
XX (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
XX Ulfendahl P, Wong K;
XX
XX WPI; 2000-679677/66.
XX
XX Identifying extendible primers for use in identification, or
XX classification of a nucleic acid of an organism, allele or gene such as
XX class 1/2 HLA comprises identifying all possible nucleotide sequences of
XX specific length.
XX
XX Claim 14; Page 53; 66pp; English.

```

XX The present invention provides a method for identifying a set of
XX extendible primers which can be used in the identification, typing and
XX classification of genes. This can then be used to predict protein
XX sequence and structure, in organ donation to match the organ with the
XX receiver, and to identify bacteria in a sample. The method can be used to
XX type the human leukocyte antigen genes (HLA) and 16S rRNA genes in
XX particular
XX
XX Sequence 25 BP; 0 A; 5 C; 2 G; 18 T; 0 U; 0 Other;
SQ
XX
XX Query Match 0.2%; Score 17.4; DB 1; Length 25;
XX Best Local Similarity 94.7%; Pred. No. 1e+03;
XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 4470 TTTTCTTTTCTTTCTT 4488
DB 1 TTTTCTTTTCTTTCTT 19

```

RESULT 1184
ACK20278/c
ID ACK20278 standard; DNA; 25 BP.
AC ACK20278;
AT 14-OCT-2003 (first entry)
DT
XX Human microarray DNA oligonucleotide SEQ ID NO 120259.
XX
XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
XX genetic variation; diallelic marker; polymorphism; human;
XX cross-species comparison.
XX
XX Homo sapiens.
XX
XX US2003104410-A1.
XX
XX 05-JUN-2003.
XX
XX 15-MAR-2002; 2002US-00098263.
XX
XX 16-MAR-2001; 2001US-0276759P.
XX
XX (AFRY-) AFRYMETRIX INC.
XX
XX Wittmann MP;
XX
XX WPI; 2003-567953/53.
XX
XX New array of nucleic acid probes, useful for in situ hybridization, in
XX Southern, Northern or dot-blot hybridization to identify or detect the
XX sequence or specific mutations of any gene.
XX
XX Claim 1; SEQ ID NO 120259; 9pp; English.
XX
XX The invention discloses a microarray comprising a plurality of nucleic
XX acid probes including one of 2,018,500 fully defined sequences, or its
XX perfect match, perfect mismatch, antisense match or antisense mismatch.
XX Also disclosed is a method of gene expression analysis. The array is used
XX in monitoring gene expression levels by hybridization to a DNA library,
XX in analysis of genetic variation or in hybridization of tag-labelled
XX compounds. The nucleic acid probes are specifically designed for analysis
XX of at least one target sequence. The method of analysis comprises
XX hybridizing at least one or more nucleic acids to at least two or more
XX nucleic acid probes and detecting the hybridization. The nucleic acid
XX probes are attached to a solid support. The analysis comprises monitoring
XX gene expression levels, identifying diallelic markers or polymorphisms,
XX or family members of a gene and a cross-species comparison. Each of the
XX nucleic acids further comprises a tag sequence. The array of nucleic acid
XX probes is useful in in situ hybridization, in Southern, Northern or dot-
XX blot hybridization to identify or detect the sequence or specific
XX mutations of any gene, in mapping the 5' termini of mRNA molecules by

CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC isolated acid previously incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html

XX Sequence 25 BP; 9 A; 6 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.4; DB 1; Length 25;

Best Local Similarity 94.7%; Pred. No. 1e+03; Mismatches 1; Indels 0; Gaps 0;

DB 4842 TATCCAGAGTTCGTCTG 4860
 22 TCTCCAGGTTCTGTCTG 4

RESULT 1185

ID ADC38183 standard; DNA; 25 BP.

AC ADC38183;

DT 18-DEC-2003 (first entry)

XX Human AMLP1a scanning 25-mer oligonucleotide SEQ ID NO:532.

XX human; angiotensin-like protein 1; AMLP1; cytosolic; gene therapy;

KM AMLP1a; ss.

XX Synthetic.

OS Homo sapiens.

PN WO2003037931-A2.

XX 08-MAY-2003.

XX 01-NOV-2002; 2002WO-US035129.

XX 01-NOV-2001; 2001US-0334773P.

XX (AMSH) AMERSHAM BIOSCIENCES SV CORP.

PI Shannon M, Phan T;

DR WPI; 2003-430501/40.

XX New isolated nucleic acid molecule encoding a human angiotensin-like
 PT protein, useful for treating or preventing a disorder associated with
 PT decreased or increased expression or activity of AMLP1.

PS Example 2; SEQ ID NO 532; 172bp; English.

CC The present invention describes the human angiotensin-like protein 1
 CC (AMLP1). human AMLP1 has cytosolic activity, and can be used in gene
 CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
 CC compositions of the present invention can be used for treating or
 CC preventing a disorder associated with decreased or increased expression
 CC or activity of AMLP1. The present sequence represents a scanning
 CC oligonucleotide for human AMLP1a, which is used in an example from the
 CC present invention.

XX Sequence 25 BP; 8 A; 7 C; 10 G; 0 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.4; DB 1; Length 25;

Best Local Similarity 94.7%; Pred. No. 1e+03; Mismatches 1; Indels 0; Gaps 0;

QY 7415 GCAGCAGCAGCAGCAG 7433
 DB 7 GCAGCAGCAGCAGCAG 25

RESULT 1186

ID ADC38192 standard; DNA; 25 BP.

AC ADC38192;

DT 18-DEC-2003 (first entry)

XX Human AMLP1a scanning 25-mer oligonucleotide SEQ ID NO:541.

XX human; angiotensin-like protein 1; AMLP1; cytosolic; gene therapy;

KM AMLP1a; ss.

XX Synthetic.

OS Homo sapiens.

PN WO2003037931-A2.

XX 08-MAY-2003.

XX 01-NOV-2002; 2002WO-US035129.

XX 01-NOV-2001; 2001US-0334773P.

XX (AMSH) AMERSHAM BIOSCIENCES SV CORP.

PI Shannon M, Phan T;

DR WPI; 2003-430501/40.

XX New isolated nucleic acid molecule encoding a human angiotensin-like
 PT protein, useful for treating or preventing a disorder associated with
 PT decreased or increased expression or activity of AMLP1.

PS Example 2; SEQ ID NO 541; 172bp; English.

CC The present invention describes the human angiotensin-like protein 1
 CC (AMLP1). human AMLP1 has cytosolic activity, and can be used in gene
 CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
 CC compositions of the present invention can be used for treating or
 CC preventing a disorder associated with decreased or increased expression
 CC or activity of AMLP1. The present sequence represents a scanning
 CC oligonucleotide for human AMLP1a, which is used in an example from the
 CC present invention.

XX Sequence 25 BP; 7 A; 7 C; 11 G; 0 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.4; DB 1; Length 25;

Best Local Similarity 94.7%; Pred. No. 1e+03; Mismatches 1; Indels 0; Gaps 0;

QY 7415 GCAGCAGCAGCAGCAG 7433
 DB 1 GCAGCAGCAGCAGCAG 19

RESULT 1187

ID ABX79828 standard; cDNA; 27 BP.

AC ABX79828;

DT 17-APR-2003 (first entry)

XX EST polymorphic DNA repeat polymorphic repeat #153.

XX EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;

KM polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;

KM Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;

KM Haw River syndrome; Huntington's disease; fragile-X syndrome;

KM Friedrich's ataxia; myotonic dystrophy; hyperandrogenaemia;

KM spinal atrophy; bulbar atrophy; spinocerebellar ataxia.

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XX OS Homo sapiens.
XX PN US6472154-B1.
XX PD 29-OCT-2002.
XX PF 31-DEC-1999; 99US-00475947.
XX PR 31-DEC-1999; 99US-00475947.
XX PA (TEXA ) UNIV TEXAS SYSTEM.
XX PI Garner HR, Wren JD, Minna JD, Fondon JW;
XX WPI; 2003-208818/20.
XX DR
XX PT Identifying a candidate polymorphic repeat within a coding sequence, for
XX PT understanding or treating genetic disease, comprises detecting tandem
XX PT repeats in a target coding sequence and scoring the repeats for
XX PT polymorphic probability.
XX PS Example; Col 717, 588bp; English.
XX CC The invention discloses a method for identifying a candidate polymorphic
XX CC repeat within a coding sequence (expressed sequence tag, EST), which
XX CC comprises detecting tandem repeats in a target coding sequence, scoring
XX CC the repeats for polymorphic probability and generating a dataset
XX CC correlating the repeats with polymorphic probability to identify a
XX CC candidate polymorphic repeat. The computational methods (polymorphic
XX CC marker prediction of ubiquitous simple sequences, POMPOS, and Rep-X) are
XX CC useful for identifying and detecting candidate polymorphic repeats in
XX CC human genes, which can be used to understand, treat or eliminate genetic
XX CC diseases, predispositions or adverse drug-treatment reactions. Examples
XX CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
XX CC syndrome, Huntington's disease, fragile-X syndrome, Friedrich's ataxia,
XX CC myoclonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
XX CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
XX CC the polymorphic repeats identified for a search of human ESTs
XX SQ
SQ Sequence 27 BP, 1 A; 0 C; 0 G; 26 T; 0 U; 0 Other;
Query Match 0.2%; Score 17.4; DB 1; Length 27;
Best Local Similarity 77.8%; Pred. No. 1.1e+03;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 4013 AATGAGAAAAAGAGAGAAAAACAAA 4039
DB 27 AATATAAAAAAAAAAAAAAAAAAAAA 1
RESULT 1189
AAK14633/c
ID AAK14633 standard; DNA; 35 BP.
XX AAK14633;
AC
XX 24-MAR-1999 (first entry)
XX DE Triple helix third strand of n-myc gene nucleotides 4791-4725.
XX KW Triple helix formation; DNA detection; triple helix; identification; bacteria;
XX OS oncogene; virus; ss.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN US5861244-A.
XX PD 19-JAN-1999.
XX PF 22-DEC-1993; 93US-00173489.
XX

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PR 29-OCT-1992; 92US-00968436.
XX PA (PROF-) PROFILE DIAGNOSTIC SCI INC.
XX PI Hepburn AG, Wang C;
XX DR WPI; 1999-130384/11.
XX PT Assay of genetic sequences based on triple helix formation from double
XX PT stranded analyte - and hybrid of anchor and reporter sequences, with
XX PT reporter released if triple helix formation occurs, used e.g. to identify
XX PT bacteria.
XX PS Disclosure; Col 13-14; 168bp; English.
XX CC The present sequence represents a polynucleotide that is able to form a
XX CC triple helix with a double stranded sequence. Cytosine bases in the
XX CC present can be replaced with 5-methylcytosine for increased triple helix
XX CC stability. The present sequence is used in the assay of the invention,
XX CC where it can be part of the anchor DNA or reporter DNA sequence. The
XX CC assay comprises adding a sample containing double-stranded DNA test
XX CC sequences to an aqueous medium containing at least one complex of anchor
XX CC DNA, attached to a solid support, and reporter DNA, where either a part
XX CC of the anchor DNA or reporter DNA is designed to form a triple-strand
XX CC structure with part of the test sequence. Triple helix formation results in
XX CC displacement of the reporter DNA which is detected as an indication of
XX CC the presence of the DNA test sequence. The method is used to detect DNA
XX CC sequences, particularly for identification of bacteria (by detecting
XX CC genes for ribosomal RNA) in clinical samples, but also detection of
XX CC oncogenes and Hepatitis B virus
XX SQ
SQ Sequence 35 BP; 0 A; 4 C; 1 G; 30 T; 0 U; 0 Other;
Query Match 0.2%; Score 17.4; DB 1; Length 35;
Best Local Similarity 77.8%; Pred. No. 1.5e+03;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 4013 AATGAGAAAAAGAGAGAAAAACAAA 4039
DB 35 AAAAGACAAAGAAAAAGAAAAA 9
RESULT 1189
AAD27123
ID AAD27123 standard; RNA; 36 BP.
XX AAD27123;
AC
XX 09-APR-2002 (first entry)
XX DE RNA template CC(AU)2GG for directing RNA synthesis by HCV RNA polymerase.
XX KW Hepatitis C virus; HCV replicase; non-structural protein 5B; NSSB;
XX KW lead compound; RNA polymerase; ss.
XX OS Unidentified.
XX OS US6322366-B1.
XX PN 27-NOV-2001.
XX PD 11-MAY-1999; 99US-00309670.
XX PF 11-MAY-1999; 99US-00309670.
XX PR 11-MAY-1999; 99US-00309670.
XX PA (ZHON/) ZHONG W.
XX PA (HONG/) HONG Z.
XX PA (LAU/) LAU J Y N.
XX PI Zhong W, Hong Z, Lau JYN;
XX WPI; 2002-096587/13.
XX

```


CC repetition of gamma, in which thymine expressed by gamma is composed of
 CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
 CC useful as primers for RT-PCR and determination of base sequences. The new
 CC sequences allow for reproductive and highly efficient analysis of gene
 CC sequences

SQ Sequence 19 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 2 Other;

Query Match 0.2%; Score 17.2; DB 1; Length 19;
 Best Local Similarity 94.4%; Pred. No. 7.7e+02;
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4467 TTTTCTTTTCTTTTCTTG 4484

Db 1 TTTTCTTTTCTTTTCTTV 18

RESULT 1192
 AAX22004/C
 ID AAX22004 standard; DNA; 22 BP.

XX AAX22004;
 XX
 XX 19-MAY-1999 (first entry)

DE PCR primer for human MED1 endonuclease coding sequence.

KW Endonuclease; MED1; human; methyl-CpG binding endonuclease-1; PCR primer;
 KM DNA fidelity; DNA manipulation; cancer; fragile X syndrome; therapy;
 KW myoconic dystrophy; Huntington's disease; spinocerebellar ataxia;
 KW Kennedy's disease; triplet repeat expansion disorder; ss.

OS Synthetic.
 OS Homo sapiens.

XX WO9904626-A1.

XX 04-FEB-1999.

XX 28-JUL-1998; 98WO-US015828.

XX 28-JUL-1997; 97US-0053936P.

PA (FOXC-) FOX CHASE CANCER CENT.

PI Bellacosa A;

DR WPI; 1999-142462/12.

PT New nucleic acid encoding human endonuclease MED1 involved in DNA
 PT mismatch repair - used for diagnosing susceptibility to cancer and
 PT fragile X syndrome, and therapeutically.

PS Example 1; Page 45; 109pp; English.

CC This sequence is a PCR primer for DNA encoding the human MED1
 CC endonuclease of the invention. MED1 (methyl-CpG binding endonuclease-1)
 CC is used to screen for specific modulators (potential therapeutic agents)
 CC particularly mimetics of MED1) and to study interactions involved in
 CC maintaining DNA fidelity, for DNA manipulation and to raise antibodies.
 CC Susceptibility or predisposition to cancer (particularly colorectal or
 CC endometrial, especially hereditary non-polypoid colorectal cancer), or
 CC its prognosis, where caused by alterations in the MED1-encoding gene, are
 CC identified by sequence comparison, amplification, detecting altered
 CC (polypeptide) and restriction fragment mapping, hybridisation
 CC (particularly to probes specific for a mutant allele). These same methods
 CC can also be used to diagnose fragile X syndrome and other diseases (e.g.,
 CC myoconic dystrophy, Huntington's disease, spinocerebellar ataxia and
 CC Kennedy's disease) associated with triplet repeat expansion. The DNA, or
 CC its fragments, are used as probes and primers in the above diagnostic
 CC methods, also to isolate homologous sequences, as sources of antisense
 CC sequences and for gene transfer, particularly to restore drug sensitivity
 CC to drug-resistant cancer cells

XX SQ Sequence 22 BP; 4 A; 12 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.2; DB 1; Length 22;
 Best Local Similarity 86.4%; Pred. No. 9.4e+02;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1099 CTGAGAGTGCACAGCTGTGG 1120

Db 22 CGGAGAGTGCACAGCTGTGG 1

RESULT 1193
 AAV71290/C
 ID AAV71290 standard; DNA; 22 BP.

XX AAV71290;

XX 01-JUL-1999 (first entry)

DE PCR primer for mouse PS1 gene.

KW PCR primer; PS1 gene; transgenic mouse; presenilin 1; APP Abeta peptide;
 KW Alzheimer's Disease; beta-amyloid precursor protein; APP; ss.

OS Synthetic.
 OS Mus sp.

XX WO9851781-A1.

XX 19-NOV-1998.

XX 13-MAY-1998; 98WO-US009709.

XX 14-MAY-1997; 97US-0046488P.

XX 18-MAR-1996; 96US-0078465P.

PA (MERI) MERCK & CO INC.

PA (UVGO) UNIV JOHNS HOPKINS.

PI Zheng H, Qian S, Van Der Ploeg LHT, Wong PC, Sisodia SS, Jiang P,

DR WPI; 1999-045226/04.

PT New transgenic mice express non-native presenilin-1 mutant or allele -
 PT provide a model system to study etiology of Familial Alzheimer's
 PT Disease.

PS Example 1; Page 7; 56pp; English.

CC This sequence represents a PCR primer for the mouse PS1 gene. The
 CC invention relates to transgenic mice that are: (a) a mouse embryo whose
 CC somatic and germ cells lack a gene encoding presenilin 1 (PS1); (b) a
 CC mouse whose somatic cells are heterozygous for a functional murine gene
 CC encoding PS1 (mPS1) and an altered PS1 gene; (c) a viable mouse whose
 CC somatic and germ cells lack a functional murine gene encoding PS1 (mPS1-
 CC), and contain and express a transgene comprising a gene for a non-native
 CC PS1 (mPS1); (d) a mouse hemizygous or homozygous for a human beta-
 CC amyloid precursor protein (APP) gene, hemizygous or homozygous for mPS1
 CC gene, and homozygous for altered PS1. The invention provides a model
 CC system that is useful to study etiology of Alzheimer's Disease,
 CC particularly the change in APP Abeta peptide production seen in
 CC conjunction with mutations affecting APP processing. The assays are
 CC useful for screening compounds that affect APP Abeta peptide production

SQ Sequence 22 BP; 10 A; 6 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.2; DB 1; Length 22;
 Best Local Similarity 86.4%; Pred. No. 9.4e+02;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2907 CTTGTTCTCTATAGAGGTG 2928

||||||| ||| ||||| ||

Db 22 CTGTTGCTGTATAGACTG 1

RESULT 1194
ACD28887/c
ID ACD28887 standard; DNA; 22 BP.
XX
AC ACD28887;
XX
DT 27-AUG-2003 (first entry)
XX
DE Wine grape lipoxygenase LOX PCR primer LOX 48L.
XX
KM Wine grape; ss; lipoxygenase; LOX; flavour; fermented beverage; wine;
KM grape juice; cheese; yogurt; pickle; tissue specificity; timing; PCR;
KM primer.
OS Vitis vinifera.
XX
PN US2003033627-A1.
XX
PD 13-FEB-2003.
XX
PF 16-OCT-2001; 2001US-00978522.
XX
PR 16-OCT-2000; 2000US-0241220P.
XX
PA (DESC/) DESCENZO R A.
PA (IREL/) IRELAN N A.
XX
PI Descenzo RA, Irelan NA;
DR WPI; 2003-492095/46.
XX
PT Novel purified and isolated Vitis vinifera lipoxygenase polypeptide,
PT useful for modifying the flavor of a comestible e.g., a beverage which is
PT a fermentation product, preferably wine.
XX
PS Example 3; Page 14; 36pp; English.
XX
CC The invention relates to a purified and isolated Vitis vinifera
CC lipoxygenase (LOX) polypeptide. The polypeptide is useful for modifying
CC the flavour of a comestible e.g. a beverage which is a fermentation
CC product, preferably wine. The polypeptide is useful for analysing the
CC effect of LOX polypeptides on flavour production in wine and grape juice.
CC The polypeptide is useful in the production of cheese, yogurt, pickles
CC etc. The polypeptide is also useful in screening assays to identify
CC modulators that modulate the activity of the Vitis vinifera LOX
CC polypeptides. The polynucleotide is useful in heterologous production of
CC pure lipoxygenase enzyme in a protein expression vector and for studying
CC the native level of gene expression in response to environmental or
CC viticultural influences. The cloned gene can be used to produce
CC transgenic plants to modify the level of gene expression to produce
CC optimal levels of lipoxygenase in the grape. Knowledge of Vitis vinifera
CC lipoxygenase coding DNA sequences allows for modification of cells to
CC permit, increase or decrease, expression of endogenous Vitis vinifera
CC lipoxygenase. Such knowledge also permits modification of timing and
CC tissue specificity of LOX expression. The DNA sequence information also
CC makes possible the development through, e.g. homologous recombination or
CC knock-out strategies of grapes that fail to express functional
CC lipoxygenase or that express a variant of Vitis vinifera lipoxygenase.
CC Such plants are useful as models for studying the in vivo activities of
CC Vitis vinifera lipoxygenase and modulators of Vitis vinifera
CC lipoxygenase. The present sequence represents a wine grape lipoxygenase
CC LOX PCR primer
XX
SQ Sequence 22 BP; 4 A; 6 C; 2 G; 10 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 9.4e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7019 TTACAGGGAATAATGGAAC 7040

Db 22 TTACAGGGAATAATGGAAC 1

RESULT 1195
ACD28882
ID ACD28882 standard; DNA; 22 BP.
XX
AC ACD28882;
XX
DT 27-AUG-2003 (first entry)
XX
DE Wine grape lipoxygenase LOX PCR primer LOX 27U.
XX
KM Wine grape; ss; lipoxygenase; LOX; flavour; fermented beverage; wine;
KM grape juice; cheese; yogurt; pickle; tissue specificity; timing; PCR;
KM primer.
OS Vitis vinifera.
XX
PN US2003033627-A1.
XX
PD 13-FEB-2003.
XX
PF 16-OCT-2001; 2001US-00978522.
XX
PR 16-OCT-2000; 2000US-0241220P.
XX
PA (DESC/) DESCENZO R A.
PA (IREL/) IRELAN N A.
XX
PI Descenzo RA, Irelan NA;
DR WPI; 2003-492095/46.
XX
PT Novel purified and isolated Vitis vinifera lipoxygenase polypeptide,
PT useful for modifying the flavor of a comestible e.g., a beverage which is
PT a fermentation product, preferably wine.
XX
PS Example 3; Page 14; 36pp; English.
XX
CC The invention relates to a purified and isolated Vitis vinifera
CC lipoxygenase (LOX) polypeptide. The polypeptide is useful for modifying
CC the flavour of a comestible e.g. a beverage which is a fermentation
CC product, preferably wine. The polypeptide is useful for analysing the
CC effect of LOX polypeptides on flavour production in wine and grape juice.
CC The polypeptide is useful in the production of cheese, yogurt, pickles
CC etc. The polypeptide is also useful in screening assays to identify
CC modulators that modulate the activity of the Vitis vinifera LOX
CC polypeptides. The polynucleotide is useful in heterologous production of
CC pure lipoxygenase enzyme in a protein expression vector and for studying
CC the native level of gene expression in response to environmental or
CC viticultural influences. The cloned gene can be used to produce
CC transgenic plants to modify the level of gene expression to produce
CC optimal levels of lipoxygenase in the grape. Knowledge of Vitis vinifera
CC lipoxygenase coding DNA sequences allows for modification of cells to
CC permit, increase or decrease, expression of endogenous Vitis vinifera
CC lipoxygenase. Such knowledge also permits modification of timing and
CC tissue specificity of LOX expression. The DNA sequence information also
CC makes possible the development through, e.g. homologous recombination or
CC knock-out strategies of grapes that fail to express functional
CC lipoxygenase or that express a variant of Vitis vinifera lipoxygenase.
CC Such plants are useful as models for studying the in vivo activities of
CC Vitis vinifera lipoxygenase and modulators of Vitis vinifera
CC lipoxygenase. The present sequence represents a wine grape lipoxygenase
CC LOX PCR primer
XX
SQ Sequence 22 BP; 10 A; 2 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 9.4e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 7019 TTACAGAGGAAATAGAAACC 7040
 |||||
 Db 1 TTACAGGGGAAATTCGAAAC 22

RESULT 1196

AAAT33701
 ID AAAT33701 standard; DNA; 23 BP.

AC AAAT33701;

DT 19-MAY-1997 (first entry)

DE Primer #1 for tissue or cell derived RNA.

KW PCR; polymerase chain reaction; primer; amplify; reverse-transcription;
 molecular indexing; class ITS restriction enzyme; cancer; causative gene;
 viral infection; hereditary disease; agricultural gene; ss.

OS Synthetic.

PH Key Location/Qualifiers

FT misc_feature 1 /tag= a
 FT /note= "hydroxylated"

PN EP735144-A1.

PD 02-OCT-1996.

PF 26-MAR-1996; 96EP-00104817.

PR 28-MAR-1995; 95JP-00069695.

PR 20-JUL-1995; 95JP-00184006.

PR 12-SEP-1995; 95JP-00234122.

PA (SHKJ) RES DEV CORP JAPAN.

PI Kato K;

DR WPI; 1996-435619/44.

PT Molecular indexing of DNA - using restriction enzymes, PCR amplification
 and electrophoresis to analyze DNA fragments.

PS Claim 3; Page 14; 20pp; English.

XX AAAT33701-733703 represent amplification primers used in the reverse-
 transcription of tissue or cell derived mRNA, in the method of the
 invention. The method of the invention is a molecular indexing method,
 and comprises digesting the cDNA amplified by these sequences with a
 class ITS restriction enzyme. Each restriction cDNA fragment is then
 ligated to a biotinylated adaptor (selected from a pool of 64 adaptors
 consesive to all possible overhangs), and digesting the products with two
 further class ITS restriction enzymes. These steps are repeated (but the
 enzyme used for the first step is different in each) to produce two
 further cDNA samples. The ligation samples are then recovered using
 streptavidin-coated paramagnetic beads, removing the strand complementary
 to an adaptor-primer. The adaptor primer and an anchored oligo-dT primer
 (such as this sequence) are then used to amplify the cDNA samples. The
 amplified products are separated, and the sizes of the fragments obtained
 is recorded. The method can be used for the analysis and diagnosis of
 diseases such as cancers or viral infections, for the search and
 isolation of the genes of physiologically active substances that are
 potential pharmaceuticals, or causative genes of hereditary diseases, as
 well as for the isolation of genes for improving agricultural products.
 Using this method, it is possible to classify (index) DNA into groups in
 a short period of time without duplication

XX Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.2; DB 1; Length 23;
 Best Local Similarity 86.4%; Pred. No. 1e+03;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 OY 4460 GGACTTTTCTTTTCTTTT 4481
 |||||
 Db 1 GGATCCTTTTCTTTTCTTTT 22

RESULT 1197

AAV61554
 ID AAV61554 standard; DNA; 23 BP.

AC AAV61554;

DT 08-DEC-1998 (first entry)

DE Double-anchored oligo-dT primer, used to synthesise apolipoprotein cDNA.

KW primer; PCR; amplification; RT-PCR; quantitate; amount ratio; liver;
 apolipoprotein; kidney; ATAC-PCR; Adaptor-tagged Competitive PCR;
 gene expression; internal standard; calibration curve; ss.

OS Synthetic.

OS Mus sp.

PN EP870842-A2.

PD 14-OCT-1998.

PF 07-APR-1998; 98EP-00302726.

PR 07-APR-1997; 97JP-00088495.

PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.

PI Kato K;

DR WPI; 1998-523164/45.

PT Determination of gene expression levels - using combinations of different
 cDNA samples tagged with different PCR adaptors.

PS Example 2; Page 9; 22pp; English.

XX The present sequence represents a primer which was used to synthesise
 CC Apolipoprotein cDNA in a RT-PCR reaction. This primer as well as primers
 CC AAV61555 and AAV61556 were added to both mouse liver-derived and mouse
 CC kidney-derived total RNA to generate single-stranded cDNA. These primers
 CC were used in the method of the invention to determine the amount ratio
 CC between a cDNA coding for mouse liver-derived Apolipoprotein and a cDNA
 CC that codes for the mouse kidney-derived Apolipoprotein by using Adaptor-
 CC tagged Competitive PCR (ATAC-PCR). This method allows gene expression to
 CC be quantitatively determined, and because internal standards are not
 CC required to prepare a calibration curve, it is a quicker and less
 CC laborious process

XX Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.2; DB 1; Length 23;
 Best Local Similarity 86.4%; Pred. No. 1e+03; Mismatches 3; Indels 0; Gaps 0;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4460 GGACTTTTCTTTTCTTTT 4481
 |||||

Db 1 GGATCCTTTTCTTTTCTTTT 22

RESULT 1198

AAA07787
 ID AAA07787 standard; DNA; 23 BP.

AC AAA07787;

DT 23-JUN-2000 (first entry)

XX	Structure of a fragment of duplex A target strand.
XX	
DE	Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW	viral infection; inflammatory response; cellular proliferation;
KW	pooriasis; duplex; ss.
XX	
OS	Synthetic.
XX	
PN	WO200011013-A1.
XX	
PD	02-MAR-2000.
XX	
PF	20-AUG-1999; 99WO-US019029.
XX	
PR	22-AUG-1998; 98US-0097712P.
XX	
PA	(UNNE-) UNIV NEBRASKA.
XX	
P1	Gold B;
XX	
DR	WPI; 2000-246530/21.
XX	
PT	Modified nucleomonomers, used in physiologically stable, non-toxic
PT	oligomers used to inhibit expression of nucleic acids and in gene
XX	regulation, antisense technology and diagnostics.
XX	
PS	Disclosure; Page 20; 42pp; English.
XX	
CC	The invention provides modified nucleomonomers of specified formula and
CC	their pharmaceutically acceptable salts. The nucleomonomers are used as
CC	monomers in oligomers, which are used in pharmaceutical compositions to
CC	inhibit expression of nucleic acid molecules including DNA and RNA in
CC	cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC	infected cells. They are used in oligomers for gene regulation, antisense
CC	technology, diagnostic applications to detect target sequences in
CC	biological samples such as those containing pathogenic bacteria, fungi
CC	and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC	encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC	molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC	interleukins associated with pathological conditions such as inflammatory
CC	conditions, cardiovascular disorders, immune reactions, cancer, viral
CC	infections and bacterial infections (see AAA07786 for details of other
CC	uses for which the oligomers are suitable for). Oligomers comprising the
CC	nucleomonomers exhibit increased duplex DNA stability when hybridizing to
CC	target nucleic acid sequences, are physiologically stable, non-toxic and
CC	able to penetrate into cells while maintaining stringent base pair
CC	fidelity for target DNA sequences. The oligomers demonstrate significant
CC	single- or double-stranded target nucleic acid binding activity to form
CC	duplexes, triplexes or other forms of stable association
XX	
SQ	Sequence 23 BP; 1 A; 2 C; 2 G; 18 T; 0 U; 0 Other;
XX	
QY	Query Match 0.2%; Score 17.2; DB 1; Length 23;
XX	Best Local Similarity 86.4%; Pred.No. 1e+03;
Db	Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX	
4465	TTTTTTTTTTTTTTTTTGGTC 4486
1	TTGGTTTTTTTTTTTTTTC 22
XX	
RESUL 1199	
AAA07786/c	
ID	AAA07786 standard; DNA; 23 BP.
XX	
AC	AAA07786;
XX	
DT	23-JUN-2000 (first entry)
XX	
DE	Structure of a fragment of duplex A target strand.
XX	
Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;	

KW viral infection; inflammatory response; cellular proliferation;
 XX psoriasis; duplex; ss.
 OS Synthetic.
 PM WO200011013-A1.
 PD 02-MAR-2000.
 PF 20-AUG-1999; 99WO-US019029.
 PR 22-AUG-1998; 98US-0097712P.
 PA (UYNE-) UNIV NEBRASKA.
 PI Gold B;
 DR WPI: 2000-246530/21.
 XX
 XX
 XX Modified nucleomonomers, used in physiologically stable, non-toxic
 PT oligomers used to inhibit expression of nucleic acids and in gene
 PR regulation, antisense technology and diagnostics.
 XX
 XX
 XX Disclosure; Page 20; 42pp; English.
 XX
 XX
 XX The invention provides modified nucleomonomers of specified formula and
 CC their pharmaceutically acceptable salts. The nucleomonomers are used as
 CC monomers in oligomers, which are used in pharmaceutical compositions to
 CC inhibit expression of nucleic acid molecules including DNA and RNA in
 CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
 CC infected cells. They are used in oligomers for gene regulation, antisense
 CC technology, diagnostic applications to detect target sequences in
 CC biological samples such as those containing pathogenic bacteria, fungi
 CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
 CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
 CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
 CC interlinking associated with pathological conditions such as inflammatory
 CC conditions, cardiovascular disorders, immune reactions, cancer, viral
 CC infections and bacterial infections. The oligomers are suitable for use
 CC in both in vivo and ex vivo therapeutic applications including treatment
 CC of cells such as bone marrow or peripheral blood in conditions such as
 CC leukemia or viral infections, genes as target for cancer treatments
 CC including oncogenes such as ras, k-ras, bcl-2, c-myc, bcr, c-abl
 CC or overexpressed sequences such as mdm2, oncostatin M, interleukin 6
 CC (Kaposi's sarcoma), HER-2 and translocation sequences such as bcr/abl or RNAs
 CC encoded by such genes, as well as viral gene sequences such as polymerase
 CC or reverse transcriptase genes of cytomegalovirus, herpes simplex virus-1
 CC or -2, HTLV-1, human immunodeficiency virus-1 or -2, hepatitis B virus,
 CC human papilloma virus, varicella zoster virus, influenza virus or
 CC rhinovirus. They can also be used to modulate inflammatory responses by
 CC modulating expression of genes such as IL-1 receptor, IL-1, ICAM-1 or E-
 CC selectin in mediating inflammation and modulation of cellular
 CC proliferation in conditions such as arterial occlusion (restenosis) after
 CC angioplasty by modulating the expression of growth or mitogenic factors
 CC such as non-muscle myosin, myc, fos, PCNA, platelet-derived growth factor
 CC or fibroblast growth factor or their receptors or cell proliferation
 CC factor such as c-myc, other extracellular proliferation factors such as
 CC transforming growth factor alpha, IL-6, approx.g-interferon, protein
 CC kinase C for treatment of psoriasis or other conditions, and epithelial
 CC growth factor, transforming growth factor or MHC alleles in autoimmune
 CC disease. Oligomers comprising the nucleomonomers exhibit increased duplex
 CC DNA stability when hybridizing to target nucleic acid sequences, are
 CC physiologically stable, non-toxic and able to penetrate into cells while
 CC maintaining stringent base pair fidelity for target DNA sequences. The
 CC oligomers demonstrate significant single- or double-stranded target
 CC nucleic acid binding activity to form duplexes, triplexes or other forms
 CC of stable association
 XX
 XX Sequence 23 BP; 18 A; 2 C; 2 G; 1 T; 0 U; 0 Other;
 XX
 XX
 XX Query Match 0.2%; Score 17.2; DB 1; Length 23;
 XX Best Local Similarity 86.4%; Pred. No. 1e+03;
 XX Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4465 TTTTGTGTC 4486
 |||||
 DB 23 TTGGTTTTTTTCTC 2

RESULT 1200
 AAA08407
 ID AAA08407 standard; DNA; 23 BP.

AC AAA08407;

DT 13-JUL-2000 (first entry)

DE Oligonucleotide primer SEQ ID NO:1.

KM Detection; primer; adapter; probe; hybridisation; gene cluster;
 KW fractionation; ss.

OS Synthetic.

PN JP2000055914-A.

PD 25-FEB-2000.

PF 13-AUG-1998; 98JP-00228944.

PR 13-AUG-1998; 98JP-00228944.

PA (TAIS) TAISHO PHARM CO LTD.

DR WPI; 2000-368733/32.

PT Gene detection method involves hybridizing probe opposite to objective
 gene out of fractional gene cluster.

PS Example 1; Page 9; 11pp; Japanese.

CC The present invention describes a gene detection method which comprises
 CC fractionating using a probe opposite to the objective gene which is
 CC hybridised out of fractioned gene cluster. The objective gene detected
 CC belongs to the group of objective genes contained in the sample. The
 CC method is used for gene detection by fractionation of cDNA by molecular
 CC index method using specific primer. It provides high detection
 CC sensitivity of objective gene. AAA08407 to AAA08414 represent
 CC oligonucleotides used in the exemplification of the present invention

XX Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.2; DB 1; Length 23;
 Best Local Similarity 86.4%; Pred. No. 1e+03;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4460 GGACTTTTTTTTTTTT 4481
 |||||

DB 1 GGATCCTTTTTTTTTTTT 22
 |||||

RESULT 1201

AA085525/c
 ID AAC85525 standard; cDNA; 23 BP.

AC AAC85525;

DT 16-MAY-2001 (first entry)

DE Primer ZC21,076.

KM Splice variant; zdicn2; mammalian adhesion protease peptide; MAPP;
 KW testis; ovary; prostate; small intestine; colon; stomach; thyroid;
 KW spinal cord; lymph node; trachea; heart; wound healing; apoptosis;
 KW neurogenesis; tumor proliferation; ischemia reperfusion; inflammation;
 KW immunologic recognition; gamete maturation; platelet aggregation;

KW infarction; brain; cancer; Alzheimer's disease; multiple sclerosis;
 KW congestive heart failure; PCR; polymerase chain reaction; amplify;
 KW primer; ss.

OS Synthetic.

PN WO200109293-A2.

PD 08-FEB-2001.

PF 02-AUG-2000; 2000MO-US021085.

PR 03-AUG-1999; 99US-00368070.

PA (ZYMO) ZYMOGENETICS INC.

PI Sheppard PO, Baidur N, Bishop PD;

DR WPI; 2001-202662/20.

PT Mammalian adhesion protease peptides useful for delivery of therapeutic
 agents, for identifying agonists and antagonists and treating disorders
 of brain, heart tissue and platelet aggregation.

PS Example 1; Page 105; 106pp; English.

CC This primer sequence was used to clone the full length cDNA encoding
 CC mammalian adhesion protease peptide (MAPP). Analysis of tissue
 CC distribution of MAPP cDNA showed a transcript of approx. 4.4kb with a
 CC strong signal in testes, ovary, prostate, small intestine and colon, and
 CC a fainter signal in stomach, thyroid, spinal cord, lymph node and
 CC trachea. Also there were two transcripts, approx. 4kb and 4.4kb, both
 CC showing medium strength signal in heart tissue

XX Sequence 23 BP; 2 A; 7 C; 6 G; 8 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.2; DB 1; Length 23;
 Best Local Similarity 86.4%; Pred. No. 1e+03;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 7413 CAGCAGCAGCAGCAGCAGC 7434
 |||||

DB 23 CAGTAGTAGCAGCAGCAGCAGC 2

RESULT 1202

ABV72153/c
 ID ABV72153 standard; DNA; 23 BP.

AC ABV72153;

DT 05-DEC-2002 (first entry)

DE PCR primer ZC21076 used to amplify cDNA encoding zdicn2.

KW Human; isoform; zdicn2; mammalian adhesion protease peptide; MAPP;
 KW disintegrin-like family member; disintegrin protease; DP; PCR; primer;
 KW anticoagulation; fertilization; muscle fusion; neurogenesis; ss.

OS Homo sapiens.

PN US6420154-B1.

PD 16-JUL-2002.

PF 02-AUG-2000; 2000US-00632098.

PR 03-AUG-1999; 99US-0146968P.

PA (ZYMO) ZYMOGENETICS INC.

PI Sheppard PO, Baidur N, Bishop PD;

DR MPI; 2002-626081/67.
 XX New Isolated Mammalian Adhesion Protease Peptides (zdintc2), which have
 PT homology to disintegrin-like family members, useful for preventing,
 PT diagnosing and treating fertility, muscular and neurogenic disorders.
 XX
 PS Example 1; Col 81-82; 42pp; English.
 XX
 CC PCR primers ABV72153-54 were used to amplify cDNA encoding human zdintc2.
 CC zdintc2 is a mammalian adhesion protease peptide (MAPP), and has homology
 CC to disintegrin-like family members (ADAMs, SVMPs and MDGs), referred to
 CC as disintegrin proteases (DIPs). MAPPs have been found to be involved in
 CC anticoagulation, fertilization, muscle fusion, and neurogenesis. Zdintc2
 CC may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate MAPP expression. The proteins may be
 CC administered to treat disorders associated with decreased expression by
 CC rectifying mutations or deletions in a patient's genome that affect the
 CC activity of MAPP by expressing inactive proteins or to supplement the
 CC patients own production of MAPPs
 XX
 SQ Sequence 23 BP; 2 A; 7 C; 6 G; 8 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 17.2; DB 1; Length 23;
 Best Local Similarity 86.4%; Pred. No. 1e+03; Mismatches 3; Indels 0; Gaps 0;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 OY 7413 CAGCAGCAGCAGCAGCAGCAGC 7434
 DB 23 CAGTAGTAGCAGCAGCAGCAAC 2
 XX
 RESULT 1203
 ABA99682
 XX ID ABA99682 standard; DNA; 23 BP.
 XX
 AC ABA99682;
 XX
 DT 31-MAY-2002 (first entry)
 XX
 DE Murine osteoporosis/arthro-rheumatism associated gene PCR primer DAPAL.
 XX
 KM Osteoporosis; murine; treatment; arthro-rheumatism; PCR; primer; ss.
 XX
 OS Mus musculus.
 XX
 PN JP2002051782-A.
 XX
 PD 19-FEB-2002.
 XX
 PF 09-AUG-2000; 2000JP-00241413.
 XX
 PR 09-AUG-2000; 2000JP-00241413.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 DR MPI; 2002-288360/33.
 XX
 PT Preventing or treating an agent for osteoporosis or arthro-rheumatism.
 XX
 PS Example 2; Page 38; 44pp; Japanese.
 XX
 CC This invention describes a novel method for testing the effect of a
 CC substance as a preventive or treating agent for osteoporosis or arthro-
 CC rheumatism. This sequence represents a PCR primer used in the
 CC amplification of a gene encoding a protein associated with osteoporosis
 CC or arthro-rheumatism which is described in the disclosure of the
 CC invention
 XX
 SQ Sequence 23 BP; 2 A; 2 C; 2 G; 17 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 17.2; DB 1; Length 23;
 Best Local Similarity 86.4%; Pred. No. 1e+03; Mismatches 3; Indels 0; Gaps 0;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4460 GGACTTTTCTTTTCTTTTCTTTT 4481
 DB 1 GGATCCTTTTCTTTTCTTTTCTTTT 22
 XX
 RESULT 1204
 ACCT1964/C
 XX ID ACCT1964 standard; DNA; 23 BP.
 XX
 AC ACCT1964;
 XX
 DT 04-AUG-2003 (first entry)
 XX
 DE N. crassa DIM-5 DNA 9a20 region amplifying primer.
 XX
 KM Histone methyltransferase; HMTase; neoplasia; cytostatic; gene therapy;
 XX DIM-5; PCR; primer; ss.
 XX
 OS Neurospora crassa.
 XX
 PN WO2003035844-A2.
 XX
 PD 01-MAY-2003.
 XX
 PF 25-OCT-2002; 2002WO-US034321.
 XX
 PR 25-OCT-2001; 2001US-0347506P.
 XX
 PA (UYOR-) UNIV OREGON STATE.
 XX
 PI Selker EU, Tamara H;
 XX
 DR MPI; 2003-441261/41.
 XX
 PT Identifying a compound with potential for treating neoplasia by
 PT determining histone methyltransferase (HMTase) inhibitory activity of the
 PT compound.
 XX
 PS Example 1; Page 97; 101pp; English.
 XX
 CC The invention relates to identifying a compound with potential for
 CC treating neoplasia. The method involves determining histone
 CC methyltransferase (HMTase) inhibitory activity of the compound, where
 CC high HMTase inhibition activity identifies that the compound has
 CC potential for treating neoplasia. The method is useful for identifying a
 CC compound with potential for treating neoplasia. Sequences ACCT1962-77
 CC represent PCR primers for amplifying the various regions of N. crassa
 CC histone methyltransferase DIM-5 DNA
 XX
 SQ Sequence 23 BP; 8 A; 1 C; 11 G; 3 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 17.2; DB 1; Length 23;
 Best Local Similarity 86.4%; Pred. No. 1e+03; Mismatches 3; Indels 0; Gaps 0;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 OY 3402 CCCGACCTTACCCTTATTCCTC 3423
 DB 23 CCCGCTTACCCTTATTCCTC 2
 XX
 RESULT 1205
 AAA10010
 XX ID AAA10010 standard; DNA; 24 BP.
 XX
 AC AAA10010;
 XX
 DT 05-JUL-2000 (first entry)
 XX
 DE Primer YHZ-2 for human YHZ gene.
 XX
 KM Foreign chromosome; microcell fusion; homologous recombination; antibody;
 KM targeting vector; transgenic animal; disease model; knockout animal;

KM PCR primer; human; ss.
 XX Homo sapiens.
 OS WO200010383-A1.
 XX
 XX
 XX 02-MAR-2000.
 PD
 XX 23-AUG-1999; 99WO-JP004518.
 PF
 XX 21-AUG-1998; 98JP-00236169.
 PR
 XX (KIRI) KIRIN BEER KK.
 PA
 XX Tomizuka K, Yoshida H, Hanaoka K, Oshimura M, Ishida I;
 PI Kuroiwa Y;
 XX WPI; 2000-246479/21.
 DR
 XX
 XX Producing a cell containing modified foreign chromosomes, useful for the
 PT generation of transgenic animals.
 XX
 XX Example 96; Page 182; 316pp; Japanese.
 PS
 XX The invention relates to a novel method of producing cells containing a
 CC modified foreign chromosome or chromosome fragment. The method comprises:
 CC (a) fusing a microcell comprising the foreign chromosome or chromosome
 CC fragment, with a cell having a high efficiency for homologous
 CC recombination; (b) marking the desired site of insertion of the foreign
 CC chromosome using a targeting vector; and (c) inducing deletion or
 CC translocation at the marked site. Transgenic animals produced by the
 CC method are useful to provide disease models and knockout animals, and in
 CC the production of human proteins, particularly human antibodies. This
 CC sequence is used in the method of the invention
 XX
 XX Sequence 24 BP; 0 A; 10 C; 1 G; 13 T; 0 U; 0 Other;
 SQ
 Query Match 0.2%; Score 17.2; DB 1; Length 24;
 Best Local Similarity 86.4%; Pred. No. 1.1e+03;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 5695 CTTGTTTGGCTTCCTTTGCTC 5716
 DB 3 CTTTTCCTTCCTTCCTTCCTC 24
 RESULT 1206
 AAF73443/C
 ID AAF73443 standard; DNA; 24 BP.
 XX
 XX AAF73443;
 AC
 XX
 XX 30-APR-2001 (first entry)
 DT
 XX
 XX Grand fir monoterpene synthase PCR primer 3elBamHIr SEQ ID NO: 100.
 DE
 XX Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;
 KM myrcene synthase; (-)-limonene synthase; (-)-pinene synthase; probe;
 KM terpinolene synthase; insect resistance; nutrition; PCR primer; ss.
 XX
 XX Abies grandis.
 OS
 XX WO200107565-A2.
 PN
 XX
 XX 01-FEB-2001.
 PD
 XX
 XX 24-JUL-2000; 2000WO-US020264.
 PF
 XX 26-JUL-1999; 99US-00360545.
 PR
 XX (UNITW) UNIV WASHINGTON STATE RES FOUND.
 PA
 XX Steele CL, Bohlmann J, Croten RB, Phillips MA;
 PI

XX WPI; 2001-182782/18.
 DR
 XX
 XX New nucleic acid encoding monoterpene synthases, for increasing terpene
 PT synthesis in plants, e.g. for increasing resistance to pests or for
 PT treatment of cancer.
 XX
 XX Example 11; Page 173; 175pp; English.
 PS
 XX The present invention provides the protein and coding sequences of
 CC monoterpene synthase from the grand fir. These include (-)-camphene
 CC synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-
 CC limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase
 CC and pinene synthase. The sequences can be used to produce transgenic
 CC plants expressing high levels of the enzymes, resulting in levels which
 CC are useful in protecting against and treating cancers, and to confer
 CC insect resistance on plants
 XX
 XX Sequence 24 BP; 6 A; 5 C; 5 G; 8 T; 0 U; 0 Other;
 SQ
 Query Match 0.2%; Score 17.2; DB 1; Length 24;
 Best Local Similarity 86.4%; Pred. No. 1.1e+03;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 7258 GAAATGCTCTGATCCCA 7279
 DB 24 GAAATGCTCTGATCCCA 3
 RESULT 1207
 AAF73444
 ID AAF73444 standard; DNA; 24 BP.
 XX
 XX AAF73444;
 AC
 XX
 XX 30-APR-2001 (first entry)
 DT
 XX
 XX Grand fir monoterpene synthase PCR primer 3elBamHIr SEQ ID NO: 101.
 DE
 XX Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;
 KM myrcene synthase; (-)-limonene synthase; (-)-pinene synthase; probe;
 KM terpinolene synthase; insect resistance; nutrition; PCR primer; ss.
 XX
 XX Abies grandis.
 OS
 XX WO200107565-A2.
 PN
 XX
 XX 01-FEB-2001.
 PD
 XX
 XX 24-JUL-2000; 2000WO-US020264.
 PF
 XX 26-JUL-1999; 99US-00360545.
 PR
 XX (UNITW) UNIV WASHINGTON STATE RES FOUND.
 PA
 XX Steele CL, Bohlmann J, Croten RB, Phillips MA;
 PI WPI; 2001-182782/18.
 DR
 XX
 XX New nucleic acid encoding monoterpene synthases, for increasing terpene
 PT synthesis in plants, e.g. for increasing resistance to pests or for
 PT treatment of cancer.
 XX
 XX Example 11; Page 174; 175pp; English.
 PS
 XX The present invention provides the protein and coding sequences of
 CC monoterpene synthase from the grand fir. These include (-)-camphene
 CC synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-
 CC limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase
 CC and pinene synthase. The sequences can be used to produce transgenic
 CC plants expressing high levels of the enzymes, resulting in levels which
 CC are useful in protecting against and treating cancers, and to confer
 CC insect resistance on plants

```

XX Sequence 24 BP; 8 A; 5 C; 5 G; 6 T; 0 U; 0 Other;
SQ
Query Match      0.2%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY      7258 GAAATGCTCTGATCCCA 7279
DB      1 GAAATGCTATGATCCCA 22
RESULT 1208
ABV74853
ID ABV74853 standard; DNA; 24 BP.
XX
AC ABV74853;
XX
DT 05-FEB-2003 (first entry)
DE Protein 16.17 PCR primer #2.
XX
KM Protein 16.17; collagenase; cancer; HIV infection; cytostatic; anti-HIV;
KM PCR; primer; ss.
XX
OS Unidentified.
XX
PN CN1351027-A.
XX
PD 29-MAY-2002.
XX
PF 26-OCT-2000; 2000CN-00125840.
XX
PR 26-OCT-2000; 2000CN-00125840.
XX
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-619851/67.
XX
PT New polypeptide-protein 16.17 containing collagenase characteristics for
PT treating diseases such as cancer and human immunodeficiency virus
PT infection.
XX
PS Example 3; Page 26 (Disclosure); 31pp; Chinese.
XX
CC The present invention relates to protein 16.17 (see ABB98830), which
CC contains collagenase characteristics. The protein and its coding sequence
CC are useful for treating diseases such as cancer and HIV infection. The
CC present sequence is a PCR primer, which was used in an example from the
CC invention. Note: The present sequence, SEQ ID 4, shown in the sequence
CC listing differs from the SEQ ID 4 shown in the disclosure (see ABV74866)
XX
SQ Sequence 24 BP; 3 A; 1 C; 3 G; 17 T; 0 U; 0 Other;
Query Match      0.2%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY      4465 TTTTGTGTTTGTGTTTGTGTC 4486
DB      2 TGTGTTTGTGTTTGTGTC 23
RESULT 1209
ABV56862
ID ABV56862 standard; DNA; 24 BP.
XX
AC ABV56862;
XX
DT 30-JAN-2003 (first entry)
XX

```

```

DE Human, glutamine enrichment factor 21.12 cDNA RT-PCR primer #1.
XX
KM Human; glutamine enrichment factor 21.12; primer; ss; angiocardiopathy;
KM cancer; nervous system disease; immunological disease; inflammation;
KM RT-PCR; reverse transcriptase.
XX
OS Homo sapiens.
XX
PN CN1345802-A.
XX
PD 24-APR-2002.
XX
PF 26-SEP-2000; 2000CN-00125420.
XX
PR 26-SEP-2000; 2000CN-00125420.
XX
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-539318/58.
XX
PT Novel polypeptide-human glutamine enrichment factor 21.12 and
PT polynucleotide for encoding the polypeptide.
XX
PS Example 2; Page 16 (Disclosure); 32pp; Chinese.
XX
CC The invention relates to human glutamine enrichment factor 21.12, a
CC polynucleotide encoding the polypeptide and a method for producing the
CC polypeptide using DNA recombination technology. The polypeptide is used
CC for curing several diseases such as cancer, angiocardiopathy, nervous
CC system disease, immunological disease and inflammation. This sequence
CC represents a reverse transcriptase PCR (RT-PCR) primer used in isolation
CC of cDNA encoding human glutamine enrichment factor 21.12
XX
SQ Sequence 24 BP; 8 A; 0 C; 11 G; 5 T; 0 U; 0 Other;
Query Match      0.2%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY      6156 TGTAGGAGGATGACATTAAGG 6177
DB      3 TGTAGGAGGAGGATTAAGG 24
RESULT 1210
ABL55230/c
ID ABL55230 standard; DNA; 24 BP.
XX
AC ABL55230;
XX
DT 14-JUN-2002 (first entry)
XX
DE Pax protein 11 RT-PCR primer, SEQ ID NO:3.
XX
KM Pax protein 11; human; recombinant production; malignant tumour; cancer;
KM blood disease; HIV infection; human immunodeficiency virus;
KM immune disorder; inflammatory condition; cytostatic; gene therapy;
KM anti-HIV; anti-inflammatory; immunomodulator; reverse transcription-PCR;
KM RT-PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN CN1329025-A.
XX
PD 02-JAN-2002.
XX
PF 21-JUN-2000; 2000CN-00116687.
XX
PR 21-JUN-2000; 2000CN-00116687.
XX
PA (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.
XX

```

XX	Mao Y, Xie Y;
P1	WPI; 2002-305398/35.
DR	A novel polypeptide-Pax protein 11 and polynucleotide for coding this
XX	polypeptide.
PT	Example 2; Page 16 (Disclosure); 32pp; Chinese.
PS	The invention relates to pax protein 11 (AA49189) and to nucleic acids
CC	encoding it (ABLS522). The protein has a molecular weight of 11 kD. The
CC	invention also relates to a method for the recombinant production of the
CC	protein, an antagonist of the protein, and the use of the protein, gene
CC	and antagonist in therapeutic applications. Pax protein 11 can be used in
CC	the treatment of a variety of diseases such as malignant tumours, blood
CC	diseases, HIV (human immunodeficiency virus) infection, immune disorders
CC	and inflammatory conditions. Sequences ABLS5230-ABLS5231 represent
CC	reverse transcription-PCR (RT-PCR) primers used in an exemplification of
CC	the invention to isolate human pax protein 11 cDNA
XX	
SQ	Sequence 24 BP; 19 A; 4 C; 1 G; 0 T; 0 U; 0 Other;
	Query Match 0.2%; Score 17.2; DB 1; Length 24;
	Best Local Similarity 86.4%; Pred.No.1.le+03;
	Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0.
OY	4464 TTTTCTTTTTTTTTTTTTTTGTG 4485
Db	24 TTCTTTTTTGTTGGTTTGT 3
RESULT 1211	
AA19218/C	
ID	AA19218 standard; DNA; 24 BP.
AC	AA19218;
XX	
DT	09-APR-2002 (first entry)
DE	Kringle protein 14, RT-PCR primer #2.
XX	
KM	Kringle protein 14; cytosolic; haemostatic; virucide; immunomodulatory;
KV	antiinflammatory; malignant tumour; haemopathy; inflammation; primer;
KW	human immunodeficiency virus; HIV; immunological disease; RT-PCR; ss;
XK	reverse transcriptase PCR.
XX	
OS	Unidentified.
XX	
PN	WO200192318-AI.
PD	06-DEC-2001.
PF	21-MAY-2001; 2001WO-CN000845.
PR	24-MAY-2000; 2000CN-00115849.
PA	(SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
P1	Mao Y, Xie Y;
XX	
DR	WPI; 2002-090030/12.
PT	Kringle protein 14 and encoding polynucleotide, used in diagnosis and
FT	treatment of malignant tumors, hemopathy, human immunodeficiency virus
XX	infection, immunological diseases and inflammation.
PS	Example 2; Page 17; 37pp; Chinese.
XX	
CC	The invention relates to an isolated polypeptide (I) of Kringle protein
CC	14 and the polynucleotide (II) encoding (I). (I) and (II) are used in
CC	diagnosis and treatment of malignant tumor, hemopathy, human
CC	immunodeficiency virus (HIV) infection, immunological diseases and

CC	various inflammations. The present sequence represents a reverse
CC	transcriptase (RT)-PCR primer used to isolate the coding sequence of
CC	kirtling protein 14 as described in the invention
XX	
SQ	Sequence 24 BP; 20 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
OY	
DB	
Query Match	0.2%; Score 17.2; DB 1; Length 24;
Best Local Similarity	86.4%; Pred. No. 1.1e+03;
Matches 19; Conservative	0; Mismatches 3; Indels 0; Gaps 0;
OY	4467 TTTTCTTTTTTTTTGCTT 4488 TTTTATTTTTTGTTTTGTTTT 3
RESULT 1212	
ID	ABX15494
AC	ABX15494 standard; DNA; 24 BP.
XX	ABX15494;
DT	15-APR-2003 (first entry)
XX	Human SDHD gene specific PCR primer 3F.
DE	
KW	Cybb; PCR; human; mitochondrial complex II; cancer; heart disease;
KW	succinate-ubiquinone oxidoreductase subunit D; SDHD; gene therapy;
KW	cyclochrom b small subunit; cybs; antiparkinsonian; cerebroprotective;
KW	cardiant; cycsostratic; gene therapy; oxygen sensing; normoxic; stroke;
KM	tissue oxygenation; neurodegenerative disease; Parkinson's disease;
KM	neoplasm; primer; se.
XX	
OS	Homo sapiens.
XX	
PN	US6468789-B1.
PD	22-OCT-2002.
PF	02-FEB-2000; 2000US-00496632.
PR	02-FEB-2000; 2000US-00496632.
PA	(UYPI-) UNIV PITTSBURGH.
PI	Bayval BE, Ferrell RE, Devlin BJ, Willett-Brozick JE;
DR	WPI; 2003-196748/19.
PS	
PT	Novel isolated mitochondrial complex II gene sequence such as SDHD DNA
PT	sequence useful as biological oxygen sensor for diagnosis, prognosis,
PT	prevention and/or treatment of undesirable biological states.
XX	
XX	Disclosure; Col 7; 19pp; English.
XX	
CC	This invention relates to an isolated mitochondrial complex II gene
CC	sequence such as the succinate-ubiquinone oxidoreductase subunit D (SDHD)
CC	gene encoding the small subunit of cytochrome b (cybs). The invention
CC	also comprises a recombinant host cell transformed with the human cybs
CC	sequence operably linked to a promoter. The sequences of the invention
CC	may have antiparkinsonian, cerebroprotective, cardiant and cytostatic
CC	activity and may be used in gene therapy. The SDHD gene of the invention
CC	is useful for correcting (or providing for) oxygen sensing in cells, for
CC	restoring oxygen sensing to affected cells in order to facilitate
CC	normoxic conditions, and for diagnosis and prognosis of mammalian cancer.
CC	The SDHD gene is useful as a biological oxygen sensor for diagnosis,
CC	prognosis, prevention and/or treatment of undesirable biological states,
CC	for improving or restoring cellular and/or tissue oxygenation to benefit
CC	undesirable states associated with tissue oxygen sensing, for correcting
CC	and/or augmenting oxygen sensing defects in cells and for creating
CC	hypoxic cells, for treating a disease, preferably a neurodegenerative
CC	disease such as Parkinson's disease, for suppressing neoplastic growth of
CC	a recipient cell, in gene therapy methods to increase the amount of the
CC	expression products of the genes in cancer cells, or to restore oxygen

CC sensing under a variety of hypoxic conditions including cancer, and for
CC the treatment of stroke or heart diseases. The present sequence
CC represents a PCR primer used to amplify exons of the human SDHD gene of
CC the invention

XX SQ Sequence 24 BP; 3 A; 4 C; 4 G; 13 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.2; DB 1; Length 24;

Best Local Similarity 86.4%; Pred. No. 1.1e+03; Mismatches 3; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6064 TTTTCTAAATCTGTCCTTTT 6085

||||| ||||||| ||||||| |||||||

2 TTTTATGAATCTGTCCTTTT 23

RESULT 1213

ABX15495

ID ABX15495 standard; DNA; 24 BP.

XX AC ABX15495;

XX DT 15-APR-2003 (first entry)

XX DE Human SDHD gene specific PCR primer 3R.

XX CYsb; PCR; human; mitochondrial complex II; cancer; heart disease;
KW succinate-ubiquinone oxidoreductase subunit D; SDHD; gene therapy;
KW cytochrome b small subunit; cybs; antiparkinsonian; cerebroprotective;
KW cardiant; cytoelastic; gene therapy; oxygen sensing; normoxic; stroke;
KW tissue oxygenation; neurodegenerative disease; Parkinson's disease;
KW neoplasm; primer; ss.

XX OS Homo sapiens.

XX PN US6468789-B1.

XX PD 22-OCT-2002.

XX PF 02-FEB-2000; 2000US-00496632.

XX PR 02-FEB-2000; 2000US-00496632.

XX PA (UYP1-) UNIV PITTSBURGH.

XX PI Bayesal BE, Ferrell RE, Devlin BJ, Willett-Brozick JR;

XX DR WPI; 2003-196748/19.

XX PT Novel isolated mitochondrial complex II gene sequence such as SDHD DNA
XX prevention and/or treatment of undesirable biological states.

XX PS Disclosure; Col 7; 19pp; English.

XX This invention relates to an isolated mitochondrial complex II gene
CC sequence such as the succinate-ubiquinone oxidoreductase subunit D (SDHD)
CC gene encoding the small subunit of cytochrome b (cybs). The invention
CC also comprises a recombinant host cell transformed with the human cybs
CC sequence operably linked to a promoter. The sequences of the invention
CC may have antiparkinsonian, cerebroprotective, cardiant and cyrostatic
CC activity and may be used in gene therapy. The SDHD gene of the invention
CC is useful for correcting (or providing for) oxygen sensing in cells, for
CC restoring oxygen sensing to affected cells in order to facilitate
CC normoxic conditions, and for diagnosis and prognosis of mammalian cancer.
CC The SDHD gene is useful as a biological oxygen sensor for diagnosis,
CC prognosis, prevention and/or treatment of undesirable biological states,
CC for improving or restoring cellular and/or tissue oxygenation to benefit
CC undesirable states associated with tissue oxygen sensing, for correcting
CC and/or augmenting oxygen sensing defects in cells and for creating
CC hypoxic cells, for treating a disease, preferably a neurodegenerative
CC disease such as Parkinson's disease, for suppressing neoplastic growth of
CC a recipient cell, in gene therapy methods to increase the amount of the

CC expression products of the genes in cancer cells, or to restore oxygen
CC sensing under a variety of hypoxic conditions including cancer, and for
CC the treatment of stroke or heart diseases. The present sequence
CC represents a PCR primer used to amplify exons of the human SDHD gene of
CC the invention

XX SQ Sequence 24 BP; 3 A; 4 C; 4 G; 13 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.2; DB 1; Length 24;

Best Local Similarity 86.4%; Pred. No. 1.1e+03; Mismatches 3; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6064 TTTTCTAAATCTGTCCTTTT 6085

||||| ||||||| ||||||| |||||||

2 TTTTATGAATCTGTCCTTTT 23

RESULT 1214

AAV57477

ID AAV57477 standard; DNA; 25 BP.

XX AC AAV57477;

XX DT 14-DEC-1998 (first entry)

XX DE Cytochrome P450ox monooxygenase PCR primer SEQ ID NO:11.

XX KW Cytochrome P450 monooxygenase; P450ox; Sorghum bicolor (L.) Moench;
KW Similis alba; biosynthetic conversion; aldoxime; nitrile; cyanohydrin;
KW cyanogenic glycoside; transgenic plant; resistance; PCR primer; ss.

XX OS Synthetic.

XX PN Sorghum bicolor.

XX PD WO9840470-A2.

XX PF 17-SEP-1998.

XX PR 05-MAR-1998; 98WO-EP001253.

XX PR 07-MAR-1997; 97EP-00810132.

XX PR 08-DEC-1997; 97EP-00810954.

XX PA (NOVS) NOVARTIS AG.

XX PI (UYRO-) UNIV ROYAL VETERINARY & AGRIC.

XX DR MPI; 1998-520808/44.

XX PT Cytochrome P450 monooxygenase of the cyanogenic glycoside pathway -
XX useful for the production of plants with improved nutritive value or pest
XX resistance.

XX PS Example 5; Page 29; 32pp; English.

XX The present sequence represents a PCR primer for cytochrome P450
CC monooxygenase from Sorghum bicolor (L.) Moench, designated P450ox.
CC Cytochrome P450 monooxygenase catalyses: (i) the conversion of aldoxime
CC to a nitrile; and (ii) the nitrile to the corresponding cyanohydrin. DNA
CC encoding cytochrome P450 monooxygenase can be used to obtain transgenic
CC plants, for the purpose of improving the nutritive value or pest
CC resistance of the plant. Cytochrome P450 monooxygenase catalyses the
CC conversion of aldoximes to nitriles to cyanohydrins, which are the
CC precursors of toxic cyanogenic glycosides, so staple food such as cassava
CC and lima beans, as well as animal feed such as white clover, can be
CC rendered less toxic by blocking the cytochrome P450 monooxygenase
CC activity. Introducing the enzyme to plants or to certain tissues could
CC help reduce crop damage since the product is also toxic to insects,
CC acarids and nematodes

XX SQ Sequence 25 BP; 1 A; 3 C; 3 G; 17 T; 0 U; 1 Other;

Query Match 0.2%; Score 17.2; DB 1; Length 25;
 Best Local Similarity 86.4%; Pred. No. 1.1e+03;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 4460 GGACTTTTCTTTTCTTTTCTT 4481
 DB 3 GGATCCTTTTCTTTTCTTTTCTT 24

RESULT 1215
 AAC95905
 ID AAC95905 standard; DNA; 25 BP.
 AC AAC95905;
 XX
 XX
 DT 26-FEB-2001 (first entry)
 XX
 DE HLA HLA-B gene PCR primer #16.
 XX
 XX DNA sequence analysis; sequencing; protein sequence; protein structure;
 KW gene typing; organ donation; bacteria identification; 16S rRNA; HLA;
 KW human leukocyte antigen; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200065088-A2.
 XX
 PD 02-NOV-2000.
 XX
 PF 20-APR-2000; 2000WO-EP003636.
 XX
 PR 26-APR-1999; 99EP-00303215.
 XX
 PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
 XX
 PI Ulfendahl P, Wong K;
 XX
 FI
 XX
 DR WPI; 2000-679677/66.
 XX
 PT Identifying extendible primers for use in identification, or
 PT classification of a nucleic acid of an organism, allele or gene such as
 PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
 PT specific length.
 XX
 PS Claim 14; Page 42; 66pp; English.
 XX
 CC The present invention provides a method for identifying a set of
 CC extendible primers which can be used in the identification, typing and
 CC classification of genes. This can then be used to predict protein
 CC sequence and structure, in organ donation to match the organ with the
 CC receiver, and to identify bacteria in a sample. The method can be used to
 CC type the human leukocyte antigen genes (HLA) and 16S rRNA genes in
 CC particular
 XX
 SQ Sequence 25 BP; 1 A; 3 C; 3 G; 18 T; 0 U; 0 Other;
 QY
 Query Match 0.2%; Score 17.2; DB 1; Length 25;
 Best Local Similarity 86.4%; Pred. No. 1.1e+03;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 4466 TTTTCTTTTCTTTTCTTCTTCT 4487
 DB 1 TTTTCTTTTCTTTTCTTCTTCTTCT 22

DE 16S rRNA gene PCR primer #37.
 XX
 XX DNA sequence analysis; sequencing; protein sequence; protein structure;
 KW gene typing; organ donation; bacteria identification; 16S rRNA; HLA;
 KW human leukocyte antigen; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200065088-A2.
 XX
 PD 02-NOV-2000.
 XX
 PF 20-APR-2000; 2000WO-EP003636.
 XX
 PR 26-APR-1999; 99EP-00303215.
 XX
 PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
 XX
 PI Ulfendahl P, Wong K;
 XX
 FI
 XX
 DR WPI; 2000-679677/66.
 XX
 PT Identifying extendible primers for use in identification, or
 PT classification of a nucleic acid of an organism, allele or gene such as
 PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
 PT specific length.
 XX
 PS Claim 14; Page 45; 66pp; English.
 XX
 CC The present invention provides a method for identifying a set of
 CC extendible primers which can be used in the identification, typing and
 CC classification of genes. This can then be used to predict protein
 CC sequence and structure, in organ donation to match the organ with the
 CC receiver, and to identify bacteria in a sample. The method can be used to
 CC type the human leukocyte antigen genes (HLA) and 16S rRNA genes in
 CC particular
 XX
 SQ Sequence 25 BP; 2 A; 2 C; 6 G; 15 T; 0 U; 0 Other;
 QY
 Query Match 0.2%; Score 17.2; DB 1; Length 25;
 Best Local Similarity 86.4%; Pred. No. 1.1e+03;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 4470 TTTTCTTTTCTTTCTTGAG 4491
 DB 1 TTTTCTTTTCTTTCTTGAGCTTGGG 22

RESULT 1217
 AAC96251
 ID AAC96251 standard; DNA; 25 BP.
 XX
 AC AAC96251;
 XX
 XX 26-FEB-2001 (first entry)
 DT
 XX
 DE HLA DPA1 gene PCR primer #8.
 XX
 XX DNA sequence analysis; sequencing; protein sequence; protein structure;
 KW gene typing; organ donation; bacteria identification; 16S rRNA; HLA;
 KW human leukocyte antigen; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200065088-A2.
 XX
 PD 02-NOV-2000.
 XX
 PF 20-APR-2000; 2000WO-EP003636.
 XX
 PR 26-APR-1999; 99EP-00303215.
 XX
 PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.

XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 48; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular.
SQ Sequence 25 BP; 3 A; 3 C; 3 G; 16 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.2; DB 1; Length 25;
Best Local Similarity 86.4%; Pred. No. 1.1e+03;
Matches 19; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4469 TTTTGTGCTGAG 4490
DB 1 TTTTGTGCTGAG 22

RESULT 1218
AAC96862
ID AAC96862 standard; DNA; 25 BP.
XX
AC AAC96862;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA HLA-C gene PCR primer #67.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 58; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to

CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 2 A; 3 C; 6 G; 14 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.2; DB 1; Length 25;
Best Local Similarity 86.4%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4472 TTTTGTGCTGAG 4493
DB 1 TTTTGTGCTGAG 22

RESULT 1219
AAC96557
ID AAC96557 standard; DNA; 25 BP.
XX
AC AAC96557;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA DRB345 gene PCR primer #28.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 53; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular.
SQ Sequence 25 BP; 2 A; 2 C; 5 G; 16 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.2; DB 1; Length 25;
Best Local Similarity 86.4%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4470 TTTTGTGCTGAG 4491
DB 1 TTTTGTGCTGAG 22

RESULT 1220
AAC96629
ID AAC96629 standard; DNA; 25 BP.

```

XX AAC96629;
AC
XX
XX 26-FEB-2001 (first entry)
DT
XX
XX HLA HLA-A gene PCR primer #6.
DE
XX
XX DNA sequence analysis; sequencing; protein sequence; protein structure;
KM gene typing; organ donation; bacteria identification; 16S rRNA; HLA;
KM human leukocyte antigen; PCR primer; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200065088-A2.
PN
XX
XX 02-NOV-2000.
PD
XX
XX 20-APR-2000; 2000WO-EP003636.
PF
XX
XX 26-APR-1999; 99EP-00303215.
PR
XX
XX (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
PA
XX
XX Ulfendahl P, Wong K;
PI
XX
XX WPI; 2000-679677/66.
DR
XX
XX Identifying extendible primers for use in identification, or
PT
XX
XX PT classification of a nucleic acid of an organism, allele or gene such as
PT
XX
XX PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT
XX
XX specific length.
XX
XX Claim 14; Page 54; 66pp; English.
XX
XX The present invention provides a method for identifying a set of
CC
XX
XX extendible primers which can be used in the identification, typing and
CC
XX
XX classification of genes. This can then be used to predict protein
CC
XX
XX sequence and structure, in organ donation to match the organ with the
CC
XX
XX receiver, and to identify bacteria in a sample. The method can be used to
CC
XX
XX type the human leukocyte antigen genes (HLA) and 16S rRNA genes in
CC
XX
XX particular
XX
XX
XX Sequence 25 BP; 1 A; 3 C; 5 G; 16 T; 0 U; 0 Other;
SQ
XX
XX
XX Query Match 0.2%; Score 17.2; DB 1; Length 25;
XX
XX Best Local Similarity 86.4%; Pred. No. 1.1e+03;
XX
XX Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX
XX 4470 TTTTCTTTTCTTGTCTTGAG 4491
QY
XX
XX 1 TTTTCTTTTCTTGTCTTGAG 22
DB
XX
XX
XX RESULT 1221
XX
XX AAH38199
ID
XX
XX AAH38199 standard; DNA; 25 BP.
XX
XX
XX AAH38199;
AC
XX
XX 14-AUG-2001 (first entry)
DT
XX
XX
XX SNP specific SNPE primer SEQ ID 995.
DE
XX
XX
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KM
XX
XX SNPE; genotyping; agammaglobulinemia; diabetes insipidus; cancer;
KM
XX
XX Leisch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolemia;
KM
XX
XX polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KM
XX
XX acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KM
XX
XX inflammation; forensic investigation; paternity analysis; primer; ss.
XX
XX
XX Homo sapiens.
OS
XX
XX WO200129262-A2.
PN
XX
XX

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XX
XX
XX 26-APR-2001.
PD
XX
XX
XX 13-OCT-2000; 2000WO-US028436.
PF
XX
XX
XX 15-OCT-1999; 99US-0160096P.
PR
XX
XX (ORCH-) ORCHID BIOSCIENCES INC.
PA
XX
XX Picoult-Newburg L, Pohl M;
PI
XX
XX WPI; 2001-290930/30.
DR
XX
XX
XX New genotyping oligonucleotide, useful for detecting the presence,
PT
XX
XX PT absence or identity of single polymorphic polymorphism in a nucleic
PT
XX
XX acid sample.
XX
XX Claim 1; Page 55; 83pp; English.
XX
XX
XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC
XX
XX primer extension (SNPE) primers, and the sequences of regions flanking
CC
XX
XX sites of single nucleotide polymorphisms SNPs. The present invention
CC
XX
XX includes kits for determining the presence or absence of a SNP, using the
CC
XX
XX oligonucleotides of the invention. The PCR primers are used to amplify a
CC
XX
XX SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC
XX
XX The oligonucleotides are useful for genotyping a nucleic acid sample by
CC
XX
XX performing a single-nucleotide primer extension reaction. The
CC
XX
XX oligonucleotides are useful for determining the presence, absence or
CC
XX
XX identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC
XX
XX assess by association analysis the genotype of an individual or group of
CC
XX
XX individuals, having a pathological phenotypic trait suspected of being
CC
XX
XX caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC
XX
XX agammaglobulinemia, diabetes insipidus, Leisch-Nyhan syndrome, muscular
CC
XX
XX dystrophy, familial hypercholesterolemia, polycystic kidney disease,
CC
XX
XX osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC
XX
XX traits also include symptoms of or susceptibility to multifactorial
CC
XX
XX disease of which a component is or may be genetic such as autoimmune
CC
XX
XX diseases, including, rheumatoid arthritis, multiple sclerosis,
CC
XX
XX inflammation, cancer, nervous system diseases and infection by pathogenic
CC
XX
XX microorganisms. The method is also useful in forensic investigations and
CC
XX
XX paternity analysis. The present sequence represents a single nucleotide
CC
XX
XX primer extension (SNPE) primer specific for a human SNP containing DNA
CC
XX
XX sequence
XX
XX
XX Sequence 25 BP; 1 A; 2 C; 1 G; 21 T; 0 U; 0 Other;
SQ
XX
XX
XX Query Match 0.2%; Score 17.2; DB 1; Length 25;
XX
XX Best Local Similarity 86.4%; Pred. No. 1.1e+03;
XX
XX Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX
XX 4462 ACTTTTCTTTTCTTTTCTTTT 4483
QY
XX
XX 3 ACTTTTCTTTTCTTTTCTTTT 24
DB
XX
XX
XX RESULT 1222
XX
XX ABK50248/C
ID
XX
XX ABK50248 standard; DNA; 25 BP.
XX
XX
XX ABK50248;
AC
XX
XX 30-JUL-2002 (first entry)
DT
XX
XX
XX Heterostigma akashiwo virus specific PCR primer PKN62B.
DE
XX
XX
XX Heterostigma akashiwo virus; Hav; primer; ss; UKCH-2; red tide; PCR;
KM
XX
XX PKN62B.
KM
XX
XX
XX Unidentified.
OS
XX
XX JP2001299358-A.
PN
XX
XX 30-OCT-2001.
PD
XX
XX

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XX 27-APR-2000; 2000JP-00128327.
XX
XX 27-APR-2000; 2000JP-00128327.
XX
XX (SUIS-) SUISSANCHO SEINANKAIKU SUISSAN KENKYUSHO.
XX
XX WPI; 2002-374710/41.
XX
XX Method for detection of Heterosigma akashiwo virus using a nucleic acid
XX amplification.
XX
XX Claim 8; Page 4; 14pp; Japanese.
XX
XX This invention relates to a novel method of detecting Heterosigma
XX akashiwo virus (Hav) by nucleic acid amplification using a target
XX sequence from the UKCH-2 gene area and all or some proximal sequences.
XX areas. The invention also comprises oligonucleotide primer sequences
XX which may be used in the method of the invention. This method can be used
XX to detect Heterosigma akashiwo virus so that red tide can be controlled.
XX Control of red tide with Hav may be used as a biological anti-red tide
XX agent. The present sequence represents a Heterosigma akashiwo virus
XX specific PCR primer used to amplify Heterosigma akashiwo viral cDNA in
XX the method of the invention
XX
XX Sequence 25 BP; 12 A; 2 C; 9 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 17.2; DB 1; Length 25;
XX Best Local Similarity 86.4%; Pred. No. 1.1e+03;
XX Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 5700 TTGCTTCTCTTCTTCTTCTTCTC 5721
XX 22 TTGCTTCTCTTCTTCTTCTTCTC 1
XX
XX RESULT 1223
XX ABQ13914
XX ID ABQ13914 standard; DNA; 25 BP.
XX
XX AC ABQ13914;
XX
XX DT 29-MAY-2002 (first entry)
XX
XX DE Human GDMLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:13906.
XX
XX KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
XX muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
XX skeletal muscle disorder; amplicon; screening; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200192524-A2.
XX
XX PD 06-DEC-2001.
XX
XX PF 25-MAY-2001; 2001WO-US016981.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX 30-JAN-2001; 2001WO-US000661.
XX 30-JAN-2001; 2001WO-US000662.
XX 30-JAN-2001; 2001WO-US000663.
XX 30-JAN-2001; 2001WO-US000664.
XX 30-JAN-2001; 2001WO-US000665.
XX 30-JAN-2001; 2001WO-US000666.
XX 30-JAN-2001; 2001WO-US000667.
XX 30-JAN-2001; 2001WO-US000668.
XX 30-JAN-2001; 2001WO-US000669.
XX 30-JAN-2001; 2001WO-US000670.
XX 05-FEB-2001; 2001US-0266860P.
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XX (AEOM-) AEOMICA INC.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
XX WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
XX or as specific biomolecule capture probes for surface-enhanced laser
XX desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
XX Disclosure; SEQ ID NO 13906; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
XX protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
XX 1 can be used in gene therapy and vaccine production. The hGDMLP-1
XX nucleic acids can be used as probes to detect, characterise and quantify
XX hGDMLP-1 nucleic acids in samples, as amplification substrates, to
XX provide initial substrates for the recombinant engineering of hGDMLP-1
XX protein variants having desired phenotypic improvements, and for
XX expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
XX used as immunogens to raise antibodies that specifically recognise hGDMLP
XX -1 proteins, as standards in assays used to determine the concentration
XX and/or amount specifically of hGDMLP proteins, as specific biomolecule
XX capture probes for surface-enhanced laser desorption ionisation, as
XX therapeutic supplement in patients having specific deficiency in hGDMLP-1
XX production, and in vaccines or for replacement therapy. The
XX polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
XX disorder associated with the expression of hGDMLP-1, in particular heart
XX and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
XX The present sequence represents an oligomer used in the screening of the
XX hGDMLP-1 sequence in the exemplification of the present invention. N.B.
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequence
XX
XX Sequence 25 BP; 5 A; 5 C; 12 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 17.2; DB 1; Length 25;
XX Best Local Similarity 86.4%; Pred. No. 1.1e+03;
XX Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 5542 GGTGTGTCATGAGATGAGAA 5563
XX 4 GGTGTGTCATGAGATGAGAA 25
XX
XX RESULT 1224
XX ABQ13041/c
XX ID ABQ13041 standard; DNA; 25 BP.
XX
XX AC ABQ13041;
XX
XX DT 11-JUN-2002 (first entry)
XX
XX DE Oligonucleotide adapter/capture probe 13032.
XX
XX KW Oligonucleotide array; adapter sequence; probe; ss.
XX
XX OS Synthetic.
XX
XX PN WO200216649-A2.
XX
XX PD 28-FEB-2002.
XX
XX PF 27-AUG-2001; 2001WO-US026519.
XX 25-AUG-2000; 2000US-0227948P.
XX 29-AUG-2000; 2000US-0228854P.
XX
XX (ILLU-) ILLUMINA INC.
XX
XX Gunderson K;
XX
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XX  WPI, 2002-292068/33.
XX
XX  Array comprising adapter sequences useful for immobilizing or detecting a
XX  target nucleic acid sequence, has different addresses comprising
XX  different specific capture probes.
XX
XX  Claim 1, Page 250, 261pp; English.
XX
XX  The invention relates to an oligonucleotide array (I) comprising at least
XX  25 different addresses (adapter sequences) with each comprising a
XX  different capture probe selected from a group consisting of the sequences
XX  given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
XX  nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
XX  ABQ13409) to a target nucleic acid to form a modified target nucleic acid
XX  and contacting the modified target nucleic acid with (I). The steps of
XX  above method is useful for detecting a target nucleic acid, which further
XX  comprises detecting the presence of the modified target nucleic acid
XX
XX  Sequence 25 BP; 4 A; 6 C; 6 G; 9 T; 0 U; 0 Other;
XX
XX  Query Match          0.2%; Score 17.2; DB 1; Length 25;
XX  Best Local Similarity 86.4%; Pred. No. 1.1e+03;
XX  Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX  433 GAAATACATGTCACGACATTCA 454
XX  22 GAAATACATGCGCCAGATTGCA 1
XX
XX  RESULT 1225
XX  ABS71671/C
XX  ID ABS71671 standard; DNA; 25 BP.
XX
XX  AC ABS71671;
XX
XX  DT 28-NOV-2002 (first entry)
XX
XX  DE T cell receptor (TCR) variable beta (BV) peptide RT-PCR primer #14.
XX
XX  KM T cell receptor; TCR; receptor; variable beta peptide; BV peptide; TCRV;
XX  KM T cell variable gene; T cell regulatory activity; autoimmune disease;
XX  KM multiple sclerosis; human; reverse transcriptase; RT-PCR; primer; ss.
XX
XX  OS Homo sapiens.
XX
XX  PN US2002107388-A1.
XX
XX  PD 08-AUG-2002.
XX
XX  PF 10-MAY-2001; 2001US-00853830.
XX
XX  PR 12-MAY-2000; 2000US-0203984P.
XX
XX  PA (VAND/) VANDENBARK A A.
XX
XX  PI Vandenbark AA;
XX
XX  DR WPI, 2002-697882/75.
XX
XX  PT Identifying a T cell receptor variable gene expressed by target T cells
XX  in an individual is useful to identify disease-associated T cells for
XX  design of individualized therapies, particularly for autoimmune disease.
XX
XX  Example 2; Page 11; 20pp; English.
XX
XX  The invention relates to a method for identifying a T cell receptor
XX  variable (TCRV) gene expressed by target T cells in an individual,
XX  comprising determining expression of TCRV genes by activated T cells from
XX  the individual and determining regulatory activity elicited in response
XX  to TCRV peptides from the individual. A preferentially expressed TCRV
XX  gene whose TCRV peptide elicits low T cell regulatory activity is
XX  identified as a variable gene expressed by target T cells. The method is

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CC  used to identify disease-associated T cells in an individual so that
CC  individualised therapies can be designed to prevent or treat the disease,
CC  particularly an autoimmune disease, especially multiple sclerosis. This
CC  sequence represents a reverse transcriptase PCR (RT-PCR) primer used in
CC  analysis of expression of DNA encoding TCR variable beta (BV) peptides
XX
XX  Sequence 25 BP; 9 A; 8 C; 5 G; 3 T; 0 U; 0 Other;
XX
XX  Query Match          0.2%; Score 17.2; DB 1; Length 25;
XX  Best Local Similarity 86.4%; Pred. No. 1.1e+03;
XX  Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX  5155 GGGGAGTTCTCTCGGACAGTG 5176
XX  22 GGGGAGTTCTCTCTGTCAGTG 1
XX
XX  RESULT 1226
XX  ABK87633
XX  ID ABK87633 standard; DNA; 25 BP.
XX
XX  AC ABK87633;
XX
XX  DT 24-SEP-2002 (first entry)
XX
XX  DE BamHI5G PCR primer.
XX
XX  KM Atopic dermatitis-associated; asthma; psoriasis; pancreatitis; PCR; ss;
XX  KM rheumatoid arthritis; nephritis; arteriosclerosis; allergic disease;
XX  KM viral disease; inflammatory colitis; bronchitis; skin disease; primer.
XX
XX  OS unidentified.
XX
XX  PN WO200251999-A1.
XX
XX  PD 04-JUL-2002.
XX
XX  PF 21-DEC-2001; 2001WO-JP011293.
XX
XX  PR 21-DEC-2000; 2000JP-00388739.
XX
XX  PA (MOCH) MOCHIDA PHARM CO LTD.
XX  PA (KAZU-) KAZUSA DNA RES INST.
XX
XX  PI Ohara O, Nagase T, Negishi T, Mizushima S, Furusako S;
XX
XX  DR WPI, 2002-519957/55.
XX
XX  PT Human spleen-originated cDNA library-isolated atopic dermatitis-
XX  associated gene, which encodes a protein, useful in diagnosis and
XX  screening of preventives or remedies for e.g. atopic dermatitis.
XX
XX  PS Example 1; Page 46; 88pp; Japanese.
XX
XX  CC The present invention relates to a new DNA containing a fully defined 568
XX  CC base sequence given in the specification. The polynucleotides and
XX  CC proteins of the invention are useful in diagnosis and screening of
XX  CC preventives or remedies for atopic dermatitis. The invention can also be
XX  CC used in treating asthma, psoriasis, pancreatitis, rheumatoid arthritis,
XX  CC nephritis, arteriosclerosis, allergic diseases, viral diseases,
XX  CC inflammatory colitis, bronchitis and skin diseases. The present nucleic
XX  CC acid sequence represents a PCR primer used in the methods of the
XX
XX  Sequence 25 BP; 1 A; 5 C; 3 G; 16 T; 0 U; 0 Other;
XX
XX  Query Match          0.2%; Score 17.2; DB 1; Length 25;
XX  Best Local Similarity 86.4%; Pred. No. 1.1e+03;
XX  Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX  6459 GGATACCTTTTTCCTGCTTTG 6480.
XX  4 GGATCCTTTTTCCTTTTTCCTTG 25
XX

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PD 05-JUN-2003.
XX
XX 15-MAR-2002; 2002US-00098263.
XX
XX 16-MAR-2001; 2001US-0276759P.
XX
XX (AFY-) AFFYMETRIX INC.
XX
XX Miltmann MP;
XX
XX WPI; 2003-567953/53.
XX
XX New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
XX
PS Claim 1; SEQ ID NO 40510; 9pp; English.
XX
XX The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridization to a DNA library,
CC in analysis of genetic variation or in hybridization of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridizing at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridization. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in situ hybridization, in Southern, Northern or dot-
CC blot hybridization to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 25 BP; 7 A; 8 C; 4 G; 6 T; 0 U; 0 Other;
Query Match 0.2%; Score 17.2; DB 1; Length 25;
Best Local Similarity 86.4%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2146 CGTAGCTCTCCATCCAAATCTT 2167
DB 1 CGAGAGCTCTCATCAAGTCT 22
RESULT 1230
AC125232/c
ID AC125232 standard; DNA; 25 BP.
XX
XX AC125232;
XX
XX 13-OCT-2003 (first entry)
XX
XX Human microarray DNA oligonucleotide SEQ ID NO 25223.
XX
XX EST; 89; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.
XX
XX Homo sapiens.
XX
XX OS
XX US2003104410-A1.
XX
XX 05-JUN-2003.
XX

PF 15-MAR-2002; 2002US-00098263.
XX
XX 16-MAR-2001; 2001US-0276759P.
XX
XX (AFY-) AFFYMETRIX INC.
XX
XX Miltmann MP;
XX
XX WPI; 2003-567953/53.
XX
XX New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
XX
PS Claim 1; SEQ ID NO 25223; 9pp; English.
XX
XX The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridization to a DNA library,
CC in analysis of genetic variation or in hybridization of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridizing at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridization. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in situ hybridization, in Southern, Northern or dot-
CC blot hybridization to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 25 BP; 4 A; 5 C; 5 G; 11 T; 0 U; 0 Other;
Query Match 0.2%; Score 17.2; DB 1; Length 25;
Best Local Similarity 86.4%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3249 CCTTAATCAGAAAGGACTAGA 3270
DB 23 CCTAATTCAGAAAGGACTTAA 2
RESULT 1231
ACKR24476
ID ACKR24476 standard; DNA; 25 BP.
XX
XX ACKR24476;
XX
XX 14-OCT-2003 (first entry)
XX
XX Human microarray DNA oligonucleotide SEQ ID NO 124457.
XX
XX EST; 89; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.
XX
XX Homo sapiens.
XX
XX OS
XX US2003104410-A1.
XX
XX 05-JUN-2003.
XX
XX 15-MAR-2002; 2002US-00098263.
XX

PI Miltmann MP;
XX
XX WPI, 2003-567953/53.
XX
PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
PS Claim 1; SEQ ID NO 19557, 9pp; English.
XX
CC The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridization to a DNA library,
CC in analysis of genetic variation or in hybridization of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridizing at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridization. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying allelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in situ hybridization, in Southern, Northern or dot-
CC blot hybridization to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 25 BP; 0 A; 9 C; 5 G; 11 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 17.2; DB 1; Length 25;
Best Local Similarity 86.4%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 6821 TTTCTGGTTTGGCTTCTCC 6842
DB 1 TTTCTGGTTTGGCTTCTCC 22
XX
RESULT 1234
ACK06297/C
ID ACK06297 standard; DNA; 25 BP.
XX
AC ACK06297;
XX
DT 14-OCT-2003 (first entry)
XX
DE Human microarray DNA oligonucleotide SEQ ID NO 106278.
XX
KW EST; 8s; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; allelic marker; polymorphism; human;
KW cross-species comparison.
XX
OS Homo sapiens.
XX
PN US2003104410-A1.
XX
PD 05-JUN-2003.
XX
PF 15-MAR-2002; 2002US-00098263.
XX
PR 16-MAR-2001; 2001US-0276759P.
XX
PA (AFY-) AFFYMETRIX INC.
XX
PI Miltmann MP;
XX

DR WPI, 2003-567953/53.
XX
XX
PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
PS Claim 1; SEQ ID NO 106278, 9pp; English.
XX
CC The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridization to a DNA library,
CC in analysis of genetic variation or in hybridization of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridizing at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridization. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying allelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in situ hybridization, in Southern, Northern or dot-
CC blot hybridization to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 25 BP; 5 A; 6 C; 7 G; 7 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 17.2; DB 1; Length 25;
Best Local Similarity 86.4%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 5070 CTAAGAGAGTGATGCTAACAC 5091
DB 23 CTAAGAGAGTGATGCTAACAC 2
XX
RESULT 1235
AC151348
ID AC151348 standard; DNA; 25 BP.
XX
AC AC151348;
XX
DT 13-OCT-2003 (first entry)
XX
DE Human microarray DNA oligonucleotide SEQ ID NO 51339.
XX
KW EST; 8s; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; allelic marker; polymorphism; human;
KW cross-species comparison.
XX
OS Homo sapiens.
XX
PN US2003104410-A1.
XX
PD 05-JUN-2003.
XX
PF 15-MAR-2002; 2002US-00098263.
XX
PR 16-MAR-2001; 2001US-0276759P.
XX
PA (AFY-) AFFYMETRIX INC.
XX
PI Miltmann MP;
XX
DR WPI, 2003-567953/53.
XX

PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
PS Claim 1; SEQ ID NO 51339; 9pp; English.
XX
XX
CC The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying allelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 25 BP; 8 A; 8 C; 5 G; 4 T; 0 U; 0 Other;
Query Match 0.2%; Score 17.2; DB 1; Length 25;
Best Local Similarity 86.4%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2808 ACTGCTAGAGAAAGCTTCC 2829
DB 1 ACTGAGAGAGAAACCTCTCC 22
RESULT 1236
AC107619
ID AC107619 standard; DNA; 25 BP.
XX
XX AC107619;
XX
DT 13-OCT-2003 (first entry)
XX
DE Human microarray DNA oligonucleotide SEQ ID NO 7610.
XX
XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
XX genetic variation; allelic marker; polymorphism; human;
XX cross-species comparison.
XX
OS Homo sapiens.
XX
XX US2003104410-A1.
XX
XX 05-JUN-2003.
XX
XX 15-MAR-2002; 2002US-00098263.
XX
XX 16-MAR-2001; 2001US-0276759P.
XX
XX (AFFY-) AFFYMETRIX INC.
XX
XX Miltmann MP;
XX
XX MPI; 2003-567953/53.
XX
XX New array of nucleic acid probes, useful for in situ hybridization, in
XX Southern, Northern or dot-blot hybridization to identify or detect the

PT sequence or specific mutations of any gene.
PS Claim 1; SEQ ID NO 7610; 9pp; English.
XX
XX
CC The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying allelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 25 BP; 8 A; 8 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 0.2%; Score 17.2; DB 1; Length 25;
Best Local Similarity 86.4%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2390 GTAACATCCAGCTGGAGCCAC 2411
DB 3 GTAACATCCAACTCGGACCAC 24
RESULT 1237
AC155796/C
ID AC155796 standard; DNA; 25 BP.
XX
XX AC155796;
XX
DT 13-OCT-2003 (first entry)
XX
DE Human microarray DNA oligonucleotide SEQ ID NO 55787.
XX
XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
XX genetic variation; allelic marker; polymorphism; human;
XX cross-species comparison.
XX
OS Homo sapiens.
XX
XX US2003104410-A1.
XX
XX 05-JUN-2003.
XX
XX 15-MAR-2002; 2002US-00098263.
XX
XX 16-MAR-2001; 2001US-0276759P.
XX
XX (AFFY-) AFFYMETRIX INC.
XX
XX Miltmann MP;
XX
XX MPI; 2003-567953/53.
XX
XX New array of nucleic acid probes, useful for in situ hybridization, in
XX Southern, Northern or dot-blot hybridization to identify or detect the
XX sequence or specific mutations of any gene.

PS Claim 1; SEQ ID NO 55787; 9pp; English.
XX
XX The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying allelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in *in situ* hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 25 BP; 3 A; 9 C; 4 G; 9 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 17.2; DB 1; Length 25;
XX Best Local Similarity 86.4%; Pred. No. 1.1e+03;
XX Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 1410 GAAGATGACATGACGAGGTG 1431
DB 23 GAAGATGACATGACGAGGTG 2
XX
XX RESULT 1238
XX ADC05714
XX ID ADC05714 standard; DNA; 25 BP.
XX AC ADC05714;
XX XX 18-DEC-2003 (first entry)
XX DT 18-DEC-2003 (first entry)
XX DE Human Na/H exchanger-like protein 1 gene oligonucleotide #2161.
XX XX
XX KM ss; gene therapy; vaccine; sodium/hydrogen exchanger like protein;
XX NHEPL1; passive replacement therapy; vaccine; diagnosis.
XX XX
XX OS Homo sapiens.
XX PN EP1273660-A2.
XX PD 08-JAN-2003.
XX PF 25-JAN-2002; 2002EP-00001160.
XX PR 30-JAN-2001; 2001WO-US000666.
XX PR 23-MAY-2001; 2001US-00864761.
XX PR 21-DEC-2001; 2001US-0343331P.
XX PA (AEOM-) AEOMICA INC.
XX PI Gu Y;
XX DR WPI; 2003-302724/30.
XX PT New human sodium-hydrogen exchanger like protein 1 (NHEPL1), useful as a
XX PT passive replacement therapy or as a vaccine for treating or preventing
XX PT disorders associated with aberrant expression or activity of human
XX NHEPL1.
XX

PS Example 2; SEQ ID NO 2201; 468pp; English.
XX
XX The invention relates to a nucleic acid molecule which encodes a Na⁺/H⁺-
CC exchanger like protein (NHEPL1). The NHEPL1 nucleic acid molecule, NHEPL1
CC polypeptide, an antibody against the protein or its antigen-binding
CC fragment is useful in therapy. The NHEPL1 nucleic acid molecule, NHEPL1
CC polypeptide and an agonist are particularly useful for manufacturing a
CC medicament for treating or preventing a disorder associated with
CC decreased expression or activity of human NHEPL1. The antibody or its
CC antigen-binding fragment, and an antagonist, are useful for manufacturing
CC a medicament for treating or preventing a disorder associated with
CC increased expression or activity of human NHEPL1. The NHEPL1 nucleic acid
CC or protein is useful as passive replacement therapy, as a vaccine, or in
CC diagnostic methods. This sequence corresponds to a 256-mer
CC oligonucleotide spanning the sequence of the human NHEPL1 gene
CC (ADC03514).
XX
SQ Sequence 25 BP; 3 A; 3 C; 4 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 17.2; DB 1; Length 25;
XX Best Local Similarity 86.4%; Pred. No. 1.1e+03;
XX Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
QY 4583 TTTCCTTACTGTTTCATTTTT 4604
DB 1 TTTCCTTACTGTTTCATTTTT 22
XX
XX RESULT 1239
XX ADC05711
XX ID ADC05711 standard; DNA; 25 BP.
XX AC ADC05711;
XX XX 18-DEC-2003 (first entry)
XX DT 18-DEC-2003 (first entry)
XX DE Human Na/H exchanger-like protein 1 gene oligonucleotide #2158.
XX XX
XX KM ss; gene therapy; vaccine; sodium/hydrogen exchanger like protein;
XX NHEPL1; passive replacement therapy; vaccine; diagnosis.
XX XX
XX OS Homo sapiens.
XX PN EP1273660-A2.
XX PD 08-JAN-2003.
XX PF 25-JAN-2002; 2002EP-00001160.
XX PR 30-JAN-2001; 2001WO-US000666.
XX PR 23-MAY-2001; 2001US-00864761.
XX PR 21-DEC-2001; 2001US-0343331P.
XX PA (AEOM-) AEOMICA INC.
XX PI Gu Y;
XX DR WPI; 2003-302724/30.
XX PT New human sodium-hydrogen exchanger like protein 1 (NHEPL1), useful as a
XX PT passive replacement therapy or as a vaccine for treating or preventing
XX PT disorders associated with aberrant expression or activity of human
XX NHEPL1.
XX
PS Example 2; SEQ ID NO 2198; 468pp; English.
XX
XX The invention relates to a nucleic acid molecule which encodes a Na⁺/H⁺-
CC exchanger like protein (NHEPL1). The NHEPL1 nucleic acid molecule, NHEPL1
CC polypeptide, an antibody against the protein or its antigen-binding
CC fragment is useful in therapy. The NHEPL1 nucleic acid molecule, NHEPL1
CC polypeptide and an agonist are particularly useful for manufacturing a
CC medicament for treating or preventing a disorder associated with
CC decreased expression or activity of human NHEPL1. The antibody or its

CC antigen-binding fragment, and an antagonist, are useful for manufacturing
CC a medicament for treating or preventing a disorder associated with
CC increased expression or activity of human NHEPL1. The NHEPL1 nucleic acid
CC or protein is useful as passive replacement therapy, as a vaccine, or in
CC diagnostic methods. This sequence corresponds to a 256-mer
CC oligonucleotide spanning the sequence of the human NHEPL1 gene
CC (ADC03514).

XX Sequence 25 BP; 4 A; 4 C; 2 G; 15 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 17.2; DB 1; Length 25;

XX Best Local Similarity 86.4%; Pred. No. 1.1e+03;

XX Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4583 TTTCCTTGACTGTTCAATTTT 4604

DB 4 TTTCAGTCACTGTTATTTT 25

RESULT 1240

ADC05712
XX ADC05712 standard; DNA; 25 BP.

XX AC ADC05712;

XX DT 18-DEC-2003 (first entry)

XX DE Human Na/H exchanger-like protein 1 gene oligonucleotide #2159.

XX KW ss; gene therapy; vaccine; sodium/hydrogen exchanger like protein;

XX KM NHEPL1; passive replacement therapy; vaccine; diagnosis.

XX OS Homo sapiens.

XX PN EP1273660-A2.

XX PD 08-JAN-2003.

XX PF 25-JAN-2002; 2002EP-00001160.

XX PR 30-JAN-2001; 2001WO-US0000666.

XX PR 23-MAY-2001; 2001US-00864761.

XX PR 21-DEC-2001; 2001US-0343331P.

XX PA (AEOM-) AEOMICA INC.

XX PS Gu Y;

XX PI WPI; 2003-302724/30.

XX DR

XX PT New human sodium-hydrogen exchanger like protein 1 (NHEPL1), useful as a

XX PT passive replacement therapy or as a vaccine for treating or preventing

XX PT disorders associated with aberrant expression or activity of human

XX PT NHEPL1.

XX PS Example 2; SEQ ID NO 2199; 468bp; English.

XX CC The invention relates to a nucleic acid molecule which encodes a Na⁺/H⁺

XX CC exchanger like protein (NHEPL1). The NHEPL1 nucleic acid molecule, NHEPL1

XX CC polypeptide, an antibody against the protein or its antigen-binding

XX CC fragment is useful in therapy. The NHEPL1 nucleic acid molecule, NHEPL1

XX CC polypeptide and an agonist are particularly useful for manufacturing a

XX CC medicament for treating or preventing a disorder associated with

XX CC decreased expression or activity of human NHEPL1. The antibody or its

XX CC antigen-binding fragment, and an antagonist, are useful for manufacturing

XX CC a medicament for treating or preventing a disorder associated with

XX CC increased expression or activity of human NHEPL1. The NHEPL1 nucleic acid

XX CC or protein is useful as passive replacement therapy, as a vaccine, or in

XX CC diagnostic methods. This sequence corresponds to a 256-mer

XX CC oligonucleotide spanning the sequence of the human NHEPL1 gene

XX CC (ADC03514).

XX SQ Sequence 25 BP; 4 A; 4 C; 3 G; 14 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 17.2; DB 1; Length 25;

XX Best Local Similarity 86.4%; Pred. No. 1.1e+03;

XX Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4583 TTTCCTTGACTGTTCAATTTT 4604

DB 3 TTTCAGTCACTGTTATTTT 24

RESULT 1241

ADC05713
XX ADC05713 standard; DNA; 25 BP.

XX AC ADC05713;

XX DT 18-DEC-2003 (first entry)

XX DE Human Na/H exchanger-like protein 1 gene oligonucleotide #2160.

XX KW ss; gene therapy; vaccine; sodium/hydrogen exchanger like protein;

XX KM NHEPL1; passive replacement therapy; vaccine; diagnosis.

XX OS Homo sapiens.

XX PN EP1273660-A2.

XX PD 08-JAN-2003.

XX PF 25-JAN-2002; 2002EP-00001160.

XX PR 30-JAN-2001; 2001WO-US0000666.

XX PR 23-MAY-2001; 2001US-00864761.

XX PR 21-DEC-2001; 2001US-0343331P.

XX PA (AEOM-) AEOMICA INC.

XX PS Gu Y;

XX PI WPI; 2003-302724/30.

XX DR

XX PT New human sodium-hydrogen exchanger like protein 1 (NHEPL1), useful as a

XX PT passive replacement therapy or as a vaccine for treating or preventing

XX PT disorders associated with aberrant expression or activity of human

XX PT NHEPL1.

XX PS Example 2; SEQ ID NO 2200; 468bp; English.

XX CC The invention relates to a nucleic acid molecule which encodes a Na⁺/H⁺

XX CC exchanger like protein (NHEPL1). The NHEPL1 nucleic acid molecule, NHEPL1

XX CC polypeptide, an antibody against the protein or its antigen-binding

XX CC fragment is useful in therapy. The NHEPL1 nucleic acid molecule, NHEPL1

XX CC polypeptide and an agonist are particularly useful for manufacturing a

XX CC medicament for treating or preventing a disorder associated with

XX CC decreased expression or activity of human NHEPL1. The antibody or its

XX CC antigen-binding fragment, and an antagonist, are useful for manufacturing

XX CC a medicament for treating or preventing a disorder associated with

XX CC increased expression or activity of human NHEPL1. The NHEPL1 nucleic acid

XX CC or protein is useful as passive replacement therapy, as a vaccine, or in

XX CC diagnostic methods. This sequence corresponds to a 256-mer

XX CC oligonucleotide spanning the sequence of the human NHEPL1 gene

XX CC (ADC03514).

XX SQ Sequence 25 BP; 4 A; 3 C; 4 G; 14 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 17.2; DB 1; Length 25;

XX Best Local Similarity 86.4%; Pred. No. 1.1e+03;

XX Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4583 TTTCCTTGACTGTTCAATTTT 4604

DB 2 TTTCAGTCACTGTTATTTT 23

RESULT 1242
 ADE15502/c
 ID ADE15502 standard; DNA; 25 BP.
 XX
 AC ADE15502;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE T cell receptor variable region beta, RT PCR primer #14.
 XX
 KM Human; T cell receptor variable region beta; TCRV beta;
 KM cytokine response; CD4+ T cell; CD25+ T cell; autoimmune disease;
 KM multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
 KM type I diabetes; non-obese diabetes; myasthenia gravis; Grave's disease;
 KM Hashimoto's thyroiditis; PCR; primer; ss; RT-PCR;
 KM reverse transcriptase PCR.
 XX
 OS Homo sapiens.
 XX
 PN US2003190665-A1.
 XX
 PD 09-OCT-2003.
 XX
 PF 14-MAY-2003; 2003US-00438729.
 XX
 PR 12-MAY-2000; 2000US-0203984P.
 PR 10-MAY-2001; 2001US-00853830.
 XX
 PA (UNOR-) UNIV OREGON HEALTH SCI.
 PA (USCG) US DEPT VETERANS AFFAIRS.
 PI Vandenbark AA;
 XX
 DR WPI; 2003-864176/80.
 XX
 PT Identifying T cell receptor variable peptides useful for treating
 PT autoimmune disease including multiple sclerosis, rheumatoid arthritis,
 PT lupus, diabetes, myasthenia gravis, Grave's disease, Hashimoto's
 PT thyroiditis and psoriasis.
 XX
 PS Example 1; SEQ ID NO 165; 68pp; English.
 XX
 CC The invention relates to identifying a T cell receptor (TCR) variable (V)
 CC peptide useful as a therapeutic agent in a subject with a disorder,
 CC comprising screening TCR V beta and/or TCR V alpha peptides to select a
 CC TCR V peptide that produces altered expression of a cytokine in response
 CC to the peptide by T cells from the subject, and determining a regulatory
 CC activity of CD4+CD25+ T cells isolated from the subject in response to
 CC the peptide. Also included are monitoring the efficacy of a TCR V peptide
 CC for treatment of a subject (comprising exposing CD4+ T cells from the
 CC subject to the peptide and determining a T cell regulatory activity of
 CC CD4+CD25+ T cells isolated from the subject, where induction or regulatory
 CC activity indicates the efficacy of the peptide for treatment of the
 CC subject), selecting a therapy for a subject (comprising: identifying a
 CC TCR V gene expressed by target T cells in the subject by screening for
 CC expression of a TCR V gene by activated T cells from the subject and
 CC determining expression of a cytokine elicited in response to one or more
 CC TCR V peptides corresponding to the TCR V gene by T cells from the
 CC subject, thereby identifying a TCR V gene expressed by target T cells)
 CC and identifying a TCR V peptide corresponding to the TCR V gene that
 CC elicits T cell regulatory activity by a T cell isolated from the subject.
 CC The method is useful for identifying a T cell receptor (TCR) variable (V)
 CC peptide useful as a therapeutic agent in a subject with a disorder. The
 CC peptide is used to treat an autoimmune disease, particularly multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus, type I
 CC diabetes, non-obese diabetes, myasthenia gravis, Grave's disease,
 CC Hashimoto's thyroiditis or psoriasis. The present sequence is a TCR V
 CC beta reverse transcriptase (RT)-PCR primer used to measure TCR gene
 CC expression levels, in the method of the invention.
 XX
 SQ Sequence 25 BP; 9 A; 8 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.2; DB 1; Length 25;
 Best Local Similarity 86.4%; Pred. No. 1.1e+03;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 5155 GGGGAGTTCCTCGGACAGTG 5176
 |||||
 DB 22 GGGGACTTCCTCGTCAAGTG 1
 RESULT 1243
 AAV06174
 ID AAV06174 standard; DNA; 26 BP.
 XX
 AC AAV06174;
 XX
 DT 20-MAY-1998 (first entry)
 XX
 DE Primer used when one of the loci in the MAR set is D3S1539.
 XX
 KM Short tandem repeat loci; D3S1539; D4S2368; D5S818; D7S820; D9S930;
 KM D10S1239; D13S317; D14S118; D14S562; D14S490; D16S539; D16S753;
 KM D17S1298; D17S1299; D19S253; D20S481; D22S683; HUMCSF1PO; HUMTPOX;
 KM HUMTH01; HUMERSFPS; HUMF13A01; HUMBRX111; HUML1POL; HUMVFA31;
 KM Multiplex amplification reaction; MAR; allele; detection; genetic marker;
 KM linkage map; identification; disease gene; PCR primer; amplify; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9739138-A1.
 XX
 PD 23-OCT-1997.
 XX
 PF 15-APR-1997; 97WO-US006293.
 XX
 PR 15-APR-1996; 96US-00632575.
 XX
 PA (PROM-) PROMEGA CORP.
 XX
 PI Schumm JW, Micka KA, Rabbach DR;
 XX
 DR WPI; 1997-526472/48.
 XX
 PT Simultaneous amplification of short tandem repeats - used to provide
 PT genetic markers for linkage maps, for identifying and characterising
 PT diseases genes and for DNA typing.
 XX
 PS Claim 32; Page 71; 122pp; English.
 XX
 CC Primers AAV06168-228 are used in a novel method for simultaneously
 CC determining the alleles present in short tandem repeat loci from one or
 CC more DNA samples. The DNA sample to be analysed has a set of at least
 CC four loci which can be amplified together. The set is selected from loci
 CC consisting of D3S1539, D4S2368, D5S818, D7S820, D9S930, D10S1239,
 CC D13S317, D14S118, D14S562, D14S490, D16S539, D16S753, D17S1298,
 CC D17S1299, D19S253, D20S481, D22S683, HUMCSF1PO, HUMTPOX, HUMTH01,
 CC HUMERSFPS, HUMF13A01, HUMBRX111, HUML1POL and HUMVFA31. Alternatively,
 CC the DNA sample to be analysed has a set of three short tandem repeat loci
 CC which can be amplified together, where the set of loci is selected from
 CC the following group of sets: (1) D3S1539, D19S253, D13S317; (2) D10S1239,
 CC D9S930, D20S481; (3) D10S1239, D4S2368, D20S481; D10S1239, D9S930,
 CC D4S2368; (4) D16S539, D7S820, D13S317; and D10S1239, D9S930, D13S317. The
 CC loci are co-amplified in a multiplex amplification reaction (MAR), where
 CC the product of the reaction is a mixture of amplified alleles from each
 CC of the co-amplified loci in the set. The amplified alleles in the mixture
 CC are evaluated to determine the alleles present at each of the loci
 CC analysed in the set within the DNA sample. The methods are used for the
 CC detection of short tandem repeats as genetic markers for the development
 CC of linkage maps, the identification and characterisation of disease
 CC genes, and the simplification and precision of DNA typing
 XX
 SQ Sequence 26 BP; 4 A; 10 C; 1 G; 11 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.2; DB 1; Length 26;
 Best Local Similarity 86.4%; Pred. No. 1.2e+03;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5329 TCTCTTGGCTCACTCTCTCCA 5350
 |||||
 DB 1 TCTCTTCCATTACTCTCTCCA 22

RESULT 1244
 AAV32729
 ID AAV32729 standard; DNA; 26 BP.
 XX
 AC AAV32729;
 XX
 DT 12-OCT-1998 (first entry)
 XX
 DE Human GST-pi gene intron 5 forward primer P1.
 XX
 KW Glutathione S-transferase; GST-pi gene; hGSTP1; human; tumour; cancer;
 KW leukemia; lymphoma; melanoma; glioma; therapy; diagnosis; PCR; primer;
 KW ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN MO821359-A1.
 XX
 PD 22-MAY-1998.
 XX
 PF 12-NOV-1997; 97MO-US020987.
 XX
 PR 12-NOV-1996; 96US-00747536.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 PA (UMIS) UNIV MISSISSIPPI.
 XX
 PI Ali-Osman F, Lopez-Berestein G, Buolamwini JK, Antoun G, Lo H;
 PI Keller C, Akande O;
 PI
 DR MPI; 1998-297961/26.
 XX
 PT New human glutathione S-transferase variant(s) - used as targets for the
 PT diagnosis, prevention and treatment of tumours, including leukaemias,
 PT lymphomas and melanomas.
 XX
 PS Example 1; Page 92; 200pp; English.
 XX
 CC Forward primer P1 was used with reverse primer P2 (see AAV32729) in the
 CC PCR amplification of the intron 5 region of the human glutathione S-
 CC transferase GST-pi gene. PCR utilizing a series of primers (see AAV32721-
 CC 34) was used to isolate overlapping GST-pi DNA segments from SuperCos-GST
 CC -pi clone, a genomic library of human glioblastoma multiform cell line
 CC MGR-3 genomic DNA. The products were used to determine the full-length
 CC sequence (see AAV32717) of the GST-pi gene. Novel methods for the
 CC diagnosis, prevention and treatment of tumours, are based on the
 CC differential involvement of variant forms of GST-pi (see AAW49013-14)
 CC
 SQ Sequence 26 BP; 6 A; 6 C; 9 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.2; DB 1; Length 26;
 Best Local Similarity 86.4%; Pred. No. 1.2e+03;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2655 CCTGTGACCAAGAGCATGAC 2676
 |||||
 DB 5 CCTGTGACATGATGATGAC 26

RESULT 1245
 AAA47213
 ID AAA47213 standard; DNA; 26 BP.
 XX

AC AAA47213;
 XX
 DT 12-SEP-2000 (first entry)
 XX
 DE Primer 1 for human genomic DNA polymorphic STR locus D3S1539.

XX
 KW Primer: short tandem repeat; STR; multiplex amplification reaction;
 KW Combined DNA Index System; CODIS; paternity test; breeding; forensic;
 KW profile; D3S1539; ss.

XX
 OS Homo sapiens.
 OS
 PN MO200031306-A2.
 XX
 PD 02-JUN-2000.
 XX
 PF 24-NOV-1999; 99WO-US027876.
 XX
 PR 25-NOV-1998; 98US-00199542.

XX
 PA (PROM-) PROMEGA CORP.
 XX
 PI Schumm JW, Sprecher CJ;
 XX
 DR MPI; 2000-400106/34.

XX
 PT New method for analyzing e.g. human tissue DNA samples comprises co-
 PT amplification of at least 13 short tandem repeat loci, useful in e.g.
 PT determining the parentage of a child.
 XX
 PS Claim 9; Page 75; 90pp; English.

XX
 CC AAA47201-307 are oligonucleotide primers used to amplify human genomic
 CC DNA short tandem repeat (STR) loci. The claimed method comprises
 CC simultaneous determination of the alleles present in a set of loci from
 CC one or more DNA samples. In particular, at least thirteen loci of genomic
 CC DNA are amplified in a single multiplex reaction. At least one of the
 CC loci is preferably a STR locus with a repeat unit of five to seven bases
 CC or base pairs in length. Preferred loci are thirteen human STR loci
 CC chosen by the United States Federal Bureau of Investigation as core loci
 CC for use in the Combined DNA Index System (CODIS) database. These loci are
 CC D3S1538, HUMTH01, D21S11, D18S51, HUMWFA31, D8S1179, HUMTPOX, HUMFIBRA,
 CC D5S818, D13S317, D7S820, D16S539 and HUMCSFPO. Some sets of loci co-
 CC amplified include pentanucleotide STR loci G475, C221 and S159 (see
 CC AAA47308-10). Loci with intermediate length repeats can be amplified with
 CC minimal incidence of artifacts, e.g. due to repeat slippage. The method
 CC comprises: (a) obtaining at least one DNA sample; (b) selecting a set of
 CC loci of the DNA sample comprising at least 13 short tandem repeats loci
 CC which can be co-amplified; (c) co-amplifying the loci in the set in a
 CC multiplex amplification reaction, the product of the reaction comprising
 CC a mixture of amplified alleles from each of the co-amplified loci in the
 CC set; and (d) evaluating the amplified alleles to determine the alleles
 CC present at each loci. The method can be used to determine the parentage
 CC of children, confirm the lineage of animals and agricultural crops. It is
 CC also of use in determining a genetic profile of DNA in human tissue
 CC samples found at a crime scene
 XX
 SQ Sequence 26 BP; 4 A; 10 C; 1 G; 11 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.2; DB 1; Length 26;
 Best Local Similarity 86.4%; Pred. No. 1.2e+03;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5329 TCTCTTGGCTCACTCTCTCCA 5350
 |||||
 DB 1 TCTCTTCCATTACTCTCTCCA 22

RESULT 1246
 ABT15367
 ID ABT15367 standard; DNA; 26 BP.
 XX
 AC ABT15367;

```

XX 06-MAR-2003 (first entry)
DT
XX
DE Amplification refractory mutation system PCR primer #39.
XX
XX Detection; mutation; fungal cytochrome b gene; fungal resistance;
XX strobilurin; single nucleotide polymorphism; crop; cereal; fruit;
XX vegetable; pathogenic; fungicide; plant; ARMS; PCR; primer; ss.
XX
XX Uncinula necator.
XX
XX WO200281742-A2.
XX
XX 17-OCT-2002.
XX
XX 25-MAR-2002; 2002MO-GB001411.
XX
XX 02-APR-2001; 2001GB-0008227.
XX
XX 20-SEP-2001; 2001GB-00022697.
XX
XX (SYGN ) SYNGENTA LTD.
XX
XX Burridge JM, Cleere SM, Stranger CP, Windaes JD;
XX WPI; 2003-046869/04.
XX
XX Detecting mutations in fungal cytochrome b gene that leads to fungal
XX resistance to strobilurin analog, by using single nucleotide polymorphism
XX detection techniques, preferably allele specific amplification technique.
XX
XX Disclosure; Page 51; 165pp; English.
XX
XX The invention relates to a novel method for detecting mutation(s) in a
XX fungal cytochrome b gene resulting in amino acid replacement at position
XX corresponding to Saccharomyces cerevisiae cytochrome b residue 129 in the
XX encoded protein. This mutation leads to fungal resistance to strobilurin
XX analogues or compounds in the same cross resistance group using a single
XX nucleotide polymorphism detection technique. The novel method is
XX particularly suitable for monitoring fungal resistance to a strobilurin
XX analogue in crops such as cereals, fruit and vegetables such as
XX sunflower, tobacco, cotton, maize, wheat, barley, rice, apple, banana,
XX potatoes, carrot, onion and turf. An allele specific oligo probe capable
XX of detecting a mutant type fungal cytochrome b polymorphism is useful for
XX detecting plant pathogenic fungal resistance to a fungicide. This
XX CC polymucleotide sequence represents a PCR primer of the amplification
XX refractory mutation system (ARMS) relating to the method of the invention
XX
XX Sequence 26 BP; 8 A; 4 C; 5 G; 9 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 17.2; DB 1; Length 26;
Best Local Similarity 86.4%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4953 TTTTCTGCTGCTGCTACGATG 4974
DB 4 TTTTATGATGCTACGATG 25

```

```

XX 16-APR-2003.
PD
XX
XX 10-OCT-2001; 2001EP-00123379.
XX
XX 10-OCT-2001; 2001EP-00123379.
XX
XX (KING-) KING CAR FOOD IND CO LTD.
XX
XX Lin C, Lin R, You C, Huang H, Lee B, Lee H, Lin Y, Pan C;
XX Hsu H, Shih C, Yen C, Kao Y, Pan C, Chan P;
XX WPI; 2003-432398/41.
XX
XX Detector for identifying human papilloma virus subtypes, comprises
XX PT carrier having two parts carrying first and second oligonucleotides that
XX PT respectively hybridize with DNA contained in first and second subtypes of
XX PT the virus.
XX
XX Claim 4; SEQ ID NO 186; 221bp; English.
XX
XX The invention comprises oligonucleotides for detecting and identifying
XX CC subtypes of human papilloma virus (HPV) contained in a sample. The
XX CC oligonucleotides of the invention are useful for simultaneously detecting
XX CC and identifying subtypes of HPVs. The present DNA sequence represents an
XX CC HPV detection oligonucleotide of the invention.
XX
XX Sequence 26 BP; 4 A; 10 C; 4 G; 8 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 17.2; DB 1; Length 26;
Best Local Similarity 86.4%; Pred. No. 1.2e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3378 GTTGCTCTCTCCCGCAGTGGCA 3399
DB 2 GAGCTCTCTCCACCATGTGCA 23

```

```

RESULT 1248
ABL56895/C
ID ABL56895 standard; DNA; 30 BP.
XX
XX ABL56895;
XX
XX 26-JUL-2002 (first entry)
XX
XX Synthetic deoxyribonucleotide poly h.
XX
XX Concentration; quantification; mutation detection; polymorphic;
XX KW polymerase chain reaction; PCR; ss.
XX
XX OS Synthetic.
XX
XX EP1046717-A2.
XX
XX 25-OCT-2000.
XX
XX 20-APR-2000; 2000EP-00108643.
XX
XX 20-APR-1999; 99JP-00111601.
XX
XX (NIBI-) JAPAN BIOINDUSTRY ASSOC.
XX PA (AGENCY OF IND SCI & TECHNOLOGY.
XX (KANK-) KANKYO ENG CO LTD.
XX
XX Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;
XX PI Koyama O, Furusho K;
XX
XX WPI; 2000-657765/64.
XX
XX Determining the concentration of a target nucleic acid, useful e.g. for
XX PT detecting genetic mutations, comprises using a fluorescently labeled
XX PT probe in which emission is reduced by binding to the target nucleic acid.

```

XX Example 5; Page 21; 55pp; English.

PS The invention relates to the determination of the concentration of a

CC nucleic acid target, using a fluorescently labeled probe which produces

CC reduced fluorescence emission when hybridised to the target nucleic acid.

CC The method comprises measuring the reduction in emission caused by

CC hybridisation. The new method is particularly used to quantify target

CC nucleic acids by a real-time polymerase chain reaction, e.g. for

CC quantifying microbial cells in co-cultures or symbiotic systems, for

CC detecting gene mutations or polymorphisms, and for analysing melting

CC curves of target nucleic acids to determine a Tm value. Methods of the

CC invention allow target nucleic acids to be quantified quickly, easily and

CC accurately. Particularly there is no need to remove unbound probe, and no

CC materials are introduced that inhibit amplification by Taq polymerase (so

CC conventional PCR conditions can be used). The specificity of PCR is kept

CC high (amplification of primer dimers is delayed), and the limit of

CC quantitation is reduced. Complex probes are not needed, and amplification

CC can be monitored in real time. The working graph for data analysis

CC (automatically generated by a computer) has a higher correlation

CC coefficient than conventional graphs so more accurate quantitation is

CC possible. The current sequence represents a synthetic

CC deoxyribooligonucleotide that was used for investigating the base

CC selectivity of a target nucleic acid

XX

SO Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.2; DB 1; Length 30;

Best Local Similarity 73.3%; Pred. No. 1.4e+03;

Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 4018 AGAAAAAGAGAAACCAAAATGTTATT 4047

DB 30 AAAAAAAAAAGAAAAAAATATATAT 1

RESULT 1249

ABLS6897/c

ID ABL56897 standard; DNA; 30 BP.

XX

AC ABL56897;

XX

DT 26-JUL-2002 (first entry)

XX

DE Synthetic deoxyribooligonucleotide poly j.

XX

KW Concentration; quantification; mutation detection; polymorphic;

XX

KM polymerase chain reaction; PCR; ss.

XX

OS Synthetic.

XX

PN EP1046717-A2.

XX

PD 25-OCT-2000.

XX

PF 20-APR-2000; 2000EP-00108643.

XX

PR 20-APR-1999; 99JP-00111601.

XX

PA (NIBI-) JAPAN BIOINDUSTRY ASSOC.

XX

PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.

XX

PA (KANK-) KANKYO ENG CO LTD.

XX

PI Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;

XX

PI Koyama O, Furusho K;

XX

DR WPI; 2000-657765/64.

XX

PT Determining the concentration of a target nucleic acid, useful e.g. for

XX

PT detecting genetic mutations, comprises using a fluorescently labeled

XX

PT probe in which emission is reduced by binding to the target nucleic acid.

XX

PS Example 5; Page 21; 55pp; English.

XX The invention relates to the determination of the concentration of a

CC nucleic acid target, using a fluorescently labeled probe which produces

CC reduced fluorescence emission when hybridised to the target nucleic acid.

CC The method comprises measuring the reduction in emission caused by

CC hybridisation. The new method is particularly used to quantify target

CC nucleic acids by a real-time polymerase chain reaction, e.g. for

CC quantifying microbial cells in co-cultures or symbiotic systems, for

CC detecting gene mutations or polymorphisms, and for analysing melting

CC curves of target nucleic acids to determine a Tm value. Methods of the

CC invention allow target nucleic acids to be quantified quickly, easily and

CC accurately. Particularly there is no need to remove unbound probe, and no

CC materials are introduced that inhibit amplification by Taq polymerase (so

CC conventional PCR conditions can be used). The specificity of PCR is kept

CC high (amplification of primer dimers is delayed), and the limit of

CC quantitation is reduced. Complex probes are not needed, and amplification

CC can be monitored in real time. The working graph for data analysis

CC (automatically generated by a computer) has a higher correlation

CC coefficient than conventional graphs so more accurate quantitation is

CC possible. The current sequence represents a synthetic

CC deoxyribooligonucleotide that was used for investigating the base

CC selectivity of a target nucleic acid

XX

SO Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 0.2%; Score 17.2; DB 1; Length 30;

Best Local Similarity 73.3%; Pred. No. 1.4e+03;

Matches 22; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 4018 AGAAAAAGAGAAACCAAAATGTTATT 4047

DB 30 AAAAAAAAAAGAAAAAAATATATAT 1

RESULT 1250

ABA97619/c

ID ABA97619 standard; DNA; 30 BP.

XX

AC ABA97619;

XX

DT 11-APR-2002 (first entry)

XX

DE Poly h nucleotide sequence.

XX

KW ss; fluorochrome; nucleic acid probe; fluorescence.

XX

KM Unidentified.

XX

PN JP2001286300-A.

XX

PD 16-OCT-2001.

XX

PF 20-APR-2000; 2000JP-00120097.

XX

PR 20-APR-1999; 99JP-00111601.

XX

PR 24-AUG-1999; 99JP-00236666.

XX

PR 30-AUG-1999; 99JP-00242693.

XX

PR 01-FEB-2000; 2000JP-00028896.

XX

PA (BIOI-) BIOINDUSTRY KYOKAI SH.

XX

PA (KANK-) KANKYO ENG KK.

XX

PA (KEIZ-) KEIZAI SANGYOSHIO SANGYO GIUTTSU SOGO KEN.

XX

DR WPI; 2002-134193/18.

XX

PT Measurement of nucleic acids, using a nucleic acid probe and analysis of

XX

PT the obtained data.

XX

PS Example 5; Page 17; 34pp; Japanese.

XX

PT This invention relates to a method for measuring nucleic acids using a

XX

CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe

CC decreases the fluorescence of the fluorochrome when hybridised with a

KM Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
 KM KDR; hamsterhead ribozyme; hairpin ribozyme; cleavage;
 KM tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 KM fms-like tyrosine kinase 1; kinase insert domain containing receptor;
 KM foetal liver kinase 1; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9715662-A2.
 XX
 PD 01-MAY-1997.
 XX
 PF 25-OCT-1996; 96WO-US017480.
 XX
 PR 26-OCT-1995; 95US-0005974P.
 PR 11-JAN-1996; 96US-00584040.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (CHIR) CHIRON CORP.
 XX
 PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
 DR WPI, 1997-259017/23.
 XX
 PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
 PT rheumatoid arthritis, etc., in a human patient.
 XX
 PS Claim 4; Page 79; 218pp; English.
 XX
 CC The present invention describes nucleic acid molecules which modulate the
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more
 CC receptors of vascular endothelial growth factor (VEGF). A patient
 CC (preferably human) having a condition associated with the level of the
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
 CC treated by administering the nucleic acid molecule or the expression
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples
 CC of nucleic acid molecules from the present invention
 XX
 SQ Sequence 17 BP; 0 A; 1 C; 0 G; 0 T; 16 U; 0 Other;
 Query Match 0.2%; Score 17; DB 1; Length 17;
 Best Local Similarity 5.9%; Pred. No. 7.1e+02;
 Matches 1; Conservative 16; Mismatches 0; Indels 0; Gaps 0;
 Oy 4463 CTTTCTTTCTTTCTTTCTTT 4479
 Db 1 CUUUUUUUUUUUUUUU 17
 RESULT 1256
 AAX69799
 ID AAX69799 standard; RNA; 17 BP.
 XX
 AC AAX69799;
 XX
 DT 28-JUL-1999 (first entry)
 XX
 DE Human flt1 VEGF receptor hamsterhead ribozyme substrate #1094.
 XX
 KM Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
 KM KDR; hamsterhead ribozyme; hairpin ribozyme; cleavage;
 KM tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 KM fms-like tyrosine kinase 1; kinase insert domain containing receptor;
 KM foetal liver kinase 1; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9715662-A2.
 XX
 PD 01-MAY-1997.

XX
 PF 25-OCT-1996; 96WO-US017480.
 XX
 PR 26-OCT-1995; 95US-0005974P.
 PR 11-JAN-1996; 96US-00584040.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (CHIR) CHIRON CORP.
 XX
 PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
 DR WPI, 1997-259017/23.
 XX
 PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
 PT rheumatoid arthritis, etc., in a human patient.
 XX
 PS Claim 4; Page 79; 218pp; English.
 XX
 CC The present invention describes nucleic acid molecules which modulate the
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more
 CC receptors of vascular endothelial growth factor (VEGF). A patient
 CC (preferably human) having a condition associated with the level of the
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
 CC treated by administering the nucleic acid molecule or the expression
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples
 CC of nucleic acid molecules from the present invention
 XX
 SQ Sequence 17 BP; 1 A; 1 C; 0 G; 0 T; 15 U; 0 Other;
 Query Match 0.2%; Score 17; DB 1; Length 17;
 Best Local Similarity 11.8%; Pred. No. 7.1e+02;
 Matches 2; Conservative 15; Mismatches 0; Indels 0; Gaps 0;
 Oy 4462 ACTTTTCTTTCTTTCTTTCTTT 4478
 Db 1 ACUUUUUUUUUUUUUU 17
 RESULT 1257
 AAA25450
 ID AAA25450 standard; DNA; 17 BP.
 XX
 AC AAA25450;
 XX
 DT 19-JUL-2000 (first entry)
 XX
 DE Oestrogen receptor hamsterhead ribozyme target sequence SEQ ID NO:1948.
 XX
 KM Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
 KM hamsterhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
 KM gene expression modification; cancer; phosphothioate; endonuclease;
 KM anticancer; breast cancer; endometrium cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9954459-A2.
 XX
 PD 28-OCT-1999.
 XX
 PF 19-APR-1999; 99WO-US008547.
 XX
 PR 20-APR-1998; 98US-0082404P.
 PR 23-JUN-1998; 98US-00103636.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Thompson JD, Belgelman L, Mcswiggen JH, Karpetsky A, Bellon L;
 PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeblerli P;
 PI Matulic-Adamic J;
 XX


```

XX PS Example 12; Page 34; 49pp; English.
CC The present sequence is that of a phosphorothioate oligonucleotide
CC containing 20 T nucleobases, each having a 2'-methoxyethoxy group on its
CC 5' riboseyl sugar moiety. It is an example of an oligomeric compound
CC produced according to the methods of the invention. The invention
CC provides compounds and methods for the preparation of mixed backbone
CC oligomeric, or chimeric, compounds having phosphodiester internucleoside
CC linkages in addition to phosphorothioate and/or phosphoramidate
CC internucleoside linkages. The methods also include incorporation of
CC boranophosphate internucleoside linkages. The methods utilize H-
CC phosphonate intermediates that are coupled together forming contiguous
CC regions of 1 or more H-phosphonate internucleoside linkages. Each
CC contiguous region is subsequently oxidized to phosphodiester,
CC phosphorothioate, phosphoramidate or boranophosphate internucleoside
CC linkages prior to further elongation. Mixed backbone oligomeric compounds
CC are prepared in this manner by oxidizing adjacent regions with different
CC reagents. Oligomeric compounds of the invention are prepared using novel
CC oxidation steps that oxidize a region of 1 or more H-phosphonate
CC internucleoside linkages without degrading existing linkages that have
CC been previously oxidized. The oligonucleotides obtained are useful as
CC primers in PCR, probes, linkers, gene fragments and for other diagnostic
CC tests on e.g. biological tissue, fluid, cells etc., as research reagents,
CC and as antiviral agents
CC
XX SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 17; DB 1; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 7.1e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 4464 TTTT TTTT TTTT TTTT TTTT 4480
XX |||||
XX 1 TTTT TTTT TTTT TTTT 17
XX
XX RESULT 1262
XX ID ADB04271 standard; DNA; 17 BP.
XX AC ADB04271;
XX DT 20-NOV-2003 (first entry)
XX DE Human MD27 scanning oligonucleotide SEQ ID 5257.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX
XX Homo sapiens.
XX OS
XX PN EP1281758-A2.
XX PD 05-FEB-2003.
XX PF 30-JUL-2002; 2002EP-00016874.
XX PR 02-AUG-2001; 2001US-00922181.
XX PA (AEOM-) AEOMICA INC.
XX PI Shannon M, Gu Y, Nguyen C;
XX PS MPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27 or MD212, e.g. cancer.
XX

```

```

PS Example 8; SEQ ID NO 5257; 103pp; English.
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
XX
XX SQ Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 17; DB 1; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 7.1e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 4463 CTTT TTTT TTTT TTTT TTTT 4479
XX |||||
XX 1 CTTT TTTT TTTT TTTT 17
XX
XX RESULT 1263
XX ID ADB04272 standard; DNA; 17 BP.
XX AC ADB04272;
XX DT 20-NOV-2003 (first entry)
XX DE Human MD27 scanning oligonucleotide SEQ ID 5258.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX
XX Homo sapiens.
XX OS
XX PN EP1281758-A2.
XX PD 05-FEB-2003.
XX PF 30-JUL-2002; 2002EP-00016874.
XX PR 02-AUG-2001; 2001US-00922181.
XX PA (AEOM-) AEOMICA INC.
XX PI Shannon M, Gu Y, Nguyen C;
XX PS MPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 5258; 103pp; English.
XX
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX

```

CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.

CC Sequence 17 BP: 0 A; 0 C; 1 G; 16 T; 0 U; 0 Other;

Query Match 0.2%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4468 TTTT TTTT TTTT TTTT TTTT G 4484
DB 1 TTTT TTTT TTTT TTTT TTTT G 17

RESULT 1264

AAD56441
ID AAD56441 standard; DNA; 17 BP.

AC AAD56441;
DT 07-AUG-2003 (first entry)

DE Antisense oligo #2, to elicit RNase H degradation of target RNA.

KM Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW antisense; ss.

XX Unidentified.

OS
FH Key Location/Qualifiers
FT misc_feature 9..10

FT /tag= a
FT /note= "Bases 9 and 10 are linked by a butanediol linker
FT which is represented as B in page 49 and X in page 59,
FT Fig 9 and 10 of the specification"

PN WO2003037909-A1.

PD 08-MAY-2003.

PF 29-OCT-2002; 2002WO-CA001628.

PR 29-OCT-2001; 2001US-0330719P.

PA (UWMC-) UNIV MCGILL.

PI Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;

DR WPI; 2003-421516/39.

PT Novel acyclic linker-containing oligonucleotide useful for preventing or
PT decreasing translation, reverse transcription and/or replication of a
PT target RNA in a system, comprises a modified deoxyribonucleotide.

PS Example 2; Page 90; 104pp; English.

CC The invention relates to an acyclic linker-containing oligonucleotide
CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC the invention are useful for preventing or decreasing translation,
CC reverse transcription and/or replication of a target RNA in a system.
CC They are useful for selectively preventing gene expression in a sequence-
CC specific manner, for hybridising to complementary RNA such as cellular
CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC RNA. They are also useful therapeutically in formulations or medicaments
CC to prevent or treat a disease characterised by the expression of a
CC particular target RNA. The invention is used in gene therapy. The present

CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC H degradation of target RNA. This sequence is used in the exemplification
CC of the invention

CC Sequence 17 BP: 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 0.2%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT T 4480
DB 1 TTTT TTTT TTTT TTTT TTTT T 17

RESULT 1265

AAD56448
ID AAD56448 standard; DNA; 17 BP.

AC AAD56448;
DT 07-AUG-2003 (first entry)

DE 2'-F-ANA antisense oligo #3, to elicit RNase H degradation of target RNA.

KM Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW antisense; ss.

XX Unidentified.

OS
FH Key Location/Qualifiers
FT modified_base 1..17

FT /tag= a
FT /mod_base= OTHER
FT misc_feature 9..10

FT /tag= b
FT /note= "Bases 9 and 10 are linked by a butanediol linker
FT which is represented as B in page 49 and Fig 5 and as X
FT in page 52, 55 and Fig 6 of the specification"

PN WO2003037909-A1.

PD 08-MAY-2003.

PF 29-OCT-2002; 2002WO-CA001628.

PR 29-OCT-2001; 2001US-0330719P.

PA (UWMC-) UNIV MCGILL.

PI Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;

DR WPI; 2003-421516/39.

PT Novel acyclic linker-containing oligonucleotide useful for preventing or
PT decreasing translation, reverse transcription and/or replication of a
PT target RNA in a system, comprises a modified deoxyribonucleotide.

PS Example 2; Fig 5; 104pp; English.

CC The invention relates to an acyclic linker-containing oligonucleotide
CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC the invention are useful for preventing or decreasing translation,
CC reverse transcription and/or replication of a target RNA in a system.
CC They are useful for selectively preventing gene expression in a sequence-
CC specific manner, for hybridising to complementary RNA such as cellular
CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC RNA. They are also useful therapeutically in formulations or medicaments
CC to prevent or treat a disease characterised by the expression of a
CC particular target RNA. The invention is used in gene therapy. The present
CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC H degradation of target RNA. This sequence is used in the exemplification

```
CC of the invention
XX
SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
Query Match 0.2%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4480
DB 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 1266
AADS6449
ID AADS6449 standard; DNA; 17 BP.
XX
AC AADS6449;
XX
DT 07-AUG-2003 (first entry)
XX
DE 2'-F-ANA antisense oligo #4, to elicit RNase H degradation of target RNA.
XX
KM Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
XX antisense; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 1..17
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluoroarabinothymidine"
FT misc_feature 12..13
FT /*tag= b
FT /note= "bases 12 and 13 are linked by a butanediol linker
FT which is represented as B in page 49 and Fig 5 and as X
FT in page 55 and Fig 6 of the specification"
XX
PN WO2003037909-A1.
XX
PD 08-MAY-2003.
XX
PF 29-OCT-2002; 2002WO-CA001628.
XX
PR 29-OCT-2001; 2001US-0330719P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;
XX WPI; 2003-421516/39.
XX
PT Novel acyclic linker-containing oligonucleotide useful for preventing or
PT decreasing translation, reverse transcription and/or replication of a
PT target RNA in a system, comprises a modified deoxyribonucleotide.
XX
PS Example 2; Fig 5; 104pp; English.
XX
CC The invention relates to an acyclic linker-containing oligonucleotide
CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC the invention are useful for preventing or decreasing translation,
CC reverse transcription and/or replication of a target RNA in a system.
CC They are useful for selectively preventing gene expression in a sequence-
CC specific manner, for hybridizing to complementary RNA such as cellular
CC mRNA or viral RNA, to hybridize to and induce cleavage of complementary
CC RNA. They are also useful therapeutically in formulations or medicaments
CC to prevent or treat a disease characterised by the expression of a
CC particular target RNA. The invention is used in gene therapy. The present
CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC H degradation of target RNA. This sequence is used in the exemplification
CC of the invention
XX
```

```
SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
Query Match 0.2%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4480
DB 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 1267
AADS6447
ID AADS6447 standard; DNA; 17 BP.
XX
AC AADS6447;
XX
DT 07-AUG-2003 (first entry)
XX
DE 2'-F-ANA antisense oligo #2, to elicit RNase H degradation of target RNA.
XX
KM Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
XX antisense; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 1..17
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-deoxy-2'-fluoroarabinothymidine"
FT misc_feature 4..5
FT /*tag= b
FT /note= "bases 4 and 5 are linked by a butanediol linker
FT which is represented as B in page 49 and Fig 5 and as X
FT in page 55 and Fig 6 of the specification"
XX
PN WO2003037909-A1.
XX
PD 08-MAY-2003.
XX
PF 29-OCT-2002; 2002WO-CA001628.
XX
PR 29-OCT-2001; 2001US-0330719P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;
XX WPI; 2003-421516/39.
XX
PT Novel acyclic linker-containing oligonucleotide useful for preventing or
PT decreasing translation, reverse transcription and/or replication of a
PT target RNA in a system, comprises a modified deoxyribonucleotide.
XX
PS Example 2; Fig 5; 104pp; English.
XX
CC The invention relates to an acyclic linker-containing oligonucleotide
CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC the invention are useful for preventing or decreasing translation,
CC reverse transcription and/or replication of a target RNA in a system.
CC They are useful for selectively preventing gene expression in a sequence-
CC specific manner, for hybridizing to complementary RNA such as cellular
CC mRNA or viral RNA, to hybridize to and induce cleavage of complementary
CC RNA. They are also useful therapeutically in formulations or medicaments
CC to prevent or treat a disease characterised by the expression of a
CC particular target RNA. The invention is used in gene therapy. The present
CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC H degradation of target RNA. This sequence is used in the exemplification
CC of the invention
XX
SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
```



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DT 27-MAR-1998 (first entry)
XX Anchored poly(T) oligonucleotide polyT-AnchA.
DE Flavonoid 3'-hydroxylase; pigmentation; flower colour; transgenic plant;
XX snapdragon; primer; ss.
XX Synthetic.
OS
XX WO9732023-A1.
XX
XX 04-SEP-1997.
XX
XX 28-FEB-1997; 97WO-AU000124.
XX
XX 01-MAR-1996; 96AU-00008386.
XX
XX (FLOR-) FLORIGENE LTD.
XX
XX Brugliera F, Holton TA, Michael MZ;
XX
XX WPI; 1997-448691/41.
XX
XX Novel flavonoid 3'-hydroxylase(s) from flowering plants - and
XX corresponding DNA, used in the manipulation of pigmentation in plants.
XX
XX Example 15; Page 59; 234pp; English.
XX
XX Anchored poly(T) oligonucleotides polyT-anchA (AAT94667), polyT-anchC
XX (AAT94668) and polyT-anchG (AAT94669) are complementary to the upstream
XX region of a polyadenylation sequence. They were used to prime cDNA
XX synthesis from snapdragon (Antirrhinum majus) petal and leaf RNA, and
XX were also utilised in the PCR amplification of plant cytochrome P450
XX sequences (see also AAT94670-73). A cDNA clone (see AAT94657) encoding
XX flavonoid 3'-hydroxylase (see AAW35704) was isolated using a differential
XX display approach. This can be used to manipulate the pigmentation of
XX transgenic plants
XX
XX Sequence 18 BP; 1 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4480
DB 1 TTTT TTTT TTTT TTTT TTTT 17
RESULT 1271
AAT94668
ID AAT94668 standard; DNA; 18 BP.
XX
XX AAT94668;
AC
XX
XX 27-MAR-1998 (first entry)
XX
XX Anchored poly(T) oligonucleotide polyT-AnchC.
XX
XX Flavonoid 3'-hydroxylase; pigmentation; flower colour; transgenic plant;
XX snapdragon; primer; ss.
XX
XX Synthetic.
XX
XX WO9732023-A1.
XX
XX 04-SEP-1997.
XX
XX 28-FEB-1997; 97WO-AU000124.
XX
XX 01-MAR-1996; 96AU-00008386.
XX
XX (FLOR-) FLORIGENE LTD.
XX
XX
XX

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XX
XX Brugliera F, Holton TA, Michael MZ;
XX
XX WPI; 1997-448691/41.
XX
XX Novel flavonoid 3'-hydroxylase(s) from flowering plants - and
XX corresponding DNA, used in the manipulation of pigmentation in plants.
XX
XX Example 15; Page 59; 234pp; English.
XX
XX Anchored poly(T) oligonucleotides polyT-anchA (AAT94667), polyT-anchC
XX (AAT94668) and polyT-anchG (AAT94669) are complementary to the upstream
XX region of a polyadenylation sequence. They were used to prime cDNA
XX synthesis from snapdragon (Antirrhinum majus) petal and leaf RNA, and
XX were also utilised in the PCR amplification of plant cytochrome P450
XX sequences (see also AAT94670-73). A cDNA clone (see AAT94657) encoding
XX flavonoid 3'-hydroxylase (see AAW35704) was isolated using a differential
XX display approach. This can be used to manipulate the pigmentation of
XX transgenic plants
XX
XX Sequence 18 BP; 0 A; 1 C; 0 G; 17 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4480
DB 1 TTTT TTTT TTTT TTTT TTTT 17
RESULT 1272
AAV54168
ID AAV54168 standard; cDNA; 18 BP.
XX
XX AAV54168;
AC
XX
XX 21-DEC-1998 (first entry)
XX
XX Nucleotide sequence PCR primer 5.
XX
XX PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
XX immunohistological staining.
XX
XX Synthetic.
XX
XX WO9839437-A1.
XX
XX 11-SEP-1998.
XX
XX 05-MAR-1996; 98WO-JP000905.
XX
XX 05-MAR-1997; 97JP-00050302.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX Sakaki Y;
XX
XX WPI; 1998-495844/42.
XX
XX Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
XX treating diseases associated with apoptosis.
XX
XX Example 1; Page 48; 70pp; Japanese.
XX
XX This is the nucleotide sequence of a PCR primer used in the method of the
XX invention, involving the use of novel apoptosis-related DNAs and
XX proteins. The inventions can be used as diagnostic reagents for apoptosis
XX e.g. (monoclonal) antibodies for the protein, as a reagent in
XX immunohistological staining, as apoptosis inhibitors. It can also be used
XX for treatment of apoptosis-related diseases
XX
XX Sequence 18 BP; 0 A; 0 C; 2 G; 16 T; 0 U; 0 Other;
SQ

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XX 16-NOV-2000 (first entry)
DT
DE Human adult ovary cDNA fragment A02_11 #2.
XX
XX Secreted protein; cytosolic; immunostimulatory; antimicrobial;
XX antiviral; immunosuppressive; antiinflammatory; vulnerary; cytokine;
XX cell proliferation; differentiation; regulator; treatment; tumor;
XX autoimmune disease; inflammatory disorder; wound; microbial infection;
XX viral disease; graft versus host reaction suppression; ss.
XX
XX Homo sapiens.
XX
XX WO200037630-A1.
XX
XX 29-JUN-2000.
XX
XX 22-DEC-1999; 99WO-US031005.
XX
XX 23-DEC-1998; 98US-00220876.
XX
XX (GEMV ) GENETICS INST INC.
XX
XX Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;
XX Merberg D, Treacy M, Bowman MR;
XX WPI; 2000-442661/38.
XX
XX P-PSDB; AAB10274.
XX
XX Secreted human proteins AS296-11 and AS34-11, useful for treating tumors,
XX autoimmune diseases, inflammatory disorders, wounds, microbial infections
XX and viral diseases.
XX
XX Disclosure; Page 269; 293pp; English.
XX
XX This invention describes novel secreted human proteins (I) which have
XX immunosuppressive, antiinflammatory and vulnerary activity and which act
XX as cytokine, cell proliferation or differentiation regulators. (I) is
XX useful for treating tumors, autoimmune diseases, inflammatory disorders,
XX wounds, microbial infections and viral diseases. (I) is also useful for
XX suppressing graft versus host reaction. AAA40490-A40580 represent cDNA
XX fragments that encode the secreted proteins AAB10226-B10288 described in
XX the method of the invention
XX
XX Sequence 18 BP; 17 A; 0 C; 1 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 17; DB 1; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 7.7e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4464 TTTT TTTT TTTT TTTT TTTT 4480
XX 18 TTTT TTTT TTTT TTTT TTTT 2
XX
XX RESULT 1276
XX AA290644
XX ID AA290644 standard; DNA; 18 BP.
XX
XX AA290644;
XX
XX 13-JUN-2000 (first entry)
XX
XX Human adipose tissue gene amplifying primer #5.
XX
XX Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
XX arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX JP2000037190-A.
XX

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PD 08-FEB-2000.
XX
XX 23-JUL-1998; 98JP-00225228.
XX
XX 23-JUL-1998; 98JP-00225228.
XX
XX (NISH ) JAPAN TOBACCO INC.
XX
XX WPI; 2000-306578/27.
XX
XX A physiologically active protein specifically derived from mammal tissue.
XX
XX Example 2; Page 18; 50pp; Japanese.
XX
XX The invention relates to identification of genes and proteins of adipose
XX tissue relating to obesity, particularly complications of visceral
XX obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
XX hyperuricemia and sleep apnea syndrome. The genes (AA290631-633) and the
XX proteins (AA67598-Y67600) are used in the genetic diagnosis, prevention
XX and treatment of adipose tissue related diseases. Sequences AA290640-51
XX represent PCR primers amplifying the human adipose tissue genes
XX
XX Sequence 18 BP; 0 A; 0 C; 2 G; 16 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 17; DB 1; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 7.7e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4469 TTTT TTTT TTTT TTTT TTTT 4485
XX 2 TTTT TTTT TTTT TTTT TTTT 18
XX
XX RESULT 1277
XX AAF75596
XX ID AAF75596 standard; DNA; 18 BP.
XX
XX AAF75596;
XX
XX 10-MAY-2001 (first entry)
XX
XX Binary encoded sequence tag method anchored primer #1.
XX
XX Binary encoded sequence tag; BEST; nucleic acid analysis;
XX gene expression; adaptor; PCR primer; ss.
XX
XX Synthetic.
XX
XX WO200112855-A2.
XX
XX 22-FEB-2001.
XX
XX 11-AUG-2000; 2000WO-US022164.
XX
XX 13-AUG-1999; 99US-0148870P.
XX
XX 06-APR-2000; 2000US-00544713.
XX
XX (UYVA ) UNITV YALE.
XX
XX Kaufman JC, Roth ME, Lizardi PM, Feng L, Latimer DR;
XX WPI; 2001-202878/20.
XX
XX Producing binary sequence tags, useful for analyzing nucleic acid
XX sequence tags, gene expression or gene-expression patterns, involves
XX generating nucleic acid fragments, which are mixed with offset adaptors
XX and adaptor-indexers.
XX
XX Disclosure; Page 100; 101pp; English.
XX
XX The present invention describes a method of producing binary sequence
XX tags from nucleic acid fragments in a sample, involving incubating the
XX sample with cleaving reagents, mixing offset adaptors with the sample,

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CC incubating with more cleaving reagents and mixing the sample with adaptor
 CC -indexers where the adaptors are coupled to binary sequence tags. The
 CC method is useful in sequence analysis, including analysis and comparison
 CC of gene expression, nucleic acid samples and genomes

XX Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;

Query Match 0.2%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 7.7e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT G 4484
 |||||
 Db 1 TTTT TTTT TTTT TTTT TTTT G 17

RESULT 1278
 AAD20091/C
 ID AAD20091 standard; mRNA; 18 BP.

XX AAD20091;

DT 03-JAN-2002 (first entry)

XX mRNA fragment used in 3' end PCR/IVT method of the invention.

XX RNA polymerase; RNAP; RNA detection; IVT; in vitro transcription; ss.

XX Undifferentiated.

XX US6271002-B1.

XX 07-AUG-2001.

XX 04-OCT-1999; 99US-00411074.

XX 04-OCT-1999; 99US-00411074.

XX (ROSE-) ROSETTA INPHARMATICS INC.

XX Linsley PS, Schelter JM;

XX WPI; 2001-624273/72.

PT Amplifying and detecting RNA derived from a population of cells by
 PT employing a primer that contains an RNA polymerase promoter in a
 PT polymerase chain reaction.

XX Example 3; Fig 1; 29pp; English.

XX The invention relates to methods and kits for amplification of mRNA using
 CC a primer in PCR that contains an RNA polymerase (RNAP) promoter. The
 CC invention provides methods for amplification and detection of RNA derived
 CC from a population of cells, preferably eukaryotic cells and most
 CC preferably mammalian cells, which methods preserve fidelity with respect
 CC to sequence and transcript representation and additionally enable
 CC amplification of extremely small amounts of mRNA. The method and kit are
 CC useful for amplifying and detecting RNA derived from a population of
 CC cells, especially eukaryotic cells like mammals. The RNAs generated are
 CC useful for profiling gene expression in different populations of cells.
 CC The present sequence is a mRNA fragment used in 3' end PCR/IVT (in vitro
 CC transcription) method of the invention

XX Sequence 18 BP; 17 A; 0 C; 0 G; 0 T; 0 U; 1 Other;

Query Match 0.2%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 7.7e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4480
 |||||
 Db 18 TTTT TTTT TTTT TTTT TTTT TTTT 2

RESULT 1279
 AAQ75552
 ID AAQ75552 standard; DNA; 19 BP.

XX AAQ75552;

DT 04-AUG-1995 (first entry)

XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;
 XX aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-00112515.

XX 16-APR-1993; 93JP-00112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.

XX Disclosure; Page 5; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

XX Sequence 19 BP; 2 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 0.2%; Score 17; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 8.3e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4480
 |||||
 Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 17

RESULT 1280
 AAQ75558
 ID AAQ75558 standard; DNA; 19 BP.

XX AAQ75558;

DT 04-AUG-1995 (first entry)

XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;
 XX aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-00112515.

XX 16-APR-1993; 93JP-00112515.

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XX 16-APR-1993; 93JP-00112515.
PR (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 19 BP; 0 A; 2 C; 0 G; 17 T; 0 U; 0 Other;
SQ
XX
XX Query Match 0.2%; Score 17; DB 1; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 8.3e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4464 TTTT TTTT TTTT TTTT TTTT 4480
XX 1 TTTT TTTT TTTT TTTT TTTT 17
XX
XX RESULT 1281
XX AAQ75556
XX ID AAQ75556 standard; DNA; 19 BP.
XX
XX AAQ75556;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX

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SQ Sequence 19 BP; 1 A; 1 C; 0 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 17; DB 1; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 8.3e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4464 TTTT TTTT TTTT TTTT TTTT 4480
XX 1 TTTT TTTT TTTT TTTT TTTT 17
XX
XX RESULT 1282
XX AAQ75554
XX ID AAQ75554 standard; DNA; 19 BP.
XX
XX AAQ75554;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 19 BP; 1 A; 1 C; 0 G; 17 T; 0 U; 0 Other;
SQ
XX
XX Query Match 0.2%; Score 17; DB 1; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 8.3e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4464 TTTT TTTT TTTT TTTT TTTT 4480
XX 1 TTTT TTTT TTTT TTTT TTTT 17
XX
XX RESULT 1283
XX AAT69640
XX ID AAT69640 standard; DNA; 19 BP.
XX
XX AAT69640;
XX
XX 20-FEB-1998 (first entry)
XX
XX Telomerase Oligo-dT-Primer P3.
XX

```

KW Telomerase; substrate; primer; detection; 5'-region; retrovirus;
 KW long terminal repeat 2; LTR-2; diagnosis; tumour; screening;
 KW effector compound; PCR; amplification; Oligo-dT-Primer; ss.
 XX
 OS Synthetic.
 XX
 XX DE19644302-A1.
 XX
 XX 05-JUN-1997.
 XX
 PD 24-OCT-1996; 96DE-01044302.
 XX
 XX 28-NOV-1995; 95DE-01044317.
 XX
 PA (BOE) BOEHRINGER MANNHEIM GMBH.
 XX
 PI Emrich T, Leying H, Hinzpeter M, Karl G;
 XX
 DR WPI; 1997-299542/28.
 XX
 PT Measuring telomerase activity, useful for tumour diagnosis and compound
 PT screening - by extending substrate primer, followed by amplification and
 PT immobilising product for detection.
 XX
 PS Example; Page 11; 21pp; German.
 XX
 CC The present sequence is a telomerase Oligo-dT-Primer, which can be used
 CC in a novel method for detecting telomerase activity. The method comprises
 CC adding to a test sample a 1st primer, that serves as telomerase
 CC substrate, and nucleoside triphosphate (dNTP) and incubating to allow
 CC primer extension by the telomerase, amplifying the extension product,
 CC immobilising the amplification product (AP) on a solid phase and
 CC qualitative and/or quantitative detection of AP, where the substrate
 CC primer is preferably from the 5'-region of the long terminal repeat 2
 CC (LTR-2) sequence of a retrovirus. The method can be used to diagnose
 CC tumours and screen compounds for effector activity. Immobilisation of AP
 CC provides a signal that is reproducibly representative of telomerase
 CC activity, eliminates the need for gel electrophoretic separation and
 CC provides high sensitivity. Radioactive labels are not required and the
 CC method can be automated for routine use. Specific detection is achieved
 CC by proper choice of hybridisation conditions, without separation of the
 CC telomerase extension product. A specific signal is generated by 1-10 cell
 CC equivalents, but for tumour analysis 10-1000 ng of tissue is usually used
 XX
 SQ Sequence 19 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 2 Other;
 Query Match 0.2%; Score 17; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 8.3e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4464 TTTT TTTT TTTT TTTT TTTT 4480
 DB 1 TTTT TTTT TTTT TTTT 17
 RESULT 1284
 ADE29541/C
 ID ADE29541 standard; RNA; 19 BP.
 XX
 AC ADE29541;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Mitogen activated protein kinase siNA oligonucleotide SEQ ID NO:163.
 XX
 KW short interfering nucleic acid; siNA; downregulation; inhibition;
 KW mitogen-activated protein kinase; MAP kinase; MAPK; RNA interference;
 KW cytostatic; anorectic; antidiabetic; antiinflammatory; antiasthmatic;
 KW immunosuppressive; antibacterial; antirheumatic; antiarthritic;
 KW antiproliferative; gastrointestinal; obesity; diabetes; tumour;
 KW inflammatory disease; asthma; septic shock; rheumatoid arthritis;
 KW psoriasis; inflammatory bowel disease; drug screening;
 KW genetic engineering; pharmacogenomic; gene mapping; ss.

XX
 OS Synthetic.
 XX
 XX WO2003072590-A1.
 XX
 PD 04-SEP-2003.
 XX
 PF 28-JAN-2003; 2003WO-US002510.
 XX
 XX 20-FEB-2002; 2002US-0358580P.
 PR 11-MAR-2002; 2002US-0363124P.
 PR 06-JUN-2002; 2002US-036782P.
 PR 29-AUG-2002; 2002US-0406784P.
 PR 05-SEP-2002; 2002US-0408378P.
 PR 09-SEP-2002; 2002US-0409293P.
 PR 15-JAN-2003; 2003US-0440129P.
 XX
 PA (SIRN-) SIRNA THERAPEUTICS INC.
 XX
 PI Mcwiggan J, Beigelman L, Ueman N, Haeblerl P, Chowitra B;
 XX
 DR WPI; 2003-689980/65.
 XX
 PT New short interfering nucleic acid, useful e.g. for treatment and
 PT diagnosis of cancer, downregulates expression of mitogen-activated
 PT protein kinase genes.
 XX
 PS Example 3; SEQ ID NO 163; 164pp; English.
 XX
 CC The present invention describes a short interfering nucleic acid (siNA)
 CC that downregulates expression of a mitogen-activated protein kinase
 CC (MAPK) genes by RNA interference. Also described: (1) a method for
 CC modulating expression of MAPK genes in cells, tissue explants or
 CC organisms by introduction of siNA; (2) kits for in vitro or in vivo
 CC delivery of siNA; (3) conjugates and/or complexes of siNA; and (4)
 CC vectors that express siNA and cells containing these vectors. MAPK siNAs
 CC have cytostatic, anorectic, antidiabetic, antiinflammatory,
 CC antiasthmatic, immunosuppressive, antibacterial, antirheumatic,
 CC antiarthritic, antiproliferative and gastrointestinal activities. The MAPK
 CC siNAs can be used to modulate the expression of MAPK genes, in cells,
 CC tissue explants or organisms, e.g. for treating obesity; diabetes types I
 CC and II; a wide range of tumours, and inflammatory diseases (asthma,
 CC septic shock, rheumatoid arthritis, psoriasis and inflammatory bowel
 CC disease). They can also be used for drug screening; diagnosis; target
 CC identification and validation; genetic engineering; pharmacogenomics;
 CC studying gene function and gene mapping (e.g. of single-nucleotide
 CC polymorphisms). The present sequence represents a MAPK siNA which is used
 CC in the exemplification of the present invention.
 XX
 SQ Sequence 19 BP; 16 A; 1 C; 0 G; 0 T; 2 U; 0 Other;
 Query Match 0.2%; Score 17; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 8.3e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4468 TTTT TTTT TTTT TTTT TTTT 4484
 DB 19 TTTT TTTT TTTT TTTT 3
 RESULT 1285
 ADE29704
 ID ADE29704 standard; RNA; 19 BP.
 XX
 AC ADE29704;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Mitogen activated protein kinase siNA oligonucleotide SEQ ID NO:326.
 XX
 KW short interfering nucleic acid; siNA; downregulation; inhibition;
 KW mitogen-activated protein kinase; MAP kinase; MAPK; RNA interference;
 KW cytostatic; anorectic; antidiabetic; antiinflammatory; antiasthmatic;

XX Disclosure, Page 5; 11pp; Japanese.
 PS
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 U; 0 Other;
 Query Match 0.2%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 8.9e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4464 TTTT TTTT TTTT TTTT TTTT 4480
 DB 1 TTTT TTTT TTTT TTTT TTTT 17
 RESULT 1288
 ID AAQ755605 standard; DNA; 20 BP.
 AC AAQ75605;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 PT Reverse transcription primer used in cDNA analysis technique.
 XX
 PS Analysis; gene expression; reverse transcription; primer; cDNA;
 XX aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 DR (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 XX WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 5; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 20 BP; 0 A; 2 C; 0 G; 18 T; 0 U; 0 Other;
 Query Match 0.2%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 8.9e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4464 TTTT TTTT TTTT TTTT TTTT 4480
 DB 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 1289
 ID AAQ75596 standard; DNA; 20 BP.
 AC AAQ75596;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 PT Reverse transcription primer used in cDNA analysis technique.
 XX
 PS Analysis; gene expression; reverse transcription; primer; cDNA;
 XX aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 DR (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 XX WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 5; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 U; 0 Other;
 Query Match 0.2%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 8.9e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4464 TTTT TTTT TTTT TTTT TTTT 4480
 DB 1 TTTT TTTT TTTT TTTT TTTT 17
 RESULT 1290
 ID AAQ75589 standard; DNA; 20 BP.
 AC AAQ75589;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 PT Reverse transcription primer used in cDNA analysis technique.
 XX
 PS Analysis; gene expression; reverse transcription; primer; cDNA;
 XX aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 XX

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PF 16-APR-1993; 93JP-00112515.
PR 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
DR
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
SQ
Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;
Query Match 0.2%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4480
Db 1 TTTT TTTT TTTT TTTT TTTT 17
RESULT 1291
AAQ75597
ID AAQ75597 standard; DNA; 20 BP.
XX
XX AAQ75597;
AC
XX
XX DT 04-AUG-1995 (first entry)
XX
XX DE Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
XX OS Synthetic.
XX
XX PN JP06303997-A.
XX
XX PD 01-NOV-1994.
XX
XX PF 16-APR-1993; 93JP-00112515.
XX
XX PR 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
DR
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily

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XX      Sequence 20 BP, 1 A, 1 C, 0 G, 18 T, 0 U, 0 Other;
SQ      Query Match          0.2%; Score 17; DB 1; Length 20;
        Best Local Similarity 100.0%; Pred. No. 8.9e+02;
        Matches 17; Conservative 0; Mismatches 0; Indels 0;
QY      4464 TTTT TTTT TTTT TTTT TTTT 4480
        |||
        1 TTTT TTTT TTTT TTTT TTTT 17
DB
RESULT 1292
AAQ75604
ID      AAQ75604 standard; DNA; 20 BP.
XX
AC      AAQ75604;
XX
DT      04-AUG-1995 (first entry)
DE      Reverse transcription primer used in cDNA analysis technique.
XX
KM      Analysis; gene expression; reverse transcription; primer; cDNA;
KW      aggregate; restriction enzyme; ss.
XX
OS      Synthetic.
XX
PN      JP0630397-A.
XX
PD      01-NOV-1994.
XX
PF      16-APR-1993; 93JP-00112515.
XX
PR      16-APR-1993; 93JP-00112515.
XX
PA      (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR      WPI; 1995-018287/03.
XX
PT      Analysis of cDNA and gene expression - by amplification of mRNA followed
PT      by digestion with restriction enzymes.
PS      Disclosure; Page 5, 11pp; Japanese.
XX
CC      A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC      double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC      labelled reverse transcription primers (GENESSEQ files AAQ75547-075798)
CC      and using the aggregate of mRNAs as the template for each reverse
CC      transcription primer; (b) digesting each of the prepared aggregates of
CC      the double-stranded cDNAs with restriction enzyme and; (c)
CC      electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC      method can be used to analyse gene expression rapidly and easily
SQ      Sequence 20 BP, 1 A, 2 C, 0 G, 17 T, 0 U, 0 Other;
QY      Query Match          0.2%; Score 17; DB 1; Length 20;
        Best Local Similarity 100.0%; Pred. No. 8.9e+02;
        Matches 17; Conservative 0; Mismatches 0; Indels 0;
DB      4464 TTTT TTTT TTTT TTTT TTTT 4480
        |||
        1 TTTT TTTT TTTT TTTT TTTT 17
RESULT 1293
AAQ75588
ID      AAQ75588 standard; DNA; 20 BP.
XX
AC      AAQ75588;
XX
DT      04-AUG-1995 (first entry)
DE      Reverse transcription primer used in cDNA analysis technique.

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XX XX Analysis: gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PS (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX PS Disclosure; Page 5; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESSEQ files AAQ75547-075798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily.
SQ Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 0.2%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4480
Db 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 1294
AAQ75581
ID AAQ75581 standard; DNA; 20 BP.
XX AC AAQ75581;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KM Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PS (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.

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PS Disclosure; Page 5; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESSEQ files AAQ75547-075798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily.
SQ Sequence 20 BP; 2 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.2%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4480
Db 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 1295
AAQ75590
ID AAQ75590 standard; DNA; 20 BP.
XX AC AAQ75590;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KM Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PS (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX PS Disclosure; Page 5; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESSEQ files AAQ75547-075798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily.
SQ Sequence 20 BP; 1 A; 2 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 0.2%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4480
Db 1 TTTT TTTT TTTT TTTT TTTT 17

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RESULT 1296
 AAQ75595
 ID AAQ75595 standard; DNA; 20 BP.
 XX
 AC AAQ75595;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KM Analysis; gene expression; reverse transcription; primer; cDNA;
 XX aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 XX by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 5; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESSEQ files AAQ75547-075798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 8.9e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4464 TTTT TTTT TTTT TTTT TTTT 4480
 DB 1 TTTT TTTT TTTT TTTT TTTT 17
 RESULT 1297
 AAQ75606
 ID AAQ75606 standard; DNA; 20 BP.
 XX
 AC AAQ75606;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KM Analysis; gene expression; reverse transcription; primer; cDNA;
 XX aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX

XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 XX by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 5; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESSEQ files AAQ75547-075798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 20 BP; 0 A; 3 C; 0 G; 17 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 8.9e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4464 TTTT TTTT TTTT TTTT TTTT 4480
 DB 1 TTTT TTTT TTTT TTTT TTTT 17
 RESULT 1298
 AAQ75582
 ID AAQ75582 standard; DNA; 20 BP.
 XX
 AC AAQ75582;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KM Analysis; gene expression; reverse transcription; primer; cDNA;
 XX aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 XX by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 5; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESSEQ files AAQ75547-075798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX

SQ Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 U; 0 Other;
 Query Match 0.2%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 8.9e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4480
 |||||
 DB 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 1299
 AAQ75603
 ID AAQ75603 standard; DNA; 20 BP.
 XX
 AC AAQ75603;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KM Analysis; gene expression; reverse transcription; primer; cDNA;
 XX aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 5; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENSEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

SQ Sequence 20 BP; 0 A; 2 C; 1 G; 17 T; 0 U; 0 Other;
 Query Match 0.2%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 8.9e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4480
 |||||
 DB 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 1300
 AAQ75580
 ID AAQ75580 standard; DNA; 20 BP.
 XX
 AC AAQ75580;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.

KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KM aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 5; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENSEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

SQ Sequence 20 BP; 3 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
 Query Match 0.2%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 8.9e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4480
 |||||
 DB 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 1301
 AAQ75587
 ID AAQ75587 standard; DNA; 20 BP.
 XX
 AC AAQ75587;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KM Analysis; gene expression; reverse transcription; primer; cDNA;
 KM aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 5; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labeled reverse transcription primers (GENESQ files AAQ7547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c) the
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 XX Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
 XX
 XX Query Match 0.2%; Score 17; DB 1; Length 20;
 XX Best Local Similarity 100.0%; Pred. No. 8.9e+02;
 XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 4464 TTTT TTTT TTTT TTTT TTTT 4480
 XX 1 TTTT TTTT TTTT TTTT TTTT 17
 XX
 XX RESULT 1302
 XX AA94391/C
 XX ID AA94391 standard; DNA; 20 BP.
 XX
 XX AA94391;
 XX
 XX 13-SEP-1999 (first entry)
 XX
 XX PCR primer used to amplify an ORF of Chlamydia pneumoniae.
 XX
 XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
 XX sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
 XX neutralising epitope; PCR primer; ss.
 XX
 XX Synthetic.
 XX
 XX Chlamydia pneumoniae.
 XX
 XX WO927105-A2.
 XX
 XX 03-JUN-1999.
 XX
 XX 20-NOV-1998; 98WO-1B001890.
 XX
 XX 21-NOV-1997; 97FR-00014673.
 XX
 XX 04-NOV-1998; 98US-0107078P.
 XX
 XX (GENSET) GENSET.
 XX
 XX Griffais R;
 XX
 XX WPI; 1999-357842/30.
 XX
 XX Genome sequence of Chlamydia pneumoniae.
 XX
 XX Page 1666; Disclosure; 1912pp; English.
 XX
 XX AA91991-X97517 represent PCR primers used to amplify open reading frames
 CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae
 CC (see AA91990). C. pneumoniae causes respiratory disease such as
 CC pneumonia and bronchitis and is thought to be a contributing factor in
 CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
 CC nodosum or pharyngitis. The polypeptides encoded by the open reading
 CC frames of the C. pneumoniae genome (see AA914584- AA915879) can be used
 CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
 CC nucleotide sequences can also be used as immunogenic compositions,
 CC especially where the vector directs the expression of a neutralising
 CC epitope of C. pneumoniae
 XX
 XX Sequence 20 BP; 5 A; 7 C; 3 G; 5 T; 0 U; 0 Other;
 XX
 XX Query Match 0.2%; Score 17; DB 1; Length 20;
 XX Best Local Similarity 100.0%; Pred. No. 8.9e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 5990 CTTGTGTGAAGTCAGCA 6006
 XX 19 CTTGTGTGAAGTCAGCA 3
 XX
 XX RESULT 1303
 XX AB285596/C
 XX ID AB285596 standard; DNA; 20 BP.
 XX
 XX AB285596;
 XX
 XX 17-OCT-2003 (first entry)
 XX
 XX Human oligonucleotide sequence.
 XX
 XX Human; antisense; lung dysfunction; nasal airway dysfunction;
 XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
 XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 XX lung inflammation; respiratory disease; ds.
 XX
 XX Homo sapiens.
 XX
 XX WO200285308-A2.
 XX
 XX 31-OCT-2002.
 XX
 XX 23-APR-2002; 2002WO-US013135.
 XX
 XX 24-APR-2001; 2001US-0286137P.
 XX
 XX (EPIC-) EPiGENESIS PHARM INC.
 XX
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 XX Miller S, Tang L, Shahabuddin S;
 XX WPI; 2003-229219/22.
 XX
 XX Pharmaceutical composition for treating ailments associated with impaired
 XX respiration, has oligo(e) antisense to specific gene(s) or its
 XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 XX ubiquinone.
 XX
 XX Claim 15; SEQ ID NO 838; 872pp; English.
 XX
 XX The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 20 BP; 0 A; 5 C; 8 G; 7 T; 0 U; 0 Other;
 XX
 XX Query Match 0.2%; Score 17; DB 1; Length 20;
 XX Best Local Similarity 100.0%; Pred. No. 8.9e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7413 CAGCAGCAGCAGCA 7429
Db 17 CAGCAGCAGCAGCA 1

RESULT 1304
ABZ89896/c
ID ABZ89896 standard; DNA; 20 BP.
XX
AC ABZ89896;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ublquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JM, Li Y, Sandrasegura A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ublquinone.
XX
PS Disclosure; SEQ ID NO 5138; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ublquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ublquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 18 A; 0 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 0.2%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT 4480
Db 20 TTTT TTTT TTTT TTTT 4

RESULT 1305
ABZ89872/c
ID ABZ89872 standard; DNA; 20 BP.
XX
AC ABZ89872;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ublquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JM, Li Y, Sandrasegura A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ublquinone.
XX
PS Disclosure; SEQ ID NO 5114; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ublquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ublquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 16 A; 2 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 0.2%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4463 CTTTCTTTCTTTCTTTCTTT 4479

DB 20 CTTTCTTTCTTTCTTTCTTT 4

RESULT 1306

AB288694/C

ID AB288694 standard; DNA; 20 BP.

AC AB288694;

DT 17-OCT-2003 (first entry)

DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;

KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;

KW antiallergic; hypotensive; immunosuppressive; cytostatic; gene therapy;

KW antisense gene therapy; respiratory; lung; adenosine sensitivity;

KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;

KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.

PN WO200285308-A2.

PD 31-OCT-2002.

PF 23-APR-2002; 2002WO-US01135.

PR 24-APR-2001; 2001US-0286137P.

XX (EPIC-) EPIGENESIS PHARM INC.

PI Nyce JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;

DR WPI; 2003-229219/22.

PT Pharmaceutical composition for treating ailments associated with impaired

PT respiration, has oligo(s) antisense to specific gene(s) or its

PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or

PT ubiquinone.

PS Disclosure; SEQ ID NO 3936; 872pp; English.

XX

CC The invention relates to a novel pharmaceutical composition, which has a

CC first active agent comprising an oligonucleotide antisense to the

CC initiation codon, coding region, 5' or 3' end genomic flanking regions,

CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

CC junctions of genes encoding a polypeptide associated with lung and/or

CC nasal airway dysfunction and a second active agent comprising an

CC antiinflammatory steroid and ubiquinone. A composition of the invention

CC has antiinflammatory, antiallergic, antiallergic, hypotensive,

CC immunosuppressive, and cytostatic activity. The composition may have a

CC use in antisense gene therapy. The composition is useful for treating or

CC preventing a respiratory, lung or malignant disease or condition, also

CC for enhancing the prophylactic or therapeutic respiratory effect of an

CC antiinflammatory steroid in a subject, for reducing or depleting levels

CC of, or reducing sensitivity to adenosine, reducing levels of adenosine

CC receptor, producing bronchodilation, increasing levels of ubiquinone or

CC lung surfactant in a subject's tissue, or treating bronchoconstriction,

CC lung inflammation, lung allergies, or a respiratory disease or condition.

CC Note: The sequence data for this patent is not represented in the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 20 BP; 17 A; 0 C; 0 G; 3 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 17; DB 1; Length 20;

XX Best Local Similarity 100.0%; Pred. No. 8.9e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTTCTTTCTTTCTTTCTTT 4480

DB 20 TTTTCTTTCTTTCTTTCTTT 4

RESULT 1307

AAQ75702

ID AAQ75702 standard; DNA; 21 BP.

AC AAQ75702;

DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;

KW aggregate; restriction enzyme; ss.

XX Synthetic.

PN JP0630397-A.

PD 01-NOV-1994.

PF 16-APR-1993; 93JP-00112515.

PR 16-APR-1993; 93JP-00112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

DR WPI; 1995-018287/03.

PT Analysis of cDNA and gene expression - by amplification of mRNA followed

PT by digestion with restriction enzymes.

PS Disclosure; Page 7; 11pp; Japanese.

XX

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of

CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of

CC labelled reverse transcription primers (GENSEQ files AAQ75547-075798)

CC and using the aggregate of mRNAs as the template for each reverse

CC transcription primer; (b) digesting each of the prepared aggregates of

CC the double-stranded cDNAs with restriction enzyme and; (c)

CC electrophoresing the digested aggregate of cDNAs in separate lanes. The

XX method can be used to analyse gene expression rapidly and easily

XX

XX Sequence 21 BP; 1 A; 3 C; 0 G; 17 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 17; DB 1; Length 21;

XX Best Local Similarity 100.0%; Pred. No. 9.5e+02;

XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

XX RESULT 1308

XX AAQ75724

XX ID AAQ75724 standard; DNA; 21 BP.

XX AC AAQ75724;

XX DT 04-AUG-1995 (first entry)

XX DE Reverse transcription primer used in cDNA analysis technique.

XX XX Analysis; gene expression; reverse transcription; primer; cDNA;

XX KW aggregate; restriction enzyme; ss.

XX OS Synthetic.

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XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI, 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 8; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 4 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 17; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 9.5e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Oy 4464 TTTTTTTTTTTTTTTT 4480
Db 1 TTTTTTTTTTTTTTTT 17

RESULT 1309
AAQ75752
ID AAQ75752 standard; DNA; 21 BP.
XX
XX AAQ75752;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI, 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 8; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 4 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 17; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 9.5e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Oy 4464 TTTTTTTTTTTTTTTT 4480
Db 1 TTTTTTTTTTTTTTTT 17

RESULT 1310
AAQ75795
ID AAQ75795 standard; DNA; 21 BP.
XX
XX AAQ75795;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI, 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 9; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 0 A; 3 C; 1 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 17; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 9.5e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Oy 4464 TTTTTTTTTTTTTTTT 4480
Db 1 TTTTTTTTTTTTTTTT 17

RESULT 1311
AAQ75798
ID AAQ75798 standard; DNA; 21 BP.
XX
XX

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CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 17; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 9.5e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Oy 4464 TTTTTTTTTTTTTTTT 4480
Db 1 TTTTTTTTTTTTTTTT 17

RESULT 1310
AAQ75795
ID AAQ75795 standard; DNA; 21 BP.
XX
XX AAQ75795;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI, 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 9; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 0 A; 3 C; 1 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 17; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 9.5e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Oy 4464 TTTTTTTTTTTTTTTT 4480
Db 1 TTTTTTTTTTTTTTTT 17

RESULT 1311
AAQ75798
ID AAQ75798 standard; DNA; 21 BP.
XX
XX

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AC AAQ75798;
XX
XX 04-AUG-1995 (first entry)
DT
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
PD
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
PR
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
DR
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 9; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 0 A; 4 C; 0 G; 17 T; 0 U; 0 Other;
SQ
XX
XX Query Match 0.2%; Score 17; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 9.5e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4480
DB 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 1312
AAQ75687
ID AAQ75687 standard; DNA; 21 BP.
XX
XX AAQ75687;
XX
XX 04-AUG-1995 (first entry)
DT
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
PD
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
PR
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX

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DR WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;
SQ
XX
XX Query Match 0.2%; Score 17; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 9.5e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4480
DB 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 1313
AAQ75693
ID AAQ75693 standard; DNA; 21 BP.
XX
XX AAQ75693;
XX
XX 04-AUG-1995 (first entry)
DT
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
PD
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
PR
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
DR
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;
SQ
XX
XX Query Match 0.2%; Score 17; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 9.5e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```


CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c) the
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX

Sequence 21 BP; 3 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.2%; Score 17; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 9.5e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4480

Db 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 1317
 AAQ75729
 ID AAQ75729 standard; DNA; 21 BP.

XX AAQ75729;

XX 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

KW Analysis; gene expression; reverse transcription; primer; cDNA;

KM aggregate; restriction enzyme; ss.

XX Synthetic.

PN JP06303997-A.

XX 01-NOV-1994.

PD 16-APR-1993; 93JP-00112515.

XX 16-APR-1993; 93JP-00112515.

PR (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

DR WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.

XX Disclosure; Page 8; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENSEQ files AAQ75547-075798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX

Sequence 21 BP; 2 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 0.2%; Score 17; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 9.5e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4480

Db 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 1318

AAQ75732

ID AAQ75732 standard; DNA; 21 BP.

XX AAQ75732;

XX 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

KW Analysis; gene expression; reverse transcription; primer; cDNA;

KM aggregate; restriction enzyme; ss.

XX Synthetic.

PN JP06303997-A.

XX 01-NOV-1994.

PD 16-APR-1993; 93JP-00112515.

XX 16-APR-1993; 93JP-00112515.

PR (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

DR WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.

XX Disclosure; Page 8; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENSEQ files AAQ75547-075798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX

Sequence 21 BP; 3 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 0.2%; Score 17; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 9.5e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4480

Db 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 1319

AAQ75690
 ID AAQ75690 standard; DNA; 21 BP.

XX AAQ75690;

XX 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

KW Analysis; gene expression; reverse transcription; primer; cDNA;

KM aggregate; restriction enzyme; ss.

XX Synthetic.

PN JP06303997-A.

XX 01-NOV-1994.

PD 16-APR-1993; 93JP-00112515.

XX 16-APR-1993; 93JP-00112515.

PR (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

DR WPI; 1995-018287/03.

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XX XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT PT by digestion with restriction enzymes.
XX XX
XX PS Disclosure; Page 7; 11pp; Japanese.
XX XX
CC CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX XX
SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 0.2%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4480
Db 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 1320
AAQ75763
ID AAQ75763 standard; DNA; 21 BP.
XX AC AAQ75763;
XX DT 04-AUG-1995 (first entry)
XX XX
DE Reverse transcription primer used in cDNA analysis technique.
XX XX
KM Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX XX
XX PS Disclosure; Page 8; 11pp; Japanese.
XX XX
CC CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX XX
SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 0.2%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4480
Db 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 1322
AAQ75694
ID AAQ75694 standard; DNA; 21 BP.
XX AC AAQ75694;
XX DT 04-AUG-1995 (first entry)
XX XX
DE Reverse transcription primer used in cDNA analysis technique.
XX XX
KM Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.

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Qy 4464 TTTT TTTT TTTT TTTT TTTT 4480
Db 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 1321
AAQ75688
ID AAQ75688 standard; DNA; 21 BP.
XX AC AAQ75688;
XX DT 04-AUG-1995 (first entry)
XX XX
DE Reverse transcription primer used in cDNA analysis technique.
XX XX
KM Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX XX
XX PS Disclosure; Page 7; 11pp; Japanese.
XX XX
CC CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX XX
SQ Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 0.2%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4480
Db 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 1322
AAQ75694
ID AAQ75694 standard; DNA; 21 BP.
XX AC AAQ75694;
XX DT 04-AUG-1995 (first entry)
XX XX
DE Reverse transcription primer used in cDNA analysis technique.
XX XX
KM Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.

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XX 01-NOV-1994.
PD 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4464 TTTT TTTT TTTT TTTT TTTT 4480
DB 1 TTTT TTTT TTTT TTTT TTTT 17
XX
RESULT 1323
AAQ75700
ID AAQ75700 standard; DNA; 21 BP.
XX
AC AAQ75700;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KM Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX

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CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4464 TTTT TTTT TTTT TTTT TTTT 4480
DB 1 TTTT TTTT TTTT TTTT TTTT 17
XX
RESULT 1324
AAQ75728
ID AAQ75728 standard; DNA; 21 BP.
XX
AC AAQ75728;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KM Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 8; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 3 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4464 TTTT TTTT TTTT TTTT TTTT 4480
DB 1 TTTT TTTT TTTT TTTT TTTT 17
XX
RESULT 1325
AAQ75758
ID AAQ75758 standard; DNA; 21 BP.
XX
AC AAQ75758;
XX

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DT 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
DE Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX Synthetic.
OS JP06303997-A.
XX
XX PN 01-NOV-1994.
XX
XX PD 16-APR-1993; 93JP-00112515.
XX
XX PF 16-APR-1993; 93JP-00112515.
XX
XX PR 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX
XX DR
XX
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX PS Disclosure; Page 8; 11pp; Japanese.
XX
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX SQ Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 17; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 9.5e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4464 TTTT TTTT TTTT TTTT TTTT 4480
XX 1 TTTT TTTT TTTT TTTT TTTT 17
XX
XX DB
XX
XX RESULT 1326
XX AAQ75786
XX ID AAQ75786 standard; DNA; 21 BP.
XX
XX AC AAQ75786;
XX
XX DT 04-AUG-1995 (first entry)
XX
XX DE Reverse transcription primer used in cDNA analysis technique.
XX
XX XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX OS Synthetic.
XX
XX PN JP06303997-A.
XX
XX PD 01-NOV-1994.
XX
XX PF 16-APR-1993; 93JP-00112515.
XX
XX PR 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX
XX DR
XX

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PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX PS Disclosure; Page 9; 11pp; Japanese.
XX
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX SQ Sequence 21 BP; 0 A; 3 C; 1 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 17; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 9.5e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4464 TTTT TTTT TTTT TTTT TTTT 4480
XX 1 TTTT TTTT TTTT TTTT TTTT 17
XX
XX DB
XX
XX RESULT 1327
XX AAQ75788
XX ID AAQ75788 standard; DNA; 21 BP.
XX
XX AC AAQ75788;
XX
XX DT 04-AUG-1995 (first entry)
XX
XX DE Reverse transcription primer used in cDNA analysis technique.
XX
XX XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX OS Synthetic.
XX
XX PN JP06303997-A.
XX
XX PD 01-NOV-1994.
XX
XX PF 16-APR-1993; 93JP-00112515.
XX
XX PR 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX
XX DR
XX
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX PS Disclosure; Page 9; 11pp; Japanese.
XX
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX SQ Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 17; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 9.5e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4464 TTTT TTTT TTTT TTTT TTTT 4480
XX 1 TTTT TTTT TTTT TTTT TTTT 17
XX
XX DB
XX

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Db      1 |||||
        TTTT
        17

RESULT 1328
AAQ75764
ID      AAQ75764 standard; DNA; 21 BP.
XX
AC      AAQ75764;
XX
DT      04-AUG-1995 (first entry)
XX
DE      Reverse transcription primer used in cDNA analysis technique.
XX
KW      Analysis; gene expression; reverse transcription; primer; cDNA;
KW      aggregate; restriction enzyme; ss.
XX
OS      Synthetic.
XX
PN      JP06303997-A.
XX
PD      01-NOV-1994.
XX
PF      16-APR-1993; 93JP-00112515.
XX
PR      16-APR-1993; 93JP-00112515.
XX
PA      (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR      WPI; 1995-018287/03.
XX
PT      Analysis of cDNA and gene expression - by amplification of mRNA followed
XX      by digestion with restriction enzymes.
XX
PS      Disclosure; Page 9; 11pp; Japanese.
XX
CC      A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC      double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC      labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)
CC      and using the aggregate of mRNAs as the template for each reverse
CC      transcription primer; (b) digesting each of the prepared aggregates of
CC      the double-stranded cDNAs with restriction enzyme and; (c)
CC      electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC      method can be used to analyse gene expression rapidly and easily
XX
SQ      Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 U; 0 Other;

Query Match      0.2%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred.No. 9.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4464 TTTT
        |||||
        TTTT
        17

Db      1 TTTT
        TTTT
        17

RESULT 1329
AAQ75796
ID      AAQ75796 standard; DNA; 21 BP.
XX
AC      AAQ75796;
XX
DT      04-AUG-1995 (first entry)
XX
DE      Reverse transcription primer used in cDNA analysis technique.
XX
KW      Analysis; gene expression; reverse transcription; primer; cDNA;
KW      aggregate; restriction enzyme; ss.
XX
OS      Synthetic.
XX
PN      JP06303997-A.
XX

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PD      01-NOV-1994.
XX
PF      16-APR-1993; 93JP-00112515.
XX
PR      16-APR-1993; 93JP-00112515.
XX
PA      (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR      WPI; 1995-018287/03.
XX
PT      Analysis of cDNA and gene expression - by amplification of mRNA followed
XX      by digestion with restriction enzymes.
XX
PS      Disclosure; Page 9; 11pp; Japanese.
XX
CC      A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC      double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC      labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)
CC      and using the aggregate of mRNAs as the template for each reverse
CC      transcription primer; (b) digesting each of the prepared aggregates of
CC      the double-stranded cDNAs with restriction enzyme and; (c)
CC      electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC      method can be used to analyse gene expression rapidly and easily
XX
SQ      Sequence 21 BP; 1 A; 3 C; 0 G; 17 T; 0 U; 0 Other;

Query Match      0.2%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred.No. 9.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4464 TTTT
        |||||
        TTTT
        17

Db      1 TTTT
        TTTT
        17

RESULT 1330
AAQ75722
ID      AAQ75722 standard; DNA; 21 BP.
XX
AC      AAQ75722;
XX
DT      04-AUG-1995 (first entry)
XX
DE      Reverse transcription primer used in cDNA analysis technique.
XX
KW      Analysis; gene expression; reverse transcription; primer; cDNA;
KW      aggregate; restriction enzyme; ss.
XX
OS      Synthetic.
XX
PN      JP06303997-A.
XX
PD      01-NOV-1994.
XX
PF      16-APR-1993; 93JP-00112515.
XX
PR      16-APR-1993; 93JP-00112515.
XX
PA      (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR      WPI; 1995-018287/03.
XX
PT      Analysis of cDNA and gene expression - by amplification of mRNA followed
XX      by digestion with restriction enzymes.
XX
PS      Disclosure; Page 8; 11pp; Japanese.
XX
CC      A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC      double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC      labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)
CC      and using the aggregate of mRNAs as the template for each reverse
CC      transcription primer; (b) digesting each of the prepared aggregates of
CC      the double-stranded cDNAs with restriction enzyme and; (c)

```

CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 0.2%; Score 17; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 9.5e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4464 TTTT TTTT TTTT TTTT TTTT 4480
 |||||
 Db 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 1331
 AAQ75723
 ID AAQ75723 standard; DNA; 21 BP.

AC AAQ75723;
 DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.

XX Synthetic.

OS JP06303997-A.

XX 01-NOV-1994.

PD 16-APR-1993; 93JP-00112515.

PF 16-APR-1993; 93JP-00112515.

PR 16-APR-1993; 93JP-00112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

DR WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 8; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESSEQ files AAQ7547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX

XX Sequence 21 BP; 3 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 0.2%; Score 17; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 9.5e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4480
 |||||
 Db 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 1332
 AAQ75726
 ID AAQ75726 standard; DNA; 21 BP.

AC AAQ75726;

DT 04-AUG-1995 (first entry)

XX Reverse transcription primer used in cDNA analysis technique.

DE Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.

XX Synthetic.

OS JP06303997-A.

XX 01-NOV-1994.

PD 16-APR-1993; 93JP-00112515.

PF 16-APR-1993; 93JP-00112515.

PR 16-APR-1993; 93JP-00112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

DR WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 8; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESSEQ files AAQ7547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX

SQ Sequence 21 BP; 3 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 0.2%; Score 17; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 9.5e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4480
 |||||
 Db 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 1333

AAQ75760
 ID AAQ75760 standard; DNA; 21 BP.

AC AAQ75760;

DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.

XX Synthetic.

OS JP06303997-A.

XX 01-NOV-1994.

PD 16-APR-1993; 93JP-00112515.

PF 16-APR-1993; 93JP-00112515.

PR 16-APR-1993; 93JP-00112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

DR WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed

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PT by digestion with restriction enzymes.
XX
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily.
XX
XX
SQ Sequence 21 BP; 3 A; 1 C; 0 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 17; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 9.5e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4480
DB 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 1334
AAQ75692
ID AAQ75692 standard; DNA; 21 BP.
XX
XX AAQ75692;
AC
XX
XX 04-AUG-1995 (first entry)
DT
XX
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
XX Synthetic.
OS
XX JP06303997-A.
PN
XX
XX 01-NOV-1994.
PD
XX
XX 16-APR-1993; 93JP-00112515.
PF
XX
XX 16-APR-1993; 93JP-00112515.
PR
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX
XX WPI; 1995-018287/03.
DR
XX
XX
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 7; 11pp; Japanese.
PS
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily.
XX
XX
SQ Sequence 21 BP; 3 A; 1 C; 0 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 17; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 9.5e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4480
DB 1 TTTT TTTT TTTT TTTT TTTT 17

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DB 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 1335
AAQ75756
ID AAQ75756 standard; DNA; 21 BP.
XX
XX AAQ75756;
AC
XX
XX 04-AUG-1995 (first entry)
DT
XX
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
XX Synthetic.
OS
XX JP06303997-A.
PN
XX
XX 01-NOV-1994.
PD
XX
XX 16-APR-1993; 93JP-00112515.
PF
XX
XX 16-APR-1993; 93JP-00112515.
PR
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX
XX WPI; 1995-018287/03.
DR
XX
XX
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 8; 11pp; Japanese.
PS
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily.
XX
XX
SQ Sequence 21 BP; 3 A; 1 C; 0 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 17; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 9.5e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4480
DB 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 1336
AAQ75757
ID AAQ75757 standard; DNA; 21 BP.
XX
XX AAQ75757;
AC
XX
XX 04-AUG-1995 (first entry)
DT
XX
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KM aggregate; restriction enzyme; ss.
XX
XX Synthetic.
OS
XX JP06303997-A.
PN
XX
XX 01-NOV-1994.
PD

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XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 8; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily.
XX
XX Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4480
DB 1 TTTT TTTT TTTT TTTT TTTT 17
RESULT 1337
AAQ75790
ID AAQ75790 standard; DNA; 21 BP.
XX
XX AAQ75790;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 9; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily.

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CC method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 1 A; 3 C; 0 G; 17 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4480
DB 1 TTTT TTTT TTTT TTTT TTTT 17
RESULT 1338
AAQ75784
ID AAQ75784 standard; DNA; 21 BP.
XX
XX AAQ75784;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 9; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESSEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily.
XX
XX Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4480
DB 1 TTTT TTTT TTTT TTTT TTTT 17
RESULT 1339
AAQ75699
ID AAQ75699 standard; DNA; 21 BP.
XX
XX AAQ75699;
XX
XX 04-AUG-1995 (first entry)
XX

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DE Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESQ files AAQ75547-075798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX
XX Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;
SQ
XX
XX Query Match 0.2%; Score 17; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 9.5e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4464 TTTT TTTT TTTT TTTT TTTT 4480
Db 1 TTTT TTTT TTTT TTTT TTTT 17
XX
XX RESULT 1340
XX AAQ75731
XX ID AAQ75731 standard; DNA; 21 BP.
XX
XX AC AAQ75731;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX

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XX
XX Disclosure; Page 8; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESQ files AAQ75547-075798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX
XX Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;
SQ
XX
XX Query Match 0.2%; Score 17; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 9.5e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4464 TTTT TTTT TTTT TTTT TTTT 4480
Db 1 TTTT TTTT TTTT TTTT TTTT 17
XX
XX RESULT 1341
XX AAQ75751
XX ID AAQ75751 standard; DNA; 21 BP.
XX
XX AC AAQ75751;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 8; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESQ files AAQ75547-075798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX
XX Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;
SQ
XX
XX Query Match 0.2%; Score 17; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 9.5e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4464 TTTT TTTT TTTT TTTT TTTT 4480
Db 1 TTTT TTTT TTTT TTTT TTTT 17
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX

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RESULT 1342
AAQ75691
ID AAQ75691 standard; DNA; 21 BP.
XX
AC AAQ75691;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PS (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
CC
SQ Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4464 TTTTTTTTTTTTTTTT 4480
DB 1 TTTTTTTTTTTTTTTT 17

```

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PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
CC
SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4464 TTTTTTTTTTTTTTTT 4480
DB 1 TTTTTTTTTTTTTTTT 17

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RESULT 1344
AAQ75734
ID AAQ75734 standard; DNA; 21 BP.
XX
AC AAQ75734;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PS (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
CC

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XX
SQ Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 U; 0 Other;

Query Match          0.2%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTTTTTTTTTTTTTT 4480
      |||||
      1 TTTTTTTTTTTTTTTT 17

Db

RESULT 1345
AAQ75755
ID AAQ75755 standard; DNA; 21 BP.
XX
AC AAQ75755;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

Query Match          0.2%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTTTTTTTTTTTTTT 4480
      |||||
      1 TTTTTTTTTTTTTTTT 17

Db

RESULT 1346
AAQ75696
ID AAQ75696 standard; DNA; 21 BP.
XX
AC AAQ75696;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.

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XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

Query Match          0.2%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTTTTTTTTTTTTTT 4480
      |||||
      1 TTTTTTTTTTTTTTTT 17

Db

RESULT 1347
AAQ75761
ID AAQ75761 standard; DNA; 21 BP.
XX
AC AAQ75761;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.

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PS Disclosure; Page 8; 11pp; Japanese.
 XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESSEQ files AAQ75547-075798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;
 QY Query Match 0.2%; Score 17; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 9.5e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 4464 TTTT TTTT TTTT TTTT TTTT 4480
 1 TTTT TTTT TTTT TTTT TTTT 17
 RESULT 1348
 AAQ75789
 ID AAQ75789 standard; DNA; 21 BP.
 XX
 AC AAQ75789;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 PS Analysis; gene expression; reverse transcription; primer; cDNA;
 KM aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 9; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESSEQ files AAQ75547-075798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;
 QY Query Match 0.2%; Score 17; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 9.5e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 4464 TTTT TTTT TTTT TTTT TTTT 4480
 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 1349
 AAQ75720
 ID AAQ75720 standard; DNA; 21 BP.
 XX
 AC AAQ75720;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 PS Analysis; gene expression; reverse transcription; primer; cDNA;
 KM aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 8; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESSEQ files AAQ75547-075798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 21 BP; 3 A; 0 C; 1 G; 17 T; 0 U; 0 Other;
 QY Query Match 0.2%; Score 17; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 9.5e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 4464 TTTT TTTT TTTT TTTT TTTT 4480
 1 TTTT TTTT TTTT TTTT TTTT 17
 RESULT 1350
 AAQ75766
 ID AAQ75766 standard; DNA; 21 BP.
 XX
 AC AAQ75766;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 PS Analysis; gene expression; reverse transcription; primer; cDNA;
 KM aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.

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XX 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX Disclosure; Page 9; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily.
XX
XX Sequence 21 BP; 1 A; 3 C; 0 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 17; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 9.5e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4464 TTTT TTTT TTTT TTTT TTTT 4480
XX 1 TTTT TTTT TTTT TTTT TTTT 17
XX
XX RESULT 1351
XX ID AAQ75783 standard; DNA; 21 BP.
XX AC AAQ75783;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX Disclosure; Page 9; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily.
XX

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XX Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 17; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 9.5e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4464 TTTT TTTT TTTT TTTT TTTT 4480
XX 1 TTTT TTTT TTTT TTTT TTTT 17
XX
XX RESULT 1352
XX ID AAQ75792 standard; DNA; 21 BP.
XX AC AAQ75792;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX Disclosure; Page 9; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESBQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily.
XX
XX Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 17; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 9.5e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4464 TTTT TTTT TTTT TTTT TTTT 4480
XX 1 TTTT TTTT TTTT TTTT TTTT 17
XX
XX RESULT 1353
XX ID AAT85350 standard; DNA; 23 BP.
XX AC AAT85350;
XX
XX 09-DEC-1997 (first entry)
XX
XX Spider silk protein target DNA primer (xv).
XX

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KM High strength film, fibre; woven article; parachutes; sails; absorber;
 KW body armour; heavy metal; biological weapon; chemical; flavour;
 KW fragrance; Nephtia clavipes; ss.
 XX
 OS Synthetic.
 XX
 XX WO9708315-A1.
 XX
 XX PD 06-MAR-1997.
 XX
 XX PF 22-AUG-1996; 96WO-US013767.
 XX
 XX PR 22-AUG-1995; 95US-00517694.
 XX
 XX PA (BASE/) BASEL R M.
 XX PA (ELIO/) ELION G R.
 XX
 XX PI Basel RM, Elion GR;
 XX
 XX DR WPI; 1997-179272/16.
 XX
 XX PT New opt. multimerised DNA sequences encoding spider silk protein - contg.
 PT both repetitive and non-repetitive sequences, useful for making high
 PT strength films, fibres, woven articles etc.
 XX
 XX PS Claim 7; Page 54; 57pp; English.
 XX
 CC A process has been developed for the production of a DNA fragment
 CC encoding silk protein. The process involves: (a) selecting target DNA,
 CC from a silk-producing spider, that contains many repetitive and non-
 CC repetitive regions; (b) selecting a single-stranded DNA primer of at
 CC least 10 nucleotides with a sequence that is complementary to a region of
 CC the target; (c) repetitively combining the primer with melted target DNA,
 CC incubating the mixture with nucleotides and a DNA polymerase with
 CC proofreading activity to produce a DNA fragment which is complementary to
 CC the target and is at least 2 kb long. The present sequence represents a
 CC specifically claimed primer for use in this process. The DNA fragment can
 CC be used to make fibres, films, woven articles, e.g. for use in
 CC parachutes, sails, body armour, and absorbers (e.g. of heavy metals,
 CC biological weapons, DNA, chemicals, flavours and fragrances). The high
 CC molecular weight (90-250 kd) of spider silk proteins can be produced on a
 CC commercial scale (at over 2 g/l cell mass). It has better tensile
 CC strength and elasticity than silkworm silk. Inclusion of both repetitive
 CC and non-repetitive regions ensures isolation of stable clones
 CC
 XX SQ Sequence 23 BP; 4 A; 6 C; 10 G; 2 T; 0 U; 1 Other;
 XX
 XX Query Match 0.2%; Score 17; DB 1; Length 23;
 XX Best Local Similarity 89.5%; Pred. No. 1.1e+03;
 XX Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 XX
 QY 7415 GCAGCAGCAGCAGCAGCAG 7433
 DB 4 GCAGCAGCAGCAGCTGCG 22
 XX
 XX RESULT 1354
 XX ABL95973
 XX ID ABL95973 standard; DNA; 23 BP.
 XX
 XX AC ABL95973;
 XX
 XX DT 19-JUN-2002 (first entry)
 XX
 XX DE Probe #48 for assaying nucleic acids.
 XX
 XX KW Probe; polymorphism detection; mutation detection; disease diagnosis;
 KW microbial identification; ss.
 XX
 XX OS Unidentified.
 XX
 XX PN WO200208414-A1.
 XX

PD 31-JAN-2002.
 XX
 XX PF 27-JUN-2001; 2001WO-IB001147.
 XX
 XX PR 27-JUN-2000; 2000JP-00193113.
 XX PR 03-AUG-2000; 2000JP-00236115.
 XX PR 26-SEP-2000; 2000JP-00292483.
 XX
 XX PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 XX PA (KANK-) KANKYO ENG CO LTD.
 XX
 XX PI Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K,
 PI Yokomaki T;
 XX
 XX DR WPI; 2002-195876/25.
 XX
 XX PT Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
 PT their polymorphism and mutation, particularly useful in science and
 PT medicine for e.g. analytical applications, disease diagnosis and
 PT microbial identification.
 XX
 XX PS Disclosure; Fig 3; 152pp; Japanese.
 XX
 CC The present invention relates to nucleic acid probes, which are useful
 CC for assaying nucleic acids by hybridising with a target nucleic acid, in
 CC which a single-stranded oligonucleotide is labelled with a fluorescent
 CC substance and a quencher in a manner that the fluorescence intensity of
 CC the hybridisation reaction system is increased after completion of the
 CC hybridisation but no stem loop structure is formed. The probes are useful
 CC for assaying nucleic acids and their polymorphism and mutation,
 CC particularly useful for e.g. analytical applications, disease diagnosis
 CC and microbial identification. The present sequence was used to illustrate
 CC the invention
 XX
 XX SQ Sequence 23 BP; 0 A; 6 C; 0 G; 17 T; 0 U; 0 Other;
 XX
 XX Query Match 0.2%; Score 17; DB 1; Length 23;
 XX Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 4464 TTTT TTTT TTTT TTTT TTTT 4480
 DB 1 TTTT TTTT TTTT TTTT TTTT 17
 XX
 XX RESULT 1355
 XX ABR85840/C
 XX ID ABR85840 standard; DNA; 23 BP.
 XX
 XX AC ABR85840;
 XX
 XX DT 24-SEP-2002 (first entry)
 XX
 XX DE Myotonic dystrophy protein kinase (DMPK) 3'UTR fragment.
 XX
 XX KW Myotonic dystrophy; DM; protein kinase; DMPK; myocardial infarction;
 KW muscle damage; dysfunction; CTG repeat; ds.
 XX
 XX OS Homo sapiens.
 XX
 XX PN US2002061571-A1.
 XX
 XX PD 23-MAY-2002.
 XX
 XX PF 20-MAR-2001; 2001US-00813289.
 XX
 XX PR 20-MAR-2000; 2000US-0190590P.
 XX
 XX PA (MAHA/) MAHADEVAN M S.
 XX PA (TISC/) TISCORNIA G.
 XX
 XX PI Mahadevan MS, Tiscornia G;
 XX

DR MPI; 2002-507644/54.
XX A new isoform of myotonic dystrophy protein kinase includes a sequence
PT encoded by exon 16 of the gene and is useful to detect presence or risk
PT of myotonic dystrophy, myocardial infarction or a condition associated
XX with muscle damage.
PS Example; Page 9; 26pp; English.
XX The invention describes an isolated and purified polypeptide, comprising
CC an amino acid sequence encoded by exon 16 of the myotonic dystrophy
CC protein kinase (DMPK) gene. The invention is used to detect presence or
CC risk of myotonic dystrophy, myocardial infarction or a condition
CC associated with muscle damage or dysfunction. This sequence represents
CC the CTG repeat isolated from the 3' UTR of the novel Myotonic dystrophy
XX protein kinase (DMPK) isoform gene
SQ Sequence 23 BP; 2 A; 5 C; 10 G; 6 T; 0 U; 0 Other;
Query Match 0.2%; Score 17; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7413 CAGCAGCAGCAGCAGCA 7429
DB 19 CAGCAGCAGCAGCAGCA 3
RESULT 1356
AAH76998
ID AAH76998 standard; DNA; 24 BP.
AC AAH76998;
XX 15-DEC-2001 (first entry)
DT Human amyloid precursor protein 9 RT-PCR primer, SEQ ID NO:4.
XX Human amyloid precursor protein 9; recombinant production;
XX malignant tumour; cancer; blood disease; HIV infection;
KW human immunodeficiency virus; immune disorder; inflammatory condition;
KW cytostatic; anti-HIV; antineoplastic; immunomodulator;
KM reverse transcription-PCR; RT-PCR primer; ss.
XX Homo sapiens.
OS WO200174878-A1.
XX 11-OCT-2001.
PD 23-MAR-2001; 2001WO-CN000391.
XX 24-MAR-2000; 2000CN-00115106.
PR (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX Mao Y, Xie Y;
PI MPI; 2001-626386/72.
XX New human amyloid precursor protein 9 and encoded polynucleotide,
PT applicable in diagnosis and treatment of cancer, hemopathy, human
PT immunodeficiency virus infection, immunological diseases and various
XX inflammations.
XX Example 2; Page 16; 37pp; Chinese.
XX The invention relates to human amyloid precursor protein 9 (AAG66809),
CC nucleic acids encoding it (AAH76996), and a method for the recombinant
CC production of amyloid precursor protein 9. The protein has a molecular
CC weight of 9 kD. The present invention additionally discloses an
CC antagonist of amyloid precursor protein 9 for therapeutic use, and an
CC antibody which specifically binds to amyloid precursor protein 9. Amyloid

CC precursor protein 9, and nucleotides which encode it may be used for
CC treating a variety of diseases, such as malignant tumours, blood
CC diseases, HIV (human immunodeficiency virus) infection, immune disorders
CC and inflammatory conditions. The protein may also be used to screen for
CC modulators of its activity or for peptide fingerprinting identification.
CC The polynucleotide can be used as a primer for nucleic acid amplification
CC reactions or as a probe for hybridisation reactions, or in producing gene
CC chips or microarrays. Sequences AAH76997-AAH76998 represent reverse
CC transcription-PCR (RT-PCR) primers used in an exemplification of the
XX invention to isolate human amyloid precursor protein 9 cDNA
SQ Sequence 24 BP; 1 A; 1 C; 4 G; 18 T; 0 U; 0 Other;
Query Match 0.2%; Score 17; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4480
DB 1 TTTT TTTT TTTT TTTT TTTT 17
RESULT 1357
AA164873
ID AA164873 standard; DNA; 24 BP.
AC AA164873;
XX 04-DEC-2001 (first entry)
DT Human serine/threonine protein kinase 48 cDNA PCR primer #2.
XX Human, serine/threonine protein kinase 48; cancer; HIV infection;
KW gene therapy; PCR primer; ss.
XX Homo sapiens.
OS CN1300831-A.
XX 27-JUN-2001.
PD 22-DEC-1999; 99CN-00125686.
XX 22-DEC-1999; 99CN-00125686.
PR (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX Mao Y, Xie Y;
PI MPI; 2001-530471/59.
XX New human serine/threonine protein kinase 48 and its encoding
PT polynucleotide, useful for treating cancer and human immunodeficiency
XX virus infection.
XX Example 3; Page 17(Disclosure); 33pp; Chinese.
XX The present invention provides the protein and coding sequences of human
CC serine/threonine protein kinase 48. The sequences can be used in the
CC treatment of cancer and HIV infection. The present sequence is a PCR
CC primer for the coding sequence of the invention.
XX Sequence 24 BP; 3 A; 1 C; 3 G; 17 T; 0 U; 0 Other;
SQ Query Match 0.2%; Score 17; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4463 TTTT TTTT TTTT TTTT TTTT 4485
DB 1 TTTT TTTT TTTT TTTT TTTT 17

```

RESULT 1358
ID AAX86505 standard; DNA; 25 BP.
XX
XX AAX86505;
AC
XX 20-MAR-2003 (revised)
DT 30-SEP-1999 (first entry)
XX
XX Internal antisense primer D used to amplify cDNA encoding beta-Trcp.
DE
XX Beta-transducin repeat containing protein; beta-Trcp; Skp1p;
KM proteasome degradation pathway; Vpu protein; beta-catenin;
KM human immune deficiency virus-1; HIV-1; cellular protein; IKKAPAB;
KM ubiquitinylation; phosphorylated protein; tumour; apoptosis; Alzheimer's;
KM antiviral; antitumour; cell cycle regulation; protein degradation;
KM and anti-inflammatory; osteo-articular inflammation; acute inflammation;
KM tumour necrosis factor; PCR primer; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX WO93938969-A1.
PN
XX 05-AUG-1999.
PD
XX 29-JAN-1999; 99WO-FR000196.
PF
XX 30-JAN-1998; 98FR-00001100.
PR 09-DEC-1998; 98FR-00015545.
XX
XX (INSP ) INST PASTEUR.
PA (INRM ) INST NAT SANTE & RECH MEDICALE.
XX
XX Benarous R, Margotcin F, Durand H, Arenzana Seisdedos F, Kroll M;
PI Concordec J;
PI WPI; 1999-469329/39.
DR
XX New human beta-transducin repeat containing protein and its fragments
PT useful as, or to screen for, antiviral, antitumour, anti-inflammatory and
PT anti-Alzheimer agents.
PT
XX
XX Example 2; Page 62; 71pp; French.
PS
XX PCR primers AAX86502-05 were used to amplify cDNA encoding a human beta-
CC transducin repeat containing protein (beta-Trcp). The protein directs
CC proteins to the proteasome degradation pathways. The protein is able to
CC interact with the Vpu protein of human immune deficiency virus-1 (HIV-1),
CC cellular proteins IKKAPAB or beta-catenin (BC) and/or protein Skp1p. The
CC protein controls ubiquitinylation of phosphorylated proteins and thus
CC their targeting to proteasomes for degradation. Depending on whether the
CC process is inhibited or promoted, the result may be delayed breakdown of
CC CD4 (in cases of HIV-1 infection); increased activity of Ikb (and thus
CC reduced activity of NFkappaB) and increased degradation of mutant bc in
CC tumour cells, or increased bc survival (and reduced apoptosis) in
CC Alzheimer's patients. The beta-Trcp protein, and its active peptide
CC fragments, or its nucleic acid, are used to screen for anti HIV-1 agents
CC (antivirals), antitumour agents that disrupt cell cycle regulation or
CC protein degradation in human tumour cells, and anti-inflammatory agents
CC that disrupt activation by NFkappaB. Fragments of the protein are also
CC useful for treating osteo-articular inflammation or acute inflammation
CC associated with release of tumour necrosis factor. (Updated on 20-MAR-
CC 2003 to correct PA field.)
XX
XX Sequence 25 BP; 4 A; 4 C; 5 G; 12 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 17; DB 1; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 4047 TTTATACCATTAAGTGTGTTG 4071
||||| ||||| ||||| ||||| |||||

```

```

DB 1 TTTATCCAGATCTGATGTGTTG 25
RESULT 1359
ID AAC96621 standard; DNA; 25 BP.
XX
XX AAC96621;
AC
XX 26-FEB-2001 (first entry)
DT
XX
XX HLA DRB345 gene PCR primer #92.
DE
XX DNA sequence analysis; sequencing; protein sequence; protein structure;
KM gene typing; organ donation; bacteria identification; 16S rRNA; HLA;
KM human leukocyte antigen; PCR primer; ss.
XX
XX Homo sapiens.
OS
XX WO200065088-A2.
PN
XX 02-NOV-2000.
PD
XX 20-APR-2000; 2000WO-EP003636.
PF
XX 26-APR-1999; 99EP-00303215.
PR
XX (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
PA
XX Ulfendahl P, Wong K;
PI WPI; 2000-679677/66.
DR
XX
XX Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
PT
XX
XX Claim 14; Page 54; 66pp; English.
PS
XX
XX The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16S rRNA genes in
CC particular
CC
XX
XX Sequence 25 BP; 2 A; 5 C; 3 G; 15 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 17; DB 1; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 4472 TTTTGTGTTGTTGACATG 4496
||||| ||||| ||||| ||||| |||||
DB 1 TTTTGTGTTGTTGACATG 25
RESULT 1360
ID AAC96765 standard; DNA; 25 BP.
XX
XX AAC96765;
AC
XX 26-FEB-2001 (first entry)
DT
XX
XX HLA HLA-A gene PCR primer #142.
DE
XX
XX DNA sequence analysis; sequencing; protein sequence; protein structure;
KM gene typing; organ donation; bacteria identification; 16S rRNA; HLA;
KM human leukocyte antigen; PCR primer; ss.
XX

```


OS Homo sapiens.
 XX
 XX WO200065088-A2.
 XX
 PD 02-NOV-2000.
 XX
 XX 20-APR-2000; 2000WO-EP003636.
 XX
 XX 26-APR-1999; 99EP-00303215.
 XX
 XX (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
 XX
 PI Ulfendahl P, Wong K;
 XX
 DR WPI; 2000-679677/66.
 XX
 PT Identifying extendible primers for use in identification, or
 PT classification of a nucleic acid of an organism, allele or gene such as
 PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
 PT specific length.
 PS Claim 14; Page 57; 66pp; English.
 XX
 CC The present invention provides a method for identifying a set of
 CC extendible primers which can be used in the identification, typing and
 CC classification of genes. This can then be used to predict protein
 CC sequence and structure, in organ donation to match the organ with the
 CC receiver, and to identify bacteria in a sample. The method can be used to
 CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
 CC particular
 XX
 SQ Sequence 25 BP; 4 A; 1 C; 5 G; 15 T; 0 U; 0 Other;
 Query Match 0.2%; Score 17; DB 1; Length 25;
 Best Local Similarity 80.0%; Pred. No. 1.2e+03;
 Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 4468 TTTT TTTT TTTT TTTT TTTT GCTT GAGA 4492
 DB 1 TTTT TTTT TTTT TTTT CATGAGT GAGA 25
 RESULT 1361
 AAC96494
 ID AAC96494 standard; DNA; 25 BP.
 XX
 AC AAC96494;
 XX
 DT 26-FEB-2001 (first entry)
 XX
 DE HLA DQB1 gene PCR primer #46.
 XX
 KW DNA sequence analysis; sequencing; protein sequence; protein structure;
 KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
 KW human leukocyte antigen; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200065088-A2.
 XX
 PD 02-NOV-2000.
 XX
 XX 20-APR-2000; 2000WO-EP003636.
 XX
 XX 26-APR-1999; 99EP-00303215.
 XX
 XX (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
 XX
 PI Ulfendahl P, Wong K;
 XX
 DR WPI; 2000-679677/66.
 XX
 PT Identifying extendible primers for use in identification, or

PT classification of a nucleic acid of an organism, allele or gene such as
 PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
 PT specific length.
 PS Claim 14; Page 52; 66pp; English.
 XX
 CC The present invention provides a method for identifying a set of
 CC extendible primers which can be used in the identification, typing and
 CC classification of genes. This can then be used to predict protein
 CC sequence and structure, in organ donation to match the organ with the
 CC receiver, and to identify bacteria in a sample. The method can be used to
 CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
 CC particular
 XX
 SQ Sequence 25 BP; 0 A; 5 C; 3 G; 17 T; 0 U; 0 Other;
 Query Match 0.2%; Score 17; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4471 TTTT TTTT TTTT TTTT TTTT GCT 4487
 DB 1 TTTT TTTT TTTT TTTT GCT 17
 RESULT 1362
 AAC96587
 ID AAC96587 standard; DNA; 25 BP.
 XX
 AC AAC96587;
 XX
 DT 26-FEB-2001 (first entry)
 XX
 DE HLA DRB345 gene PCR primer #58.
 XX
 KW DNA sequence analysis; sequencing; protein sequence; protein structure;
 KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
 KW human leukocyte antigen; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200065088-A2.
 XX
 PD 02-NOV-2000.
 XX
 XX 20-APR-2000; 2000WO-EP003636.
 XX
 XX 26-APR-1999; 99EP-00303215.
 XX
 XX (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
 XX
 PI Ulfendahl P, Wong K;
 XX
 DR WPI; 2000-679677/66.
 XX
 PT Identifying extendible primers for use in identification, or
 PT classification of a nucleic acid of an organism, allele or gene such as
 PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
 PT specific length.
 PS Claim 14; Page 54; 66pp; English.
 XX
 CC The present invention provides a method for identifying a set of
 CC extendible primers which can be used in the identification, typing and
 CC classification of genes. This can then be used to predict protein
 CC sequence and structure, in organ donation to match the organ with the
 CC receiver, and to identify bacteria in a sample. The method can be used to
 CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
 CC particular
 XX
 SQ Sequence 25 BP; 4 A; 2 C; 5 G; 14 T; 0 U; 0 Other;
 Query Match 0.2%; Score 17; DB 1; Length 25;

Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 4470 TTTTCTTTTCTTGTGCTGAGACA 4494
DB 1 TTTTCTTTTCTTGTGCTGAGACA 25

RESULT 1363
AAC96454
ID AAC96454 standard; DNA; 25 BP.
AC AAC96454;
DT 26-FEB-2001 (first entry)
DE HLA DQB1 gene PCR primer #6.
XX DNA sequence analysis; sequencing; protein structure;
KM gene typing; organ donation; bacteria identification; 16S rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX Homo sapiens.
OS WO200065088-A2.
PN 02-NOV-2000.
PD 20-APR-2000; 2000WO-EP003636.
XX 26-APR-1999; 99EP-00303215.
PR (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
PA Ulfendahl P, Wong K;
PI WPI; 2000-679677/66.
DR Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX Claim 14; Page 51; 66pp; English.
PS The present invention provides a method for identifying a set of
XX extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16S rRNA genes in
CC particular.
XX Sequence 25 BP; 3 A; 3 C; 3 G; 16 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 17; DB 1; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 4470 TTTTCTTTTCTTGTGCTGAGACA 4494
DB 1 TTTTCTTTTCTTGTGCTGAGACA 25

RESULT 1364
AAC95968
ID AAC95968 standard; DNA; 25 BP.
XX AAC95968;
AC AAC95968;
DT 26-FEB-2001 (first entry)
XX HLA HLA-B gene PCR primer #79.
DE

XX DNA sequence analysis; sequencing; protein structure;
KM gene typing; organ donation; bacteria identification; 16S rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX Homo sapiens.
OS WO200065088-A2.
PN 02-NOV-2000.
PD 20-APR-2000; 2000WO-EP003636.
XX 26-APR-1999; 99EP-00303215.
PR (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
PA Ulfendahl P, Wong K;
PI WPI; 2000-679677/66.
DR Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX Claim 14; Page 43; 66pp; English.
PS The present invention provides a method for identifying a set of
XX extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16S rRNA genes in
CC particular.
XX Sequence 25 BP; 2 A; 5 C; 1 G; 17 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 17; DB 1; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 4466 TTTTCTTTTCTTGTGCTGGA 4490
DB 1 TTTTCTTTTCTTGTGCTGGA 25

RESULT 1365
AAC96030
ID AAC96030 standard; DNA; 25 BP.
XX AAC96030;
AC AAC96030;
DT 26-FEB-2001 (first entry)
DE HLA HLA-C gene PCR primer #42.
XX DNA sequence analysis; sequencing; protein structure;
KM gene typing; organ donation; bacteria identification; 16S rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX Homo sapiens.
OS WO200065088-A2.
PN 02-NOV-2000.
PD 20-APR-2000; 2000WO-EP003636.
XX 26-APR-1999; 99EP-00303215.
PR (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
PA

PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
XX classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
XX
PS Claim 14; Page 44; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16S rRNA genes in
CC particular.
XX
SQ Sequence 25 BP; 3 A; 2 C; 6 G; 14 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 17; DB 1; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 4473 TTTTCTTTTCTGCTTGAGACATGG 4497
DB 1 TTTTCTTTTCTGCTTGAGACATGG 25
XX
RESULT 1366
AAC96199
ID AAC96199 standard; DNA; 25 BP.
XX
AC AAC96199;
XX
DT 26-FEB-2001 (first entry)
XX
DE 16S rRNA gene PCR primer #166.
XX
XX DNA sequence analysis; sequencing; protein structure; protein structure;
XX gene typing; organ donation; bacteria identification; 16S rRNA; HLA;
XX human leukocyte antigen; PCR primer; 8S.
XX
OS Homo sapiens.
XX
XX WO200065088-A2.
XX
XX 02-NOV-2000.
XX
XX 20-APR-2000; 2000WO-EP003636.
XX
XX 26-APR-1999; 99EP-00303215.
XX
XX (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
XX Ulfendahl P, Wong K;
XX
XX WPI; 2000-679677/66.
XX
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
XX
PS Claim 14; Page 47; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16S rRNA genes in

CC particular
XX
SQ Sequence 25 BP; 3 A; 6 C; 2 G; 14 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 17; DB 1; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 4470 TTTTCTTTTCTGCTTGAGACA 4494
DB 1 TTTTCTTTTCTGCTTGAGACA 25
XX
RESULT 1367
AAC95820
ID AAC95820 standard; DNA; 25 BP.
XX
XX AAC95820;
XX
DT 26-FEB-2001 (first entry)
XX
XX
XX HLA DRB345 gene PCR primer #20.
XX
XX
XX DNA sequence analysis; sequencing; protein structure; protein structure;
XX gene typing; organ donation; bacteria identification; 16S rRNA; HLA;
XX human leukocyte antigen; PCR primer; 8S.
XX
XX Homo sapiens.
XX
XX WO200065088-A2.
XX
XX 02-NOV-2000.
XX
XX 20-APR-2000; 2000WO-EP003636.
XX
XX 26-APR-1999; 99EP-00303215.
XX
XX (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
XX Ulfendahl P, Wong K;
XX
XX WPI; 2000-679677/66.
XX
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
XX
PS Claim 14; Page 40; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16S rRNA genes in
CC particular.
XX
XX
SQ Sequence 25 BP; 2 A; 5 C; 3 G; 15 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 17; DB 1; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 4472 TTTTCTTTTCTGCTTGAGACATG 4496
DB 1 TTTTCTTTTCTGCTTGAGACATG 25
XX
RESULT 1368
AAC95660
ID AAC95660 standard; DNA; 25 BP.
XX

```

AC AAC95660;
XX
XX DT 26-FEB-2001 (first entry)
XX
XX DE HLA DPA1 gene PCR primer #5.
XX
XX DNA sequence analysis; sequencing; protein sequence; protein structure;
XX KW gene typing; organ donation; bacteria identification; 16S rRNA; HLA;
XX KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
XX WO200065088-A2.
XX
XX PD 02-NOV-2000.
XX
XX PF 20-APR-2000; 2000WO-EP003636.
XX
XX PR 26-APR-1999; 99EP-00303215.
XX
XX PA (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
XX Ulfendahl P, Wong K;
XX
XX WPI; 2000-679677/66.
XX
XX PT Identifying extendible primers for use in identification, or
XX PT classification of a nucleic acid of an organism, allele or gene such as
XX PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
XX PT specific length.
XX
XX PS Claim 14; Page 37; 66pp; English.
XX
XX CC The present invention provides a method for identifying a set of
XX CC extendible primers which can be used in the identification, typing and
XX CC classification of genes. This can then be used to predict protein
XX CC sequence and structure, in organ donation to match the organ with the
XX CC receiver, and to identify bacteria in a sample. The method can be used to
XX CC type the human leukocyte antigen genes (HLA) and 16S RNA genes in
XX CC particular
XX
SQ Sequence 25 BP; 4 A; 4 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 17; DB 1; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matrix 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0.

Cy 4470 TTTTTCCTTGCTGAGACA 4494
Db 1 TTTTTCCTTGCTGAGACC 25

RESULT 1369
AAC96480
AAC96480 standard; DNA; 25 BP.
XX
XX AAC96480;
XX AC
XX XX.
XX DT 26-FEB-2001 (first entry)
XX
XX HTL DOB1 gene PCR primer #32.
XX
XX DNA sequence analysis; sequencing; protein sequence; protein structure;
XX KW gene typing; organ donation; bacteria identification; 16S rRNA; HLA;
XX KW human leukocyte antigen; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200065088-A2.
XX
XX PN 02-NOV-2000.
XX
XX PD 20-APR-2000; 2000WO-EP003636.
XX
XX PF

```

PR 26-APR-1999; 99EP-00303215.
 XX (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
 XX
 XX
 PI Ulfendahl P, Wong K;
 XX
 DR WPI; 2000-679677/66.
 XX
 PT Identifying extendible primers for use in identification, or
 PT classification of a nucleic acid of an organism, allele or gene such as
 PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
 PT specific length.
 XX
 PS
 CC Claim 14; Page 52; 66pp; English.
 CC
 CC The present invention provides a method for identifying a set of
 CC extendible primers which can be used in the identification, typing and
 CC classification of genes. This can then be used to predict protein
 CC sequence and structure, in organ donation to match the organ with the
 CC receiver, and to identify bacteria in a sample. The method can be used to
 CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
 CC particular
 CC
 SQ Sequence 25 BP; 0 A; 4 C; 3 G; 18 T; 0 U; 0 Other;
 Query Match 0.2%; Score 17; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0
 QY 4471 TTTT TTTT TTTT TTTT GCT 4487
 |||||
 Db 1 TTTT TTTT TTTT GCT 17
 |||||
 RESULT 1370
 AAC96050
 ID AAC96050 standard; DNA; 25 BP.
 XX
 AC AAC96050;
 XX
 DT 26-FEB-2001 (first entry)
 XX
 DE 16s rRNA gene PCR primer #17.
 XX
 KW DNA sequence analysis; sequencing; protein sequence; protein structure;
 KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
 KW human leukocyte antigen; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200065088-A2.
 XX
 PD 02-NOV-2000.
 XX
 PF 20-APR-2000; 2000WO-EP003636.
 XX
 PR 26-APR-1999; 99EP-00303215.
 XX
 PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
 XX
 PI Ulfendahl P, Wong K;
 XX
 DR WPI; 2000-679677/66.
 XX
 PT Identifying extendible primers for use in identification, or
 PT classification of a nucleic acid of an organism, allele or gene such as
 PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
 PT specific length.
 XX
 PS
 CC Claim 14; Page 44; 66pp; English.
 CC
 CC The present invention provides a method for identifying a set of

CC extendible primers which can be used in the identification, typing and
 CC classification of genes. This can then be used to predict protein
 CC sequence and structure, in organ donation to match the organ with the
 CC receiver, and to identify bacteria in a sample. The method can be used to
 CC type the human leukocyte antigen genes (HLA) and 16S rRNA genes in
 CC particular

XX Sequence 25 BP; 3 A; 3 C; 5 G; 14 T; 0 U; 0 Other;

Query Match 0.2%; Score 17; DB 1; Length 25;

Best Local Similarity 80.0%; Pred. No. 1.2e+03;

Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4472 TTTTCTTTTGTCTTGAGACATG 4496

Db 1 TTTTCTTTTGTCTTGAGACATG 25

RESULT 1371

1D AAC96075 standard; DNA; 25 BP.

XX AAC96075;

DT 26-FEB-2001 (first entry)

XX 16S rRNA gene PCR primer #42.

XX DNA sequence analysis; sequencing; protein sequence; protein structure;

KW gene typing; organ donation; bacteria identification; 16S rRNA; HLA;

KW human leukocyte antigen; PCR primer; ss.

OS Homo sapiens.

PN WO200065088-A2.

PD 02-NOV-2000.

PF 20-APR-2000; 2000WO-EP003636.

PR 26-APR-1999; 99EP-00303215.

PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.

PI Ulendahl P, Wong K;

DR WPI; 2000-679677/66.

XX Identifying extendible primers for use in identification, or

PT classification of a nucleic acid of an organism, allele or gene such as

PS Claim 14; Page 45; 66pp; English.

XX The present invention provides a method for identifying a set of

CC extendible primers which can be used in the identification, typing and

CC classification of genes. This can then be used to predict protein

CC sequence and structure, in organ donation to match the organ with the

CC receiver, and to identify bacteria in a sample. The method can be used to

CC type the human leukocyte antigen genes (HLA) and 16S rRNA genes in

XX particular

SQ Sequence 25 BP; 3 A; 2 C; 4 G; 16 T; 0 U; 0 Other;

Qy 4471 TTTTCTTTTGTCTTGAGACAT 4495

Db 1 TTTTCTTTTGTCTTGAGACAT 25

RESULT 1372

1D AAC96531 standard; DNA; 25 BP.

XX AAC96531;

DT 26-FEB-2001 (first entry)

XX HLA DRB345 gene PCR primer #2.

KW DNA sequence analysis; sequencing; protein sequence; protein structure;

KW gene typing; organ donation; bacteria identification; 16S rRNA; HLA;

KW human leukocyte antigen; PCR primer; ss.

OS Homo sapiens.

PN WO200065088-A2.

PD 02-NOV-2000.

PF 20-APR-2000; 2000WO-EP003636.

PR 26-APR-1999; 99EP-00303215.

PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.

PI Ulendahl P, Wong K;

DR WPI; 2000-679677/66.

XX Identifying extendible primers for use in identification, or

PT classification of a nucleic acid of an organism, allele or gene such as

PS Claim 14; Page 53; 66pp; English.

XX The present invention provides a method for identifying a set of

CC extendible primers which can be used in the identification, typing and

CC classification of genes. This can then be used to predict protein

CC sequence and structure, in organ donation to match the organ with the

CC receiver, and to identify bacteria in a sample. The method can be used to

CC type the human leukocyte antigen genes (HLA) and 16S rRNA genes in

XX particular

SQ Sequence 25 BP; 3 A; 2 C; 5 G; 15 T; 0 U; 0 Other;

Qy 4470 TTTTCTTTTGTCTTGAGACA 4494

Db 1 TTTTCTTTTGTCTTGAGACA 25

RESULT 1373

1D AAC96600 standard; DNA; 25 BP.

XX AAC96600;

DT 26-FEB-2001 (first entry)

XX HLA DRB345 gene PCR primer #71.

KW DNA sequence analysis; sequencing; protein sequence; protein structure;

KW gene typing; organ donation; bacteria identification; 16S rRNA; HLA;

KW human leukocyte antigen; PCR primer; ss.

OS Homo sapiens.

```
PN WO200065088-A2.
XX
XX 02-NOV-2000.
XX
XX 20-APR-2000; 2000WO-EP003636.
XX
XX 26-APR-1999; 99EP-00303215.
XX
XX (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
XX Ulfendahl P, Wong K;
XX
XX WPI; 2000-679677/66.
XX
XX Identifying extendible primers for use in identification, or
XX classification of a nucleic acid of an organism, allele or gene such as
XX class 1/2 HLA comprises identifying all possible nucleotide sequences of
XX specific length.
XX
XX Claim 14; Page 54; 66pp; English.
XX
XX The present invention provides a method for identifying a set of
XX extendible primers which can be used in the identification, typing and
XX classification of genes. This can then be used to predict protein
XX sequence and structure, in organ donation to match the organ with the
XX receiver, and to identify bacteria in a sample. The method can be used to
XX type the human leukocyte antigen genes (HLA) and 16S rRNA genes in
XX particular
XX
XX Sequence 25 BP; 3 A; 3 C; 4 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 17; DB 1; Length 25;
XX Best Local Similarity 80.0%; Pred. No. 1.2e+03;
XX Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Oy 4470 TTTT TTTT TTTT TTTT TTTT GCTT GCTT GAGACA 4494
Db 1 TTTT TTTT TTTT TTTT TTTT GCTT GCTT GATAGA 25

RESULT 1374
ABN13475/c
ID ABN13475 standard; DNA; 25 BP.
XX
XX AC ABN13475;
XX
XX 29-MAY-2002 (first entry)
XX
XX Human GDMLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:13467.
XX
XX Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
XX muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
XX skeletal muscle disorder; amplicon; screening; ss.
XX
XX Homo sapiens.
XX
XX WO200192524-A2.
XX
XX 06-DEC-2001.
XX
XX 25-MAY-2001; 2001WO-US016981.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX
XX 21-SEP-2000; 2000US-0234687P.
XX
XX 27-SEP-2000; 2000US-0236359P.
XX
XX 04-OCT-2000; 2000GB-00024263.
XX
XX 30-JAN-2001; 2001WO-US000661.
XX
XX 30-JAN-2001; 2001WO-US000662.
XX
XX 30-JAN-2001; 2001WO-US000663.
XX
XX 30-JAN-2001; 2001WO-US000664.
XX
XX 30-JAN-2001; 2001WO-US000665.
XX
XX 30-JAN-2001; 2001WO-US000666.
XX
XX 30-JAN-2001; 2001WO-US000667.
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PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
XX WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognise hGDMLP-1 proteins,
XX or as specific biomolecule capture probes for surface-enhanced laser
XX desorption/ionization, comprises human myosin-like protein hGDMLP-1.
XX
XX Disclosure; SEQ ID NO 13467; 21pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
XX protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
XX 1 can be used in gene therapy and vaccine production. The hGDMLP-1
XX nucleic acids can be used as probes to detect, characterise and quantify
XX hGDMLP-1 nucleic acids in samples, as amplification substrates, to
XX provide initial substrates for the recombinant engineering of hGDMLP-1
XX protein variants having desired phenotypic improvements, and for
XX expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
XX used as immunogens to raise antibodies that specifically recognise hGDMLP
XX -1 proteins, as standards in assays used to determine the concentration
XX and/or amount specifically of hGDMLP proteins, as specific biomolecule
XX capture probes for surface-enhanced laser desorption/ionisation, as
XX therapeutic supplement in patients having specific deficiency in hGDMLP-1
XX production, and in vaccines or for replacement therapy. The
XX polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
XX disorder associated with the expression of hGDMLP-1, in particular heart
XX and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
XX The present sequence represents an oligomer used in the screening of the
XX hGDMLP-1 sequence in the exemplification of the present invention. N.B.
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequence
XX
XX Sequence 25 BP; 7 A; 5 C; 8 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 17; DB 1; Length 25;
XX Best Local Similarity 80.0%; Pred. No. 1.2e+03;
XX Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Oy 1749 GCTG CAGCTCAT TTTGTCAT CCG 1773
Db 25 GCATCAGCTCAT TCGAGTCAT CCG 1

RESULT 1375
ABN05306
ID ABN05306 standard; DNA; 25 BP.
XX
XX AC ABN05306;
XX
XX 29-MAY-2002 (first entry)
XX
XX Human GDMLP-1 25-mer scanning SEQ ID NO:4 sequence SEQ ID NO:5298.
XX
XX Human; genome-derived myosin-like protein 1; hGDMLP-1; heart;
XX muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
XX skeletal muscle disorder; amplicon; screening; ss.
XX
XX Homo sapiens.
XX
XX WO200192524-A2.
XX
XX 06-DEC-2001.
XX
XX 25-MAY-2001; 2001WO-US016981.
XX
```

PR 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 05-FEB-2001; 2001US-0266860P.
 PA (ABOM-) ABOMICA INC.
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX WPI; 2002-179446/23.
 DR
 PR New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
 XX
 PS Disclosure; SEQ ID NO 5298; 214pp; English.
 XX
 CC The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
 CC nucleic acids can be used as probes to detect, characterise and quantify
 CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption/ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX
 SQ Sequence 25 BP; 5 A; 11 C; 5 G; 4 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 17; DB 1; Length 25;
 Best Local Similarity 80.0%; Pred. No. 1.2e+03;
 Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 2523 CCGTTTCACAGCAGATGAGCTCCAG 2547
 DB 1 CCGATCACAGCTGCTCAGCTCCAG 25
 RESULT 1376
 ABN05307
 ID ABN05307 standard; DNA; 25 BP.
 AC ABN05307;
 XX
 DT 29-MAY-2002 (first entry)
 XX
 DE Human GDMLP-1 25-mer scanning SEQ ID NO:4 sequence SEQ ID NO:5299.
 XX
 KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;

KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 OS Homo sapiens.
 PN WO200192524-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 25-MAY-2001; 2001WO-US016981.
 XX
 PR 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 05-FEB-2001; 2001US-0266860P.
 PA (ABOM-) ABOMICA INC.
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX WPI; 2002-179446/23.
 DR
 PR New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
 XX
 PS Disclosure; SEQ ID NO 5299; 214pp; English.
 XX
 CC The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
 CC nucleic acids can be used as probes to detect, characterise and quantify
 CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption/ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX
 SQ Sequence 25 BP; 6 A; 10 C; 5 G; 4 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 17; DB 1; Length 25;
 Best Local Similarity 80.0%; Pred. No. 1.2e+03;
 Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 2524 CCGTTTCACAGCAGATGAGCTCCAG 2548
 DB 1 CCGATCACAGCTGCTCAGCTCCAG 25

Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 828 CCTGCCATGTGGAGATGCTC 852
Db 1 CCTTACATGTGACGCTCTCTC 25

RESULT 1381
AB284413/c
AB284413 standard; DNA; 25 BP.

AB284413;
14-MAY-2003 (first entry)

Toxicologically relevant human PCR primer #1572.

Toxicologically relevant gene; toxicological response; PCR primer; ss.

Homo sapiens.
Synthetic.

MO2003016500-A2.

27-FEB-2003.

16-AUG-2002; 2002MO-US026514.

16-AUG-2001; 2001US-0313080P.

(PHASE-) PHASE-1 MOLECULAR TOXICOLOGY INC.

Nett RE, Dunn RT, Adkins K, Pickett GG, Kier LD, Schmeisler K;
Alen P;

WPI; 2003-268322/26.

Determining a toxicological response to an agent, useful for screening of drugs, comprises comparing the expression profile of one or more human toxic response genes to a reference gene expression profile indicative of toxicity.

Claim 1; Page 348; 455pp; English.

The present invention describes a method (M1) for determining a toxicological response to an agent, which comprises comparing the expression profile of one or more human toxic response genes to a reference gene expression profile indicative of toxicity, and so determining the presence of a toxic response to the agent. Also described: (1) an array comprising one or more polynucleotides selected from the genes corresponding to the partial sequences given in AB282842 to AB284764, or their fragments of at least 20 nucleotides, or homologues; and (2) determining if a gene putatively identified to be a toxic response gene plays a role on toxic response pathways by determining the expression profile of the gene after exposure of cells or a human subject to a known toxic pharmaceutical or industrial agent, comprising: (a) exposing cells to an agent or isolating cells from a human subject who was exposed to an agent; (b) obtaining the test gene expression profile for a putatively identified toxic response gene after exposure to a known toxic pharmaceutical or industrial agent; and (c) comparing the test profile to the expression profile of a gene with a similar function or comparing the test profile to the expression profile of that gene after exposure to other known toxic compounds. The methods are useful for predicting and determining toxicological responses on a cellular, organ or system level. The arrays comprising the human genes are useful for toxicological screening of drugs, pharmaceutical compounds and chemicals

Query Match 0.2%; Score 17; DB 1; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 6313 CTGGGCTACTGTGCTGGACTT 6337
Db 25 CTGGCCATATGTGTGGGATTT 1

RESULT 1382
ADB01140/c
ADB01140 standard; DNA; 25 BP.

ADB01140;
20-NOV-2003 (first entry)

Human MD23 scanning oligonucleotide SEQ ID 2126.

Cytosolic; immunostimulant; gene therapy; vaccine; human;
zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
developmental disorder; ss.

Homo sapiens.

EP1281758-A2.

05-FEB-2003.

30-JUL-2002; 2002EP-00016874.

02-AUG-2001; 2001US-00922181.

(AEOM-) AEOMICA INC.

Shannon M, Gu Y, Nguyen C;
WPI; 2003-423107/40.

New zinc finger-containing proteins and nucleic acids, useful in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MD23, MD24, MD27 or MD212, e.g. cancer.

Example 8; SEQ ID NO 2126; 103pp; English.

The present invention relates to novel human zinc finger-containing proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2, MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy, or in manufacturing a medicament for treating or preventing a disorder associated with decreased or increased expression or activity of MD23, MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic acids and proteins are also useful for diagnosing or monitoring a disease caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic acids can also be used as probes to detect and characterize gross alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are useful in constructing microarrays for measuring gene expression. The proteins are useful as therapeutic agents for gene therapy or as vaccines. The present sequence was used to illustrate the invention.

Sequence 25 BP; 4 A; 5 C; 13 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 17; DB 1; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 3382 CTCCTCCCGAGTCGACCCGCCA 3406
Db 25 CTCCTCCCGAGGCGCATCCCCA 1

RESULT 1383
ACT174658/c

ID AC174658 standard; DNA; 25 BP.
 AC AC174658;
 DT 14-OCT-2003 (first entry)
 DE Human microarray DNA oligonucleotide SEQ ID NO 74649.
 XX EST; ss; probe: expressed sequence tag; microarray; gene expression;
 KM genetic variation; biallelic marker; polymorphism; human;
 KW cross-species comparison.
 XX *
 OS Homo sapiens.
 XX US2003104410-A1.
 PN 05-JUN-2003.
 PD 15-MAR-2002; 2002US-00098263.
 PF 16-MAR-2001; 2001US-0276759P.
 PR (AFY-) AFFYMETRIX INC.
 PA Miltmann MP;
 XX WPI; 2003-567953/53.
 DR New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.
 PS Claim 1; SEQ ID NO 74649; 9pp; English.
 XX The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying biallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html
 CC XX
 SQ Sequence 25 BP; 11 A; 2 C; 6 G; 6 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 17; DB 1; Length 25;
 Best Local Similarity 80.0%; Pred. No. 1.2e+03;
 Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 4932 TGAGTACTCTCCCTTACTTTT 4956
 DB 25 TAAAGTACTCAACTTACTCTTT 1
 RESULT 1384
 AC15542
 ID AC15542 standard; DNA; 25 BP.
 XX

AC AC15542;
 XX 14-OCT-2003 (first entry)
 DT Human microarray DNA oligonucleotide SEQ ID NO 115523.
 DE EST; ss; probe: expressed sequence tag; microarray; gene expression;
 KM genetic variation; biallelic marker; polymorphism; human;
 KW cross-species comparison.
 XX *
 OS Homo sapiens.
 XX US2003104410-A1.
 PN 05-JUN-2003.
 PD 15-MAR-2002; 2002US-00098263.
 PF 16-MAR-2001; 2001US-0276759P.
 PR (AFY-) AFFYMETRIX INC.
 PA Miltmann MP;
 XX WPI; 2003-567953/53.
 DR New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.
 PS Claim 1; SEQ ID NO 115523; 9pp; English.
 XX The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying biallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html
 CC XX
 SQ Sequence 25 BP; 6 A; 6 C; 4 G; 9 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 17; DB 1; Length 25;
 Best Local Similarity 80.0%; Pred. No. 1.2e+03;
 Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 6605 ACGTTTCTTCCCATCAGGTGAA 6629
 DB 1 ACTTATTTCCTCAGGTGAA 25
 RESULT 1385
 AC19545/C
 ID AC19545 standard; DNA; 25 BP.
 XX AC19545;
 XX

DT 14-OCT-2003 (first entry)
 XX Human microarray DNA oligonucleotide SEQ ID NO 99536.
 DE EST; sg; probe; expressed sequence tag; microarray; gene expression;
 XX genetic variation; diallelic marker; polymorphism; human;
 KM cross-species comparison.
 XX Homo sapiens.
 OS
 XX US2003104410-A1.
 XX 05-JUN-2003.
 XX 15-MAR-2002; 2002US-00098263.
 XX 16-MAR-2001; 2001US-0276759P.
 XX (AFFY-) AFFYMETRIX INC.
 XX Miltmann MP;
 XX WPI, 2003-567953/53.
 DR New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.
 XX
 XX Claim 1; SEQ ID NO 99536; 9pp; English.
 PS
 XX The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying diallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html
 XX
 XX Sequence 25 BP; 12 A; 5 C; 7 G; 1 T; 0 U; 0 Other;
 SQ
 Query Match 0.2%; Score 17; DB 1; Length 25;
 Best Local Similarity 80.0%; Pred. No. 1.2e+03;
 Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Oy 5688 TGTACCACTGTTTGGCTTCTCTTT 5712
 Db 25 TGCACCTCTGTGTGCTGTCTTT 1
 RESULT 1386
 ACK31032
 ID ACK31032 standard; DNA; 25 BP.
 XX
 XX AC31032;
 XX 14-OCT-2003 (first entry)
 XX

DE Human microarray DNA oligonucleotide SEQ ID NO 131013.
 XX EST; sg; probe; expressed sequence tag; microarray; gene expression;
 KM genetic variation; diallelic marker; polymorphism; human;
 KM cross-species comparison.
 XX Homo sapiens.
 OS
 XX US2003104410-A1.
 XX 05-JUN-2003.
 XX 15-MAR-2002; 2002US-00098263.
 XX 16-MAR-2001; 2001US-0276759P.
 XX (AFFY-) AFFYMETRIX INC.
 XX Miltmann MP;
 XX WPI, 2003-567953/53.
 DR New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.
 XX
 XX Claim 1; SEQ ID NO 131013; 9pp; English.
 PS
 XX The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying diallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html
 XX
 XX Sequence 25 BP; 11 A; 5 C; 4 G; 5 T; 0 U; 0 Other;
 SQ
 Query Match 0.2%; Score 17; DB 1; Length 25;
 Best Local Similarity 80.0%; Pred. No. 1.2e+03;
 Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Oy 7056 AAGTAAAGACCTTGTGATGCAC 7080
 Db 1 AAGTAAAGACCTTGTGAAACAC 25
 RESULT 1387
 AC174659/c
 ID AC174659 standard; DNA; 25 BP.
 XX
 XX AC174659;
 XX 14-OCT-2003 (first entry)
 XX Human microarray DNA oligonucleotide SEQ ID NO 74650.
 XX

KW EST; ss; probe: expressed sequence tag; microarray; gene expression;
 KW genetic variation; biallelic marker; polymorphism; human;
 KW cross-species comparison.
 OS Homo sapiens.
 XX
 XX US2003104410-A1.
 XX
 XX 05-JUN-2003.
 PD
 XX 15-MAR-2002; 2002US-00098263.
 XX
 XX 16-MAR-2001; 2001US-0276759P.
 PR
 XX (AFPMETRIX INC.
 XX
 XX Miltmann MP;
 XX
 XX WPI; 2003-567953/53.
 DR
 XX New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.
 PS
 XX Claim 1; SEQ ID NO 74650; 9pp; English.
 XX
 XX The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridization to a DNA library,
 CC in analysis of genetic variation or in hybridization of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridizing at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridization. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying biallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in in situ hybridization, in Southern, Northern or dot-
 CC blot hybridization to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html
 CC
 XX
 SQ Sequence 25 BP; 12 A; 2 C; 6 G; 5 T; 0 U; 0 Other;
 Query Match 0.2%; Score 17; DB 1; Length 25;
 Best Local Similarity 80.0%; Pred. No. 1.2e+03;
 Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

KW Cross-species comparison.
 XX
 XX Homo sapiens.
 OS
 XX
 XX US2003104410-A1.
 XX
 XX 05-JUN-2003.
 PD
 XX 15-MAR-2002; 2002US-00098263.
 XX
 XX 16-MAR-2001; 2001US-0276759P.
 PR
 XX (AFPMETRIX INC.
 XX
 XX Miltmann MP;
 XX
 XX WPI; 2003-567953/53.
 DR
 XX New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.
 PS
 XX Claim 1; SEQ ID NO 6431; 9pp; English.
 XX
 XX The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridization to a DNA library,
 CC in analysis of genetic variation or in hybridization of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridizing at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridization. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying biallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in in situ hybridization, in Southern, Northern or dot-
 CC blot hybridization to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html
 CC
 XX
 SQ Sequence 25 BP; 5 A; 7 C; 6 G; 7 T; 0 U; 0 Other;
 Query Match 0.2%; Score 17; DB 1; Length 25;
 Best Local Similarity 80.0%; Pred. No. 1.2e+03;
 Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

XX	Homo sapiens.
XX	US2003104410-A1.
XX	05-JUN-2003.
XX	15-MAR-2002; 2002US-00098263.
XX	16-MAR-2001; 2001US-0276755P.
XX	(AFYY-) AFFYMETRIX INC.
XX	Mitmann MP;
XX	WPI; 2003-567953/53.
XX	New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
XX	Claim 1; SEQ ID NO 69192; 9pp; English.
PS	The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying allelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern or dot-blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' terminl of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html
SQ	Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 U; 0 Other;
Oy	Query Match 0.2%; Score 17; DB 1; Length 25; Best Local Similarity 80.0%; Pred. No. 1.2e+03; Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
25	CAATAGGAAAGAATAATTCTTT 7125 CAATAGGAAAGACAAATTAACCTT 1
ID	RESULT 1390 ACI13534/C ACI13534 standard; DNA; 25 BP. ACI13534; 13-OCT-2003 (first entry)
DE	Human microarray DNA oligonucleotide SEQ ID NO 13525.
KM	EST; ss; probe; expressed sequence tag; microarray; Gene expression; KM genetic variation; biallelic marker; polymorphism; human; cross-species comparison.
OS	Homo sapiens.

PN	US2003104410-A1.
XX	
PD	05-JUN-2003.
XX	
PP	15-MAR-2002; 2002US-00098263.
XX	
PR	16-MAR-2001; 2001US-0276759P.
XX	
PA	(AFFY-) AFFYMETRIX INC.
XX	
PI	Miltmann MP;
XX	
DR	WPI; 2003-567953/53.
XX	
PT	New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
XX	
PS	Claim 1; SEQ ID NO 13525; 9pp; English.
XX	
CC	The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying diallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern or dot-blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html
CC	
CC	Sequence 25 BP; 6 A; 8 C; 8 G; 3 T; 0 U; 0 Other;
XX	
SC	
SC	Query Match 0.2%; Score 17; DB 1; Length 25;
SC	Best Local Similarity 80.0%; Pred. No. 1.2e+03;
SC	Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY	4185 GTGGTTATCGCCCAAGATGGGGTTC 4209
DB	25 GTCTCGTCGCTCCAGATCGGGTC 1
XX	
XX	RESULT 1391
XX	ACK26873/c
XX	ID ACK26873 standard; DNA; 25 BP.
XX	
XX	ACK26873;
XX	
DT	14-OCT-2003 (first entry)
XX	
DE	Human microarray DNA oligonucleotide SEQ ID NO 126854.
XX	
KW	EST; ss; probe; expressed sequence tag; microarray; gene expression;
XX	genetic variation; diallelic marker; polymorphism; human;
XX	cross-species comparison.
OS	Homo sapiens.
XX	
XX	US2003104410-A1.
XX	

PD 05-JUN-2003.
 XX
 PF 15-MAR-2002; 2002US-00098263.
 XX
 PR 16-MAR-2001; 2001US-0276759P.
 XX
 PA (AFFY-) AFFYMETRIX INC.
 XX
 PI Miltmann MP;
 XX
 DR WPI; 2003-567953/53.
 XX
 PT New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.
 XX
 PS Claim 1; SEQ ID NO 126854; 9pp; English.
 XX
 CC The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying biallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html
 XX
 SQ Sequence 25 BP; 8 A; 6 C; 5 G; 6 T; 0 U; 0 Other;
 Query Match 0.2%; Score 17; DB 1; Length 25;
 Best Local Similarity 80.0%; Pred. No. 1.2e+03;
 Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 2265 CATTCTGATGCTGCATCAACTG 2289
 DB 25 CATTCTGATGCTGCATCAACTG 1
 RESULT 1392
 ACI98785
 ID ACT198785 standard; DNA; 25 BP.
 XX
 AC ACI98785;
 XX
 DT 14-OCT-2003 (first entry)
 XX
 DE Human microarray DNA oligonucleotide SEQ ID NO 98776.
 XX
 KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
 KW genetic variation; biallelic marker; polymorphism; human;
 KW cross-species comparison.
 XX
 OS Homo sapiens.
 XX
 PN US2003104410-A1.
 XX
 PD 05-JUN-2003.
 XX

PF 15-MAR-2002; 2002US-00098263.
 XX
 PR 16-MAR-2001; 2001US-0276759P.
 XX
 PA (AFFY-) AFFYMETRIX INC.
 XX
 PI Miltmann MP;
 XX
 DR WPI; 2003-567953/53.
 XX
 PT New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.
 XX
 PS Claim 1; SEQ ID NO 98776; 9pp; English.
 XX
 CC The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying biallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html
 XX
 SQ Sequence 25 BP; 4 A; 9 C; 7 G; 5 T; 0 U; 0 Other;
 Query Match 0.2%; Score 17; DB 1; Length 25;
 Best Local Similarity 80.0%; Pred. No. 1.2e+03;
 Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 5028 GGAGCGAGCTCACTGAGAGCTTAC 5052
 DB 1 GGAGCTCGCTTCTCTGGAGGCTTAC 25
 RESULT 1393
 ACK31033
 ID ACK31033 standard; DNA; 25 BP.
 XX
 AC ACK31033;
 XX
 DT 14-OCT-2003 (first entry)
 XX
 DE Human microarray DNA oligonucleotide SEQ ID NO 131014.
 XX
 KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
 KW genetic variation; biallelic marker; polymorphism; human;
 KW cross-species comparison.
 XX
 OS Homo sapiens.
 XX
 PN US2003104410-A1.
 XX
 PD 05-JUN-2003.
 XX
 PF 15-MAR-2002; 2002US-00098263.
 XX

PR 16-MAR-2001; 2001US-0276759P.
 XX (AFVY-) AFFYMETRIX INC.
 XX
 XX Miltmann MP;
 XX WPI; 2003-567953/53.
 XX
 PT New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.
 XX
 PS Claim 1; SEQ ID NO 131014; 9pp; English.
 XX
 CC The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridization to a DNA library,
 CC in analysis of genetic variation or in hybridization of tag-labeled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridizing at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridization. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying allelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in in situ hybridization, in Southern, Northern or dot-
 CC blot hybridization to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' terminus of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html
 XX
 SQ Sequence 25 BP; 11 A; 4 C; 5 G; 5 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 17; DB 1; Length 25;
 Best Local Similarity 80.0%; Pred. No. 1.2e+03;
 Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 XX
 QY 7056 AAGTAAGACATTGTGTGATGCAC 7080
 DB 1 AAGTAAGACGCTGCTTGAACAC 25
 XX
 RESULT 1394
 ACH53795/C
 ID ACH53795 standard; DNA; 25 BP.
 XX
 AC ACH53795;
 XX
 DT 16-OCT-2003 (first entry)
 XX
 DE DNA target sequence #2931 useful in array for genetic analyses.
 XX
 KW Gene expression analysis; array; hybridization; genetic variation;
 KW tag-labelled compound; gene family; in situ hybridization;
 KW library screening; Southern hybridization; northern hybridization;
 KW dot-blot hybridization; gene sequence; mutation detection;
 KW target sequence; probe; PCR; primer; ss.
 XX
 OS Unidentified.
 XX
 US2003082596-A1.
 XX
 PD 01-MAY-2003.
 XX
 PF 08-AUG-2002; 2002US-00215112.
 XX

PR 08-AUG-2001; 2001US-0311040P.
 XX (MITT/) MITTMANN M.
 XX
 XX Miltmann M;
 XX WPI; 2003-576608/54.
 XX
 PT New probe array useful e.g. for monitoring gene expression levels, for
 PT analyzing genetic variations, or for hybridizing tag-labeled compounds,
 PT comprising multiple nucleic acid probes.
 XX
 PS Claim 1; SEQ ID NO 2931; 9pp; English.
 XX
 CC The present invention relates to nucleic acid sequences that are
 CC complementary to particular genes, and can be used as probes for a
 CC variety of analyses such as gene expression analysis. Each probe
 CC comprises 9 or more consecutive nucleotides from at least one of 14936
 CC nucleotide sequences defined in the patent, or their perfect sense match,
 CC sense mismatch, antisense match or antisense mismatch oligonucleotides.
 CC The probes may be used in an array comprising at least 10 distinct
 CC nucleic acid probes. The array is useful in monitoring gene expression
 CC levels by hybridization to a DNA library, in analyzing genetic
 CC variations, and in hybridizing tag-labeled compounds. The probes are
 CC useful for identifying family members of a gene. The probes are also
 CC useful in in situ hybridizations, in screening cDNA or genomic libraries
 CC (or derived subclones) for additional clones containing segments of DNA
 CC that have been previously isolated and sequenced, in Southern, northern,
 CC or dot-blot hybridization of genomic DNA to identify or detect the
 CC sequence of any gene or detect specific mutations in any gene, and in
 CC mapping the 5' terminus of mRNA molecules by primer extensions. The
 CC nucleic acid sequences of the invention are also useful as PCR primers.
 CC The invention provides a large collection of nucleic acid sequences
 CC complementary to particular genes with a wide range of analytical uses.
 CC ACH5085-ACH6260 represent the target sequences of the invention. Note:
 CC The sequence data for this patent was obtained in electronic format
 CC directly from the USPTO web site at seqdata.uspto.gov/patseqIDentity.html
 XX
 SQ Sequence 25 BP; 5 A; 10 C; 3 G; 7 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 17; DB 1; Length 25;
 Best Local Similarity 80.0%; Pred. No. 1.2e+03;
 Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 XX
 QY 1511 GGACATCGGGGGAACAGTTCTA 1535
 DB 25 GGCACTGCTCGAGAACAGTTCA 1
 XX
 RESULT 1395
 ACH53669/C
 ID ACH53669 standard; DNA; 25 BP.
 XX
 AC ACH53669;
 XX
 DT 16-OCT-2003 (first entry)
 XX
 DE DNA target sequence #2805 useful in array for genetic analyses.
 XX
 KW Gene expression analysis; array; hybridization; genetic variation;
 KW tag-labelled compound; gene family; in situ hybridization;
 KW library screening; Southern hybridization; northern hybridization;
 KW dot-blot hybridization; gene sequence; mutation detection;
 KW target sequence; probe; PCR; primer; ss.
 XX
 OS Unidentified.
 XX
 US2003082596-A1.
 XX
 PD 01-MAY-2003.
 XX
 PF 08-AUG-2002; 2002US-00215112.
 XX


```

PR 08-AUG-2001; 2001US-0311040P.
XX
PA (MITT/) MITTMANN M.
XX
PI Miltmann M;
XX
DR WPI; 2003-576608/54.
XX
PT New probe array useful e.g. for monitoring gene expression levels, for
PT analyzing nucleic acid variations, or for hybridizing tag-labeled compounds,
PT comprises multiple nucleic acid probes.
XX
PS Claim 1; SEQ ID NO 2805; 9pp; English.
XX
CC The present invention relates to nucleic acid sequences that are
CC complementary to particular genes, and can be used as probes for a
CC variety of analyses such as gene expression analysis. Each probe
CC comprises 9 or more consecutive nucleotides from at least one of 14936
CC nucleotide sequences defined in the patent, or their perfect sense match,
CC sense mismatch, antisense match or antisense mismatch oligonucleotides.
CC The probes may be used in an array comprising at least 10 distinct
CC nucleic acid probes. The array is useful in monitoring gene expression
CC levels by hybridisation to a DNA library, in analysing genetic
CC variations, and in hybridising tag-labelled compounds. The probes are
CC useful for identifying family members of a gene. The probes are also
CC useful in situ hybridisations, in screening cDNA or genomic libraries
CC (or derived subclones) for additional clones containing segments of DNA
CC that have been previously isolated and sequenced, in Southern, northern,
CC or dot-blot hybridisation of genomic DNA to identify or detect the
CC sequence of any gene or detect specific mutations in any gene, and in
CC mapping the 5' termini of mRNA molecules by primer extensions. The
CC nucleic acid sequences of the invention are also useful as PCR primers.
CC The invention provides a large collection of nucleic acid sequences
CC complementary to particular genes with a wide range of analytical uses.
CC ACH50865-ACH65260 represent the target sequences of the invention. Note:
CC The sequence data for this patent was obtained in electronic format
CC directly from the USPTO web site at seqdata.uspto.gov/patidIDentry.html
XX
SQ Sequence 25 BP; 6 A; 10 C; 3 G; 6 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 17; DB 1; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
QY 1511 GGGACATCGCGGGGAAACAGTTCTA 1535
DB 25 GGGAGTTGCTGCTGCAACAGTTGCA 1
XX
RESULT 1396
AAQ47178 ID AAQ47178 standard; DNA; 26 BP.
XX
AC AAQ47178;
XX
DT 25-MAR-2003 (revised)
DT 25-JAN-1994 (first entry)
XX
DE MHC DR A intron binding oligomer Tcon.
XX
KM MHC; major histocompatibility complex; class II; control oligomers; DR A;
KM transplacation; antigen; autoimmune disease; ss.
XX
OS Synthetic.
XX
PN WO9314769-A1.
XX
PD 05-AUG-1993.
XX
PF 29-JAN-1993; 93WO-US000797.
XX
PR 31-JAN-1992; 92US-00830427.
PR 14-SEP-1992; 92US-00944868.

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XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Weiss TL, Garovoy MR, Hunt A, Huey B, Tam S;
XX
DR WPI; 1993-258367/32.
XX
PT Depletion of transplacation antigens in donor cells - using anti-sense
PT or triplex-forming oligonucleotide(s), used for treating auto-immune
PT disease and in transplants.
XX
PS Example; Page 22; 71pp; English.
XX
CC The sequences given in AAQ47176-77 represent triplex forming oligo-
CC nucleotides which bind to the mRNA sequence of the MHC class II locus DR
CC A structural gene at positions 851-876. The sequences given in AAQ47178-
CC 80 represent control oligomers which contain base compositions similar to
CC that around this DR A region but not containing the correct sequences. DR
CC A is a transplacation antigen. Binding of this sequence to the DR A gene
CC inhibits antigen production. This method may be used for treating
CC individuals with autoimmune disease, characterised by dysfunctional
CC expression of a transplacation antigen. It may also be used to produce
CC cells which are more easily transplanted into a recipient. (Updated on 25
CC -MAR-2003 to correct PN field.)
XX
SQ Sequence 26 BP; 0 A; 0 C; 4 G; 22 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 17; DB 1; Length 26;
Best Local Similarity 80.0%; Pred. No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
QY 4459 TGGACCTTTTCTTTTCTTTTCTTTT 4483
DB 2 TTGCTGTTTGTGTTTCTTTTCTTTT 26
XX
RESULT 1397
AAK89364 ID AAK89364 standard; DNA; 26 BP.
XX
AC AAK89364;
XX
DT 24-SEP-1999 (first entry)
XX
DE Chromosomal binding site for p53 protein (Seq ID No: 10 of US5936079).
XX
KM Cell growth inhibition; chromosomal binding site; p53 protein;
KM cellular replication; cancer; ss.
XX
OS Synthetic.
XX
PN US5936079-A.
XX
PD 10-AUG-1999.
XX
PF 15-AUG-1994; 94US-00291011.
XX
PR 06-APR-1992; 92US-00863661.
PR 01-MAY-1992; 92US-00879618.
XX
PA (ALTO-) ALTON OCHSNER MEDICAL FOUND.
XX
KM Cook J, Re R;
XX
PI WPI; 1999-457628/38.
XX
DR WPI; 1999-457628/38.
XX
PT New oligonucleotide useful for treating and preventing cancer.
XX
PS Example 1; Col 12; 12pp; English.
XX
CC The invention provides methods for inhibiting cell growth by providing a
CC growing cell with an oligonucleotide capable of binding to a chromosomal
CC binding site for p53 protein. Sequences AAK89362, AAK89363 and AAK89366

```

CC represent oligonucleotides that are derived from the sequence AAX89355.
 CC The oligonucleotides are used for inhibiting mammalian cellular
 CC replication and the treatment and prevention of cancer in a human. The
 CC oligonucleotides can be used in vitro to inhibit the growth of cultured
 CC mammalian cells e.g. human, monkey, mouse, rat and hamster cells which
 CC have chromosomal DNA encoding a binding site for p53 protein. Sequences
 CC AAX89355-366 represent oligonucleotides that are based on chromosomal
 CC binding sites for p53 protein
 XX
 SQ Sequence 26 BP; 0 A; 7 C; 0 G; 19 T; 0 U; 0 Other;
 Query Match 0.2%; Score 17; DB 1; Length 26;
 Best Local Similarity 80.0%; Pred. No. 1.3e+03;
 Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 4463 CTTTCTTTTCTTTTCTTCT 4487
 DB 2 CCTTTTCTCTTTTCTTTTCT 26
 RESULT 1398
 AA25387
 ID AA25387 standard; DNA; 26 BP.
 XX
 AC AA25387;
 XX
 DT 16-DEC-1999 (first entry)
 XX
 DE Infectious pancreatic necrosis virus PCR primer #1.
 XX
 KM Infectious pancreatic necrosis virus; IPNV; strain West Buxton;
 KM strain SP; segment A; segment B; nonpathogenic; Birnaviridae family;
 KM infection; live attenuated vaccine; aquaculture industry; Rainbow trout;
 KM Brook trout; Atlantic salmon; PCR primer; ss.
 XX
 OS Synthetic.
 OS Infectious pancreatic necrosis virus.
 XX
 PN WO950419-A2.
 XX
 PD 07-OCT-1999.
 XX
 PF 31-MAR-1999; 99WO-US004285.
 XX
 PR 31-MAR-1998; 98US-0080178P.
 XX
 PA (UMMA-) UNITV MARYLAND BIOTECHNOLOGY INST.
 PI Vakharia VN, Yao K;
 XX
 PI WPI; 1999-591321/50.
 DR
 XX
 PT Preparing nonpathogenic infectious pancreatic necrosis virus, IPNV,
 PT useful for producing attenuated virus for vaccines useful in the
 PT aquaculture industry.
 XX
 PS Example 1; Page 21, 63pp; English.
 XX
 CC A method has been developed for preparing nonpathogenic, infectious
 CC pancreatic necrosis virus (IPNV). The method comprises: 1) preparing cDNA
 CC containing the IPNV genome segments A and B where A is modified to
 CC prevent expression of an arginine-rich non-structural (NS) protein; 2)
 CC transcribing the cDNA to produce RNA; 3) incubating the host cells in a
 CC culture medium; and 4) isolating live IPNV from the culture medium. The
 CC method is useful to produce live nonpathogenic IPNV, useful to study
 CC viral pathogenesis and for the production of live, nonpathogenic IPNV
 CC vaccines, since it was demonstrated that the NS protein-deficient virus
 CC could replicate but did not invoke a pathological response in hosts.
 CC Combination vaccines may also be produced by combining the IPNV with
 CC bacterial antigens (especially from gram negative bacteria e.g. Aeromonas
 CC salmonicida) and/or antigens from aquatic viruses other than Birnaviruses
 CC (the family to which IPNV belongs) e.g. infectious haematopoietic
 CC necrosis virus. The method may also be used to generate a nonpathogenic

CC chimeric virus when the cDNA of segment A encodes epitopic determinants
 CC from at least two different IPNV strains. IPNV causes a highly contagious
 CC and destructive disease of juvenile Rainbow and Brook trout and Atlantic
 CC salmon (e.g. highly virulent strains can cause more than 90 % mortality
 CC in hatchery stocks less than 4 months old and survivors can remain
 CC lifelong carriers and reservoirs of infection); IPNV is therefore a
 CC pathogen of major economic importance to the aquaculture industry. The
 CC present sequence represents an IPNV PCR primer used in an example from
 CC the present invention
 XX
 SQ Sequence 26 BP; 0 A; 6 C; 4 G; 16 T; 0 U; 0 Other;
 Query Match 0.2%; Score 17; DB 1; Length 26;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4463 CTTTCTTTTCTTTTCTT 4479
 DB 10 CTTTCTTTTCTTTTCTT 26
 RESULT 1399
 AAAS5837
 ID AAAS5837 standard; DNA; 26 BP.
 XX
 AC AAAS5837;
 XX
 DT 01-SEP-2000 (first entry)
 XX
 DE Histone deacetylase HD1 and HD2 antisense oligonucleotide SEQ ID NO:82.
 XX
 KM Human; DNA methyltransferase; DNA Methylase; antisense oligonucleotide;
 KM modulation; inhibition; gene expression; combination therapy; p16;
 KM histone deacetylase; HDAC; thymidylate synthase; tumour suppressor;
 KM methylation; gene therapy; tumour; cytosolic; antiaschmatic;
 KM antiinflammatory; inflammation; asthma; ss.
 XX
 OS Homo sapiens.
 OS
 PN WO200023112-A1.
 XX
 PD 27-APR-2000.
 XX
 PF 19-OCT-1999; 99WO-US024278.
 XX
 PR 19-OCT-1998; 98US-0104804P.
 XX
 PA (METH-) METHYLENE INC.
 PI Besterman JM, Macleod AR, Siders WM;
 XX
 PI WPI; 2000-339532/29.
 DR
 XX
 PT Inhibiting gene expression e.g. DNA methyltransferase, by treating cells
 PT with a synergistic amount of antisense oligonucleotide and protein
 PT effectors e.g. 5-aza-cytidine of gene products, useful for gene therapy
 PT of e.g. tumore.
 XX
 PS Example 9; Page 58; 99pp; English.
 XX
 CC The present invention describes a method for inhibiting the expression of
 CC a gene in a cell comprising contacting the cell with an effective
 CC synergistic amount of an antisense oligonucleotide which inhibits
 CC expression of the gene, and an effective synergistic amount of a protein
 CC effector of a product of the gene. Also described are: (1) a method for
 CC treating a disease responsive to inhibition of a gene in a mammal; (2) a
 CC method for inhibiting tumour growth in mammal; (3) an inhibitor of a gene
 CC comprising an antisense oligonucleotide which inhibits expression of the
 CC gene in operable association with a protein effector of a gene product;
 CC and (4) a pharmaceutical composition comprising the inhibitor of (3). The
 CC methods and compositions are useful as analytical tools for transgenic
 CC studies and as therapeutic tools, e.g. as gene therapy tools for human
 CC diseases including benign and malignant tumours, inflammation or asthma.

CC The methods, inhibitors and compositions of the invention that inhibit
CC expression or activity of a gene or gene product may be used to treat
CC patients having, or predisposed to developing, a disease responsive to
CC inhibition of the gene. These may also be used to activate silenced genes
CC to provide missing gene functions and improve a given condition.
CC Furthermore, the methods and compositions are useful as probes of the
CC physiological function of a gene product in an experimental cell culture
CC or animal system; and to evaluate the effect of inhibiting gene activity
CC or expression. AA55758 to AA55842 represent oligonucleotide sequences
CC which are used in the exemplification of the present invention
XX

SO Sequence 26 BP; 7 A; 4 C; 8 G; 5 T; 2 U; 0 Other;

Query Match 0.2%; Score 17; DB 1; Length 26;
Best Local Similarity 72.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 5574 CAGCAAGCTTGGCTCATGTCGATT 5598
DB 1 CAGCAAAATTATGAGTCATGCGGAU 25

RESULT 1400
AA55838
ID AA55838 standard; DNA; 26 BP.
AC AA55838;
XX
XX
DT 01-SEP-2000 (first entry)
XX
DE Histone deacetylase HD1 and HD2 antisense oligonucleotide SEQ ID NO:63.
XX
XX Human; DNA methyltransferase; DNA Methylase; antisense oligonucleotide;
XX modulation; inhibition; gene expression; combination therapy; p16;
XX histone deacetylase; HDAC; thymidylate synthase; tumour suppressor;
XX methylation; gene therapy; tumour; cytostatic; antiasthmatic;
XX antiinflammatory; inflammation; asthma; ss.
XX
XX Homo sapiens.
XX
XX WO200023112-A1.
XX
XX PD 27-APR-2000.
XX
XX PF 19-OCT-1999; 99WO-US024278.
XX
XX PR 19-OCT-1998; 98US-0104804P.
XX
XX (METH-) METHYLGENE INC.
XX
XX Beesterman JM, Macleod AR, Siders WM;
XX
XX WPI; 2000-339532/29.
XX
XX PT Inhibiting gene expression e.g. DNA methyltransferase, by treating cells
XX with a synergistic amount of antisense oligonucleotide and protein
XX effectors e.g. 5-aza-cytidine of gene products, useful for gene therapy
XX of e.g. tumors.
XX
XX PS Example 9; Page 58; 99pp; English.
XX
XX CC The present invention describes a method for inhibiting the expression of
XX a gene in a cell comprising contacting the cell with an effective
XX synergistic amount of an antisense oligonucleotide which inhibits
XX expression of the gene, and an effective synergistic amount of a protein
XX effector of a product of the gene. Also described are: (1) a method for
XX treating a disease responsive to inhibition of a gene in a mammal; (2) a
XX method for inhibiting tumour growth in mammal; (3) an inhibitor of a gene
XX comprising an antisense oligonucleotide which inhibits expression of a gene
XX gene in operable association with a protein effector of a gene product;
XX and (4) a pharmaceutical composition comprising the inhibitor of (3). The
XX methods and compositions are useful as analytical tools for transgenic
XX studies and as therapeutic tools, e.g. as gene therapy tools for human

CC diseases including benign and malignant tumours, inflammation or asthma.
CC The methods, inhibitors and compositions of the invention that inhibit
CC expression or activity of a gene or gene product may be used to treat
CC patients having, or predisposed to developing, a disease responsive to
CC inhibition of the gene. These may also be used to activate silenced genes
CC to provide missing gene functions and improve a given condition.
CC Furthermore, the methods and compositions are useful as probes of the
CC physiological function of a gene product in an experimental cell culture
CC or animal system; and to evaluate the effect of inhibiting gene activity
CC or expression. AA55758 to AA55842 represent oligonucleotide sequences
CC which are used in the exemplification of the present invention
XX

SO Sequence 26 BP; 7 A; 4 C; 8 G; 5 T; 2 U; 0 Other;

Query Match 0.2%; Score 17; DB 1; Length 26;
Best Local Similarity 72.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 5574 CAGCAAGCTTGGCTCATGTCGATT 5598
DB 1 CAGCAAGTTATGAGTCATGCGGAU 25

RESULT 1401
AAC92118
ID AAC92118 standard; DNA; 26 BP.
AC AAC92118;
XX
XX
DT 19-MAR-2001 (first entry)
XX
XX Human MLT gene intron-exon boundary #2.
XX
XX
XX Human; API2-MLT chimera; chimeric; apoptosis inhibitor 2; MLT; API2;
XX mucosa-associated lymphoid tissue lymphoma associated translocation;
XX chromosome 11 region q21-22.3; chromosome 18 region q21.1-22;
XX molecular characterisation; chromosome translocation; carcinogenesis;
XX fusion protein; malignancy; ss.
XX
XX Homo sapiens.
XX
XX WO200073500-A1.
XX
XX PD 07-DEC-2000.
XX
XX PF 26-MAY-2000; 2000WO-EP004796.
XX
XX PR 27-MAY-1999; 99EP-00201683.
XX
XX (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX
XX Baens M, Marynen P, Dierlam J;
XX
XX WPI; 2001-061556/07.
XX
XX PT Determining if a tissue sample has a chromosome (11:18) translocation
XX associated with malignancies by amplifying a nucleic acid sample using
XX primers complementary to chromosome 11 region q21-22.3 and chromosome 18
XX region q21.1-22.
XX
XX PS Example 3; Page 22; 47pp; English.
XX
XX CC The present invention describes a method for determining if a tissue
XX sample comprises a cell with a chromosome (11:18) translocation
XX associated with malignancies such as mucosa-associated lymphoid tissue
XX (MALT) lymphomas. The method comprises subjecting a sample nucleic acid
XX to amplification using primers complementary to sequences which are on
XX chromosome 11 region q21-22.3 and on chromosome 18 region q21.1-22. The
XX method can be used for determining if a tissue sample or analogue
XX comprises a chromosome (11:18) translocation associated with malignancies
XX such as mucosa-associated lymphoid tissue lymphomas. The nucleic acid or
XX the antibody may be used as a probe for detection, for hybridisation to
XX southern blot cell DNAs or for in situ hybridisation of cells, or for

CC determining the presence of complementary DNA. The present sequence
 CC represents an intron-exon boundary oligonucleotide from the human MALT-
 CC lymphoma associated translocation (MLT) gene, which is used in an example
 CC from the present invention

XX Sequence 26 BP; 6 A; 0 C; 3 G; 17 T; 0 U; 0 Other;

Query Match 0.2%; Score 17; DB 1; Length 26;
 Best Local Similarity 80.0%; Pred. No. 1.3e+03;
 Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 6465 TTTTCTGTTGTTGTAATAGG 6489

DB 2 TTTTCTGTTGTTGTAATAGG 26

RESULT 1402

AAC89541 AAC89541 standard; DNA; 26 BP.

XX AAC89541;

AC 08-MAR-2001 (first entry)

DE Human HDAC-1/HDAC-2 antisense sequence SEQ ID NO: 11.

XX Histone deacetylase; HDAC-1; HDAC-2; HDAC-3; HDAC-4; HDAC-5; HDAC-C;

KM HDAC-D; cell cycle; tumorigenesis; cancer; inhibitor; antisense;

XX gene therapy; PCR primer; ss.

OS Homo sapiens.

XX WO200071703-A2.

XX 30-NOV-2000.

PF 03-MAY-2000; 2000WO-IB001252.

PR 03-MAY-1999; 99US-0132287P.

XX (METH-) METHYLENE INC.

PI Macleod AR, Li Z, Besterman JM;

DR WPI; 2001-016407/02.

XX Antisense oligonucleotide that inhibits expression of a histone
 PT deacetylase, useful for treating and/or alleviating the symptoms of
 PT neoplasia, or for inhibiting neoplastic cell growth in an animal.

XX Example 1; Page 23; 125pp; English.

CC The present invention provides inhibitors of histone deacetylase enzymes
 CC such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-C and HDAC-D. These
 CC inhibitors may be antisense strands or they may be compounds identified
 CC by contacting the enzyme with the compound and measuring the resulting
 CC enzyme activity. These inhibitors are useful for treating cancers and for
 CC identifying which histone deacetylase is involved in a neoplasia

XX Sequence 26 BP; 7 A; 5 C; 7 G; 5 T; 2 U; 0 Other;

Query Match 0.2%; Score 17; DB 1; Length 26;
 Best Local Similarity 72.0%; Pred. No. 1.3e+03;
 Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 5574 CAGCAAGCTTGGCTCATGTGATT 5598

DB 1 CAGCAAGTTATGGTCATGCGGAAU 25

RESULT 1403

AAC89533 AAC89533 standard; DNA; 26 BP.

XX AAC89533;

XX 08-MAR-2001 (first entry)

DE Human HDAC-1/HDAC-2 PCR primer SEQ ID NO: 3.

XX Histone deacetylase; HDAC-1; HDAC-2; HDAC-3; HDAC-4; HDAC-5; HDAC-C;

KM HDAC-D; cell cycle; tumorigenesis; cancer; inhibitor; antisense;

XX gene therapy; PCR primer; ss.

OS Homo sapiens.

XX WO200071703-A2.

XX 30-NOV-2000.

PF 03-MAY-2000; 2000WO-IB001252.

PR 03-MAY-1999; 99US-0132287P.

XX (METH-) METHYLENE INC.

PI Macleod AR, Li Z, Besterman JM;

DR WPI; 2001-016407/02.

XX Antisense oligonucleotide that inhibits expression of a histone
 PT deacetylase, useful for treating and/or alleviating the symptoms of
 PT neoplasia, or for inhibiting neoplastic cell growth in an animal.

XX Example 2; Page 12; 125pp; English.

CC The present invention provides inhibitors of histone deacetylase enzymes
 CC such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-C and HDAC-D. These
 CC inhibitors may be antisense strands or they may be compounds identified
 CC by contacting the enzyme with the compound and measuring the resulting
 CC enzyme activity. These inhibitors are useful for treating cancers and for
 CC identifying which histone deacetylase is involved in a neoplasia

XX Sequence 26 BP; 7 A; 5 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 0.2%; Score 17; DB 1; Length 26;
 Best Local Similarity 80.0%; Pred. No. 1.3e+03;
 Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5574 CAGCAAGCTTGGCTCATGTGATT 5598

DB 1 CAGCAAGTTATGGTCATGCGGATT 25

RESULT 1404

AAC89532 AAC89532 standard; DNA; 26 BP.

XX AAC89532;

AC 08-MAR-2001 (first entry)

DE Human HDAC-1/HDAC-2 PCR primer SEQ ID NO: 2.

XX Histone deacetylase; HDAC-1; HDAC-2; HDAC-3; HDAC-4; HDAC-5; HDAC-C;

KM HDAC-D; cell cycle; tumorigenesis; cancer; inhibitor; antisense;

XX gene therapy; PCR primer; ss.

OS Homo sapiens.

XX WO200071703-A2.

XX 30-NOV-2000.

PF 03-MAY-2000; 2000WO-IB001252.

PR 03-MAY-1999; 99US-0132287P.
XX (METH-) METHYLGENE INC.
XX
XX Macleod AR, Li Z, Besterman JM;
PI
XX WPI; 2001-016407/02.
DR
XX Antisense oligonucleotide that inhibits expression of a histone
PT deacetylase, useful for treating and/or alleviating the symptoms of
PT neoplasia, or for inhibiting neoplastic cell growth in an animal.
XX
XX
PS Example 2; Page 12; 125pp; English.
XX
XX The present invention provides inhibitors of histone deacetylase enzymes
CC such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-C and HDAC-D. These
CC inhibitors may be antisense strands or they may be compounds identified
CC by contacting the enzyme with the compound and measuring the resulting
CC enzyme activity. These inhibitors are useful for treating cancers and for
CC identifying which histone deacetylase is involved in a neoplasia
XX
SQ Sequence 26 BP; 7 A; 5 C; 7 G; 7 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 17; DB 1; Length 26;
Best Local Similarity 80.0%; Pred. No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 5574 CAGCAAGCTTGGCTCATGCGATT 5598
Db 1 CAGCAATTATGGCTCATGCGATT 25
RESULT 1405
AAC89542
ID AAC89542 standard; DNA; 26 BP.
XX
XX AAC89542;
AC
XX 08-MAR-2001 (first entry)
DT
XX
XX Human HDAC-1/HDAC-2 antisense sequence SEQ ID NO: 12.
DE
XX
XX Histone deacetylase; HDAC-1; HDAC-2; HDAC-3; HDAC-4; HDAC-5; HDAC-C;
KM HDAC-D; cell cycle; tumorigenesis; cancer; inhibitor; antisense;
KW gene therapy; PCR primer; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200071703-A2.
PN
XX
XX 30-NOV-2000.
PD
XX
XX 03-MAY-2000; 2000WO-IB001252.
PF
XX
XX 03-MAY-1999; 99US-0132287P.
PR
XX (METH-) METHYLGENE INC.
PA
XX
XX Macleod AR, Li Z, Besterman JM;
PI
XX WPI; 2001-016407/02.
DR
XX
XX Antisense oligonucleotide that inhibits expression of a histone
PT deacetylase, useful for treating and/or alleviating the symptoms of
PT neoplasia, or for inhibiting neoplastic cell growth in an animal.
XX
XX
PS Example 1; Page 23; 125pp; English.
XX
XX The present invention provides inhibitors of histone deacetylase enzymes
CC such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-C and HDAC-D. These
CC inhibitors may be antisense strands or they may be compounds identified
CC by contacting the enzyme with the compound and measuring the resulting
CC enzyme activity. These inhibitors are useful for treating cancers and for

CC identifying which histone deacetylase is involved in a neoplasia
XX
SQ Sequence 26 BP; 7 A; 5 C; 7 G; 5 T; 2 U; 0 Other;
XX
Query Match 0.2%; Score 17; DB 1; Length 26;
Best Local Similarity 72.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
OY 5574 CAGCAAGCTTGGCTCATGCGATT 5598
Db 1 CAGCAAGTTATGATCATGCGAUV 25
RESULT 1406
ABL55293/C
ID ABL55293 standard; DNA; 26 BP.
XX
XX ABL55293;
AC
XX 28-JUN-2002 (first entry)
DT
XX
XX Olive pollen allergen Ole e 1 PCR primer OL4.
DE
XX
XX Olive; pollen allergen; Ole e 1; plant; recombinant production; Oleaceae;
KM Pichia pastoris; allergy; diagnosis; immunotherapy; vaccine;
KW T cell epitope; hypoallergenic isoforn production; PCR; primer; ss.
XX
XX Olea europaea.
OS
XX Synthetic.
OS
XX WO200212503-A1.
PN
XX
XX 14-FEB-2002.
PD
XX
XX 19-JUL-2001; 2001WO-ES000287.
PF
XX
XX 28-JUL-2000; 2000ES-00001919.
PR
XX (UYMA-) UNIV COMPLUTENSE MADRID.
PA
XX
XX Rodriguez Garcia R, Villalba Diaz MT, Monsalve Clemente R;
PI Batanero Cremades B;
PI
XX
XX WPI; 2002-227154/28.
DR
XX
XX New recombinant DNA encoding plant allergens, useful for diagnosis and
PT immunotherapy of allergens, encodes the major allergen of olive or
PT related species.
XX
XX
XX Disclosure; Page 9; 38pp; Spanish.
PS
XX
XX The invention relates to recombinant DNA molecules which encode the olive
CC pollen allergen Ole e 1 (ABL55282-ABL55284), the lilac pollen allergen
CC Syr v 1 (ABL55285-ABL55287) and the privet pollen allergen Lig v 1
CC (ABL55388-ABL55289) and to the recombinantly produced pollen allergen
CC polypeptides (AAM49230-AAM49237). The invention also encompasses
CC recombinant DNA with at least 60% identity to the DNA sequences mentioned
CC above, and also relates to eukaryotic expression vectors and host cells
CC comprising the DNA sequences of the invention, a method for the
CC recombinant production of the pollen allergens in the yeast Pichia
CC pastoris and a system for purifying the recombinant allergens. The pollen
CC allergens of olive, lilac and privet (all members of the Oleaceae family)
CC exhibit high structural homology, and are also similar in structure to
CC pollen allergens from other Oleaceae family members. The recombinant Ole
CC e 1, Syr v 1 and Lig v 1 DNA sequences and their encoded proteins may be
CC used in the diagnosis and treatment of allergy. In particular, they may
CC be used for in vitro diagnosis of allergy; in the design of vaccines for
CC immunotherapy; in the production of peptides containing one or more T
CC cell epitopes for use as vaccines; and to produce hypoallergenic isoforms
CC of the pollen proteins that have little or no IgE (immunoglobulin E) -
CC binding capacity which may be used to treat allergy. The recombinant DNA
CC and methods of the invention provide high yield production of correctly
CC folded allergen protein with the same immunological properties as the

CC native allergen. Typically yields are about 60 mg of protein/l and the
CC recombinantly produced allergen has a high degree of purity (99%)
CC compared with allergen extracted directly from pollen. Sequences AB155290
CC -AB155293 represent O1e e 1 PCR primers used to amplify nucleic acids of
CC the invention for cloning
XX
SQ Sequence 26 BP; 5 A; 5 C; 9 G; 7 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 17; DB 1; Length 26;
Best Local Similarity 80.0%; Pred. No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 5980 ACCTGCCCACTGTGTGAAGTCAG 6004
DB 25 ACCCGCCCACTGTGAATTCG 1
XX
RESULT 1407
AB1554659
ID AB1554659 standard; DNA; 26 BP.
XX
AC AB1554659;
XX
DT 03-DEC-2002 (first entry)
XX
DE Human p53 protein chromosomal binding region oligonucleotide Hoog3.
XX
KW 86; p53; chromosomal binding region; cancer; carcinoma; sarcoma;
KW breast cancer; adrenal cortex cancer; colon cancer; bladder cancer;
KW prostate cancer; lung cancer; leukemic cancer.
XX
OS Synthetic.
XX
PN US2002103153-A1.
XX
PD 01-AUG-2002.
XX
PF 22-AUG-2001; 2001US-00935247.
XX
PR 06-APR-1992; 92US-00863661.
PR 01-MAY-1992; 92US-00879618.
PR 15-AUG-1994; 94US-00291011.
PR 10-MAR-1999; 99US-00266065.
XX
PA (REBR/) RE R.
PA (COOK/) COOK J.
XX
PI Re R, Cook J;
XX
DR MPI; 2002-674027/72.
XX
PT Composition for treating cancer comprises an oligonucleotide that binds a
PT chromosomal binding site for p53.
XX
PS Example 1; Page 7; 13pp; English.
XX
CC The invention relates to composition comprising an oligonucleotide that
CC can bind a chromosomal binding site for p53 protein, and a
CC pharmacologically acceptable carrier. The composition is useful for
CC inhibiting mammalian (e.g. human, ape, monkey, cow, mouse, rat, hamster,
CC rabbit, cat, sheep or bull, dog, horse) cell growth and replication,
CC especially cancer (e.g. carcinoma, sarcoma, breast cancer, adrenal cortex
CC cancer, colon cancer, bladder cancer, prostate cancer, lung cancer or
CC leukemic cancer). The present sequence is human p53 protein chromosomal
CC binding region scrambled control oligonucleotide Hoog3
XX
SQ Sequence 26 BP; 0 A; 7 C; 0 G; 19 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 17; DB 1; Length 26;
Best Local Similarity 80.0%; Pred. No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 4463 CTTTTTTTTTTTTTTTTTGTCT 4487

DB 2 CTTTTTCTTTTTTTTTTTTCT 26
XX
RESULT 1408
AB156896/c
ID AB156896 standard; DNA; 30 BP.
XX
AC AB156896;
XX
DT 26-JUL-2002 (first entry)
XX
DE Synthetic deoxyribonucleotide poly 1.
XX
KW Concentration; quantification; mutation detection; polymorphic;
KW polymerase chain reaction; PCR; ss.
XX
OS Synthetic.
XX
PN EP1046717-A2.
XX
PD 25-OCT-2000.
XX
PF 20-APR-2000; 2000EP-00108643.
XX
PR 20-APR-1999; 99JP-00111601.
XX
PA (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
PI Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;
PI Koyama O, Furusho K;
XX
DR MPI; 2000-657765/64.
XX
PT Determining the concentration of a target nucleic acid, useful e.g. for
PT detecting genetic mutations, comprises using a fluorescently labeled
PT probe in which emission is reduced by binding to the target nucleic acid.
XX
PS Example 5; Page 21; 55pp; English.
XX
CC The invention relates to the determination of the concentration of a
CC nucleic acid target, using a fluorescently labeled probe which produces
CC reduced fluorescence emission when hybridised to the target nucleic acid.
CC The method comprises measuring the reduction in emission caused by
CC hybridisation. The new method is particularly used to quantify target
CC nucleic acids by a real-time polymerase chain reaction, e.g. for
CC quantifying microbial cells in co-cultures or symbiotic systems, for
CC detecting gene mutations or polymorphisms, and for analysing melting
CC curves of target nucleic acids to determine a Tm value. Methods of the
CC invention allow target nucleic acids to be quantified quickly, easily and
CC accurately. Particularly there is no need to remove unbound probe, and no
CC materials are introduced that inhibit amplification by Taq polymerase (so
CC conventional PCR conditions can be used). The specificity of PCR is kept
CC high (amplification of primer dimers is delayed), and the limit of
CC quantitation is reduced. Complex probes are not needed, and amplification
CC can be monitored in real time. The working graph for data analysis
CC (automatically generated by a computer) has a higher correlation
CC coefficient than conventional graphs so more accurate quantitation is
CC possible. The current sequence represents a synthetic
CC deoxyribonucleotide that was used for investigating the base
CC selectivity of a target nucleic acid
XX
SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 17; DB 1; Length 30;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 4018 AGAAAAAGAGAGAAACAAATGT 4042
DB 29 AAAAAAAAAAGAAAAAAAAAATAT 5

```

RESULT 1409
ABL56894/c
ID ABL56894 standard; DNA; 30 BP.
XX
AC ABL56894;
XX
DT 26-JUL-2002 (first entry)
XX
DE Synthetic deoxyribonucleotide poly g.
XX
KM Concentration; quantification; mutation detection; polymorphic;
KM polymerase chain reaction; PCR; ss.
XX
OS Synthetic.
XX
PN BP1046717-A2.
XX
PD 25-OCT-2000.
XX
PF 20-APR-2000; 2000EP-00108643.
XX
PR 20-APR-1999; 99JP-00111601.
XX
PA (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA (AGEN-) AGENCY OF IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
PI Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;
PI Koyama O, Furusho K;
DR WPI; 2000-657765/64.
XX
PT Determining the concentration of a target nucleic acid, useful e.g. for
PT detecting genetic mutations, comprises using a fluorescently labeled
PT probe in which emission is reduced by binding to the target nucleic acid.
XX
PS Example 5; Page 21; 55pp; English.
XX
CC The invention relates to the determination of the concentration of a
CC nucleic acid target, using a fluorescently labeled probe which produces
CC reduced fluorescence emission when hybridised to the target nucleic acid.
CC The method comprises measuring the reduction in emission caused by
CC hybridisation. The new method is particularly used to quantify target
CC nucleic acids by a real-time polymerase chain reaction, e.g. for
CC quantifying microbial cells in co-cultures or symbiotic systems, for
CC detecting gene mutations or polymorphisms, and for analysing melting
CC curves of target nucleic acids to determine a Tm value. Methods of the
CC invention allow target nucleic acids to be quantified quickly, easily and
CC accurately. Particularly there is no need to remove unbound probe, and no
CC materials are introduced that inhibit amplification by Taq polymerase (so
CC conventional PCR conditions can be used). The specificity of PCR is kept
CC high (amplification of primer dimers is delayed), and the limit of
CC quantitation is reduced. Complex probes are not needed, and amplification
CC can be monitored in real time. The working graph for data analysis
CC (automatically generated by a computer) has a higher correlation
CC coefficient than conventional graphs so more accurate quantitation is
CC possible. The current sequence represents a synthetic
CC deoxyribonucleotide that was used for investigating the base
CC selectivity of a target nucleic acid
XX
SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;
Query Match 0.2%; Score 17; DB 1; Length 30;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 4018 AGAAAAAGAGAGAAAAAATAATGT 4042
DB 29 AAAAAAAAAAGAAAAAAATAT 5

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RESULT 1410
ABA97620/c
ID ABA97620 standard; DNA; 30 BP.
XX
AC ABA97620;
XX
DT 11-APR-2002 (first entry)
XX
DE Poly i nucleotide sequence.
XX
KM ss; fluorochrome; nucleic acid probe; fluorescence.
XX
OS Unidentified.
XX
PN JP2001286300-A.
XX
PD 16-OCT-2001.
XX
PF 20-APR-2000; 2000JP-00120097.
XX
PR 20-APR-1999; 99JP-00111601.
PR 24-AUG-1999; 99JP-00236666.
PR 30-AUG-1999; 99JP-00242693.
PR 01-FEB-2000; 2000JP-00028896.
XX
PA (BIOT-) BIOINDUSTRY KYOKAI SH.
PA (KANK-) KANKYO ENG KK.
PA (KEIZ-) KEIZAI SANGYOSHO SANGYO GIUTSU SOGO KEN.
XX
PI WPI; 2002-134193/18.
XX
PT Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT the obtained data.
XX
PS Example 5; Page 17; 34pp; Japanese.
XX
CC This invention relates to a method for measuring nucleic acids using a
CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC decreases the fluorescence of the fluorochrome when hybridised with a
CC target nucleic acid, the decrease in the fluorescence is measured. The
CC method can be used for measuring a target nucleic acid
XX
SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;
Query Match 0.2%; Score 17; DB 1; Length 30;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 4018 AGAAAAAGAGAGAAAAAATAATGT 4042
DB 29 AAAAAAAAAAGAAAAAAATAT 5

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PR 20-APR-1999; 99JP-00111601.
PR 24-AUG-1999; 99JP-00236666.
PR 30-AUG-1999; 99JP-00242693.
PR 01-FEB-2000; 2000JP-00028896.
XX
XX (BIOI-) BIOINDUSTRY KYOKAI SH.
PA (KANK-) KANKYO ENG KK.
PA (KEIZ-) KEIZAI SANGYOSHIO SANGYO GIJUTSU SOGO KEN.
XX
XX WPI; 2002-134193/18.
XX
XX Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT the obtained data.
XX
XX Example 5; Page 17; 34pp; Japanese.
XX
XX This invention relates to a method for measuring nucleic acids using a
CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC decreases the fluorescence of the fluorochrome when hybridised with a
CC target nucleic acid, the decrease in the fluorescence is measured. The
CC method can be used for measuring a target nucleic acid
XX
XX Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;
SQ
XX
XX Query Match 0.2%; Score 17; DB 1; Length 30;
XX Best Local Similarity 80.0%; Pred. No. 1.5e+03;
XX Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 4018 AGAAAAAGAGAGAGAAAAACAAATGT 4042
DB 29 AAAAAAAAAAGAAAAAAATAT 5
XX
XX RESULT 1412
XX ABL95891/C
XX ID ABL95891 standard; DNA; 30 BP.
XX
XX ABL95891;
XX
XX 19-JUN-2002 (first entry)
XX
XX Probe poly g for assaying nucleic acids.
XX
XX Probe; polymorphism detection; mutation detection; disease diagnosis;
XX microbial identification; ss.
XX
XX Unidentified.
XX
XX WO200208414-A1.
XX
XX 31-JAN-2002.
XX
XX 27-JUN-2001; 2001WO-IB001147.
XX
XX 27-JUN-2000; 2000JP-00193133.
XX
XX 03-AUG-2000; 2000JP-00236115.
XX
XX 26-SEP-2000; 2000JP-00292483.
XX
XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX (KANK-) KANKYO ENG CO LTD.
XX
XX Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;
XX Yokomaku T;
XX
XX WPI; 2002-195876/25.
XX
XX Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
XX their polymorphism and mutation, particularly useful in science and
XX medicine for e.g. analytical applications, disease diagnosis and
XX microbial identification.
XX
XX Example 12; Page 60; 152pp; Japanese.
XX

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CC The present invention relates to nucleic acid probes, which are useful
CC for assaying nucleic acids by hybridising with a target nucleic acid, in
CC which a single-stranded oligonucleotide is labelled with a fluorescent
CC substance and a quencher in a manner that the fluorescence intensity of
CC the hybridisation reaction system is increased after completion of the
CC hybridisation but no stem loop structure is formed. The probes are useful
CC for assaying nucleic acids and their polymorphism and mutation,
CC particularly useful for e.g. analytical applications, disease diagnosis
CC and microbial identification. The present sequence was used to illustrate
CC the invention
XX
XX Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;
SQ
XX
XX Query Match 0.2%; Score 17; DB 1; Length 30;
XX Best Local Similarity 80.0%; Pred. No. 1.5e+03;
XX Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 4018 AGAAAAAGAGAGAGAAAAACAAATGT 4042
DB 29 AAAAAAAAAAGAAAAAAATAT 5
XX
XX RESULT 1413
XX ABL95893/C
XX ID ABL95893 standard; DNA; 30 BP.
XX
XX ABL95893;
XX
XX 19-JUN-2002 (first entry)
XX
XX Probe poly I for assaying nucleic acids.
XX
XX Probe; polymorphism detection; mutation detection; disease diagnosis;
XX microbial identification; ss.
XX
XX Unidentified.
XX
XX WO200208414-A1.
XX
XX 31-JAN-2002.
XX
XX 27-JUN-2001; 2001WO-IB001147.
XX
XX 27-JUN-2000; 2000JP-00193133.
XX
XX 03-AUG-2000; 2000JP-00236115.
XX
XX 26-SEP-2000; 2000JP-00292483.
XX
XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX (KANK-) KANKYO ENG CO LTD.
XX
XX Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;
XX Yokomaku T;
XX
XX WPI; 2002-195876/25.
XX
XX Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
XX their polymorphism and mutation, particularly useful in science and
XX medicine for e.g. analytical applications, disease diagnosis and
XX microbial identification.
XX
XX Example 12; Page 60; 152pp; Japanese.
XX
XX The present invention relates to nucleic acid probes, which are useful
XX for assaying nucleic acids by hybridising with a target nucleic acid, in
XX which a single-stranded oligonucleotide is labelled with a fluorescent
XX substance and a quencher in a manner that the fluorescence intensity of
XX the hybridisation reaction system is increased after completion of the
XX hybridisation but no stem loop structure is formed. The probes are useful
XX for assaying nucleic acids and their polymorphism and mutation,
XX particularly useful for e.g. analytical applications, disease diagnosis
XX and microbial identification. The present sequence was used to illustrate
XX the invention
XX

```


SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;
 Query Match 0.2%; Score 17; DB 1; Length 30;
 Best Local Similarity 80.0%; Pred. No. 1.5e+03;
 Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 4018 AGAAAAAGAGAGAAACAAATGT 4042
 DB 29 AAAAAAAAAAAAAAAAAAAAAAT 5
 RESULT 1414
 AAS17761/c
 ID AAS17761 standard; DNA; 31 BP.
 AC AAS17761;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Oligo d(T) PCR primer.
 XX
 KM Oligo d(T); ss; differential subtraction; PCR primer;
 KM double exponential elimination; tumour.
 OS Synthetic.
 XX
 PN US6316192-B1.
 PD 13-NOV-2001.
 PF 11-MAR-1999; 99US-00268505.
 PR 11-MAR-1999; 99US-00268505.
 XX
 PA (LUOJ/) LUO J.
 PI Lwo J;
 DR WPI; 2002-074371/10.
 PT Selective elimination of non-targeted DNA sequences for rapid isolation
 PT and enrichment of the differences of DNA fragments between two pools of
 PT DNA, comprises converting testers to drivers.
 PS Claim 6; Col 5; 23pp; English.
 XX
 CC The invention comprises rapid isolation and enrichment of the differences
 CC of DNA fragments between two pools of DNA, comprises converting
 CC undesirable testers (DNA being subtracted) to drivers (DNA used to
 CC subtract) and re-utilising converted drivers in repeats of subtraction to
 CC achieve double exponential elimination of undesirable tester sequences.
 CC The method comprises (a) attaching a nucleic acid fragment to 1 or more
 CC polymerase chain reaction (PCR) adapters to form an adapter-attached
 CC nucleic acid fragment, followed by amplifying the adapter-attached
 CC nucleic acid fragment through PCR with primers containing nucleic acid
 CC sequences complementary to nucleic acid sequences of the adapter to form
 CC an adapter-attached nucleic acid tester, (b) mixing the adapter-attached
 CC nucleic acid tester with a nucleic acid driver that contains no attached
 CC adapter or contains an attached adapter whose sequence differs from the
 CC adapter, to form a nucleic acid mixture, (c) denaturing and re-annealing
 CC the tester/driver nucleic acid mixture, (d) adding to the nucleic acid
 CC mixture an effective amount of reagents necessary for removing the
 CC step (c) to (d) at least once (no amplification takes place and no
 CC additional driver is added). The method is used for rapid isolation and
 CC enrichment of the differences of DNA fragments between two pools of DNA
 CC e.g. in the search for tumour specific sequences. The method has 2
 CC improvements over the methods disclosed by Yang et al. (1996), Lisitsyn
 CC et al. (1993), Straus et al. (1990) by (1) bypassing the need of a
 CC polymerase chain reaction (PCR) amplification or physical separation of
 CC desirable testers from undesirable ones in each repeat of subtraction, it
 CC eliminates the necessity of tester dilution in each repeat of
 CC subtraction, and (11) by utilising the converted driver from each repeat

CC of subtraction, it eliminates the need for re-introducing additional
 CC driver into hybridisation in each repeat of subtraction. The present
 CC sequence is an Oligo d(T) PCR primer used in the method of the invention
 XX
 SQ Sequence 31 BP; 0 A; 0 C; 0 G; 30 T; 0 U; 1 Other;
 Query Match 0.2%; Score 17; DB 1; Length 31;
 Best Local Similarity 72.4%; Pred. No. 1.5e+03;
 Matches 21; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
 QY 4011 TAAATGAGAAAAAGAGAAACAAA 4039
 DB 31 BAAAAAAAAAAAAAAAAAAAAAAA 3
 RESULT 1415
 AAS09500/c
 ID AAS09500 standard; DNA; 32 BP.
 AC AAS09500;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE SMART PCR primer #2.
 XX
 KM Heat-labile uracil-DNA glycosylase; UNG; UDG; PCR primer; SMART;
 KM PCR control; LCR control; ligase chain reaction; carry-over prevention;
 KM ss.
 OS Synthetic.
 XX
 PN WO200151623-A1.
 PD 19-JUL-2001.
 PF 10-JAN-2001; 2001WO-N00000008.
 PR 12-JAN-2000; 2000NO-00000163.
 PR 27-OCT-2000; 2000NO-00005428.
 XX
 PA (BIOT-) BIOTEC ASA.
 PI Lanes O, Willasen NP, Guddal PH, Gjellesvik DR;
 DR WPI; 2001-451854/48.
 XX
 CC New cod liver uracil-DNA glycosylase enzyme, useful in monitoring or
 CC controlling a reaction system multiplying DNA sequences or in carry-over
 CC prevention procedures.
 PS Example 2; Page 20; 59pp; English.
 XX
 CC The sequence represents a SMART PCR primer used to synthesise first
 CC strand cDNA from Atlantic cod in order to isolate cDNAs encoding heat-
 CC labile uracil-DNA glycosylase, (UNG/UDG). The enzyme is useful in
 CC monitoring and/or controlling a reaction system multiplying DNA
 CC sequences, e.g. PCR (polymerase chain reaction) or LCR (ligase chain
 CC reaction). The enzyme is also useful in carry-over prevention procedures
 XX
 SQ Sequence 32 BP; 0 A; 0 C; 0 G; 30 T; 0 U; 2 Other;
 Query Match 0.2%; Score 17; DB 1; Length 32;
 Best Local Similarity 70.0%; Pred. No. 1.6e+03;
 Matches 21; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
 QY 4010 CTAATGAGAAAAAGAGAAACAAA 4039
 DB 32 BAAAAAAAAAAAAAAAAAAAAAAA 3
 RESULT 1416
 ABA01204/c
 ID ABA01204 standard; DNA; 32 BP.

XX ABA01204;
AC 11-SEP-2003 (revised)
XX 28-JAN-2002 (first entry)
DT
XX Mamushi fibrinolytic enzyme, brevinase, PCR primer, BbRP1.
DE
XX Fibrinolytic enzyme; brevinase; thermostable; thrombolytic agent;
KM mamushi; PCR primer; ss.
XX
OS Agkistrodon blomhoffi; brevicandus.
XX
XX KR001045716-A.
PN
PD 05-JUN-2001.
XX
XX 06-NOV-1999; 99KR-00049115.
PF
XX 06-NOV-1999; 99KR-00049115.
PR
XX 06-NOV-1999; 99KR-00049115.
XX
PA (LEEJ/) LEE J W.
PA (PARK/) PARK W.
XX
PI Lee JW, Park W;
XX
XX WPI; 2001-636862/73.
DR
XX Fibrinolytic enzyme, brevinase, separated from poison of viper,
PT agkistrodon blomhoffi brevicandus.
XX
XX
PS Example 5; Page 6; 23pp; Korean.
XX
CC The present invention relates to fibrinolytic enzyme, brevinase (see
CC AAG79000), which is separated from the poison of Agkistrodon blomhoffi
CC brevicandus (mamushi). The enzyme shows stability at high temperatures
CC and is thus useful in developing thrombolytic agents. The present
CC sequence is a PCR primer, which was used in an example from the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
SO Sequence 32 BP; 0 A; 0 C; 0 G; 30 T; 0 U; 2 Other;
Query Match 0.2%; Score 17; DB 1; Length 32;
Best Local Similarity 72.4%; Pred. No. 1.6e+03;
Matches 21; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
QY 4011 TAAATGAGAAAAGAGACAAA 4039
DB 31 BAAAAAAAAAAAAAAAAAAAAA 3
RESULT 1417
AAV31770/C
ID AAV31770 standard; DNA; 20 BP.
XX
XX AAV31770;
AC
XX 27-AUG-2003 (revised)
DT 21-AUG-1998 (first entry)
XX
DE Canine herpes virus PCR primer PPFnl-2.
XX
XX PCR; primer; amplification; recombinant canine herpes virus; vaccine;
KM canine herpes; ss.
XX
XX Synthetic.
OS Canine herpesvirus.
XX
XX WO9808936-A1.
PN
XX 05-MAR-1998.
PD
XX 31-JAN-1997; 97WO-UP000236.
PF

XX 28-AUG-1996; 96JP-00226832.
PR
XX (NIPP) NIPPON INST BIOLOGICAL SCIENCE.
PA
XX Xuan X, Tuchiya K, Ueda S, Mikami T, Otsuka H;
XX WPI; 1998-230257/20.
DR
XX Recombinant canine herpes virus - useful as vaccine against canine herpes
PT and distemper.
XX
XX Disclosure; Page 17; 54pp; Japanese.
PS
XX This is the nucleotide sequence of the canine Herpes virus (CHV) PCR
CC primer used for amplification in the method of the invention which
CC involved the formation of a recombinant canine herpes virus, containing
CC foreign nucleic acid sequences. The recombinant CHV is used in the
CC production of vaccines against canine herpes. (Updated on 27-AUG-2003 to
CC correct OS field.)
XX
SO Sequence 20 BP; 7 A; 9 C; 3 G; 1 T; 0 U; 0 Other;
Query Match 0.2%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 9.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4493 CATGGGCTTGCGTCGCTTG 4512
DB 20 CATGGGCTTGCGTCGCTTG 1
RESULT 1418
AAV12302/C
ID AAV12302 standard; DNA; 20 BP.
XX
XX AAV12302;
AC
XX 17-JUN-1998 (first entry)
DT
XX Ribonucleotide reductase R1 3'UTR fragment SEQ ID NO:46.
DE
XX Ribonucleotide reductase R1; 3'-untranslated region; 3'UTR; tumour;
KW housekeeping gene; identification; modulator; metastasis; neoplastic;
KM papilloma; atherosclerosis; angiogenesis; viral infection; ss.
XX
XX Homo sapiens.
OS
XX WO9800532-A2.
PN
XX 08-JAN-1998.
PD
XX 30-JUN-1997; 97WO-CA000454.
PF
XX 01-JUL-1996; 96US-0021152P.
PR
XX (WRIG/) WRIGHT J A.
PA (YOUNG/) YOUNG A H.
XX
XX Wright JA, Young AH;
PI
XX WPI; 1998-086958/08.
DR
XX New oligo-nucleotide(s) complementary to untranslated regions of
PT housekeeping genes - are useful in, e.g. identifying modulators of tumour
PT growth/metastasis and inhibiting growth of neoplastic cells.
XX
XX Claim 4; Page 29; 64pp; English.
PS
XX The present sequence represents a 3'-untranslated region (3'UTR) fragment
CC of ribonucleotide reductase R1. The present invention describes: (1) (nt)
CC oligonucleotides (ON) comprising at least 7 consecutive nucleotides
CC or their analogues of a UTR of a housekeeping gene; (2) antisense ON

CC (AON) complementary to ON; (3) ribozymes (Rb) complementary or homologous
 CC to ON, and able to cleave it; (4) DNA sequence encoding ON, OAN and Rb;
 CC (5) an antibody (Ab) that binds to ON, OAN and Rb; (6) a nt probe ncp
 CC that hybridise to ON, OAN and Rb. ON, AON, Rb and Ab are used to modulate
 CC (especially inhibit) growth of tumour cells (especially neoplastic cells)
 CC and to reduce their capacity for metastasis. The above may also be used
 CC to treat benign proliferative disorders e.g. papillomas, atherosclerosis,
 CC angiogenesis and viral infections, e.g. human immunodeficiency virus,
 CC hepatitis or herpes. ON may further be used: (i) to identify modulators
 CC of tumour growth/metastasis; (ii) to identify compounds (especially
 CC potential anticancer agents) that inhibit or enhance interaction between
 CC ON and its binding substances; (iii) as probes for detecting related
 CC sequences, and (iv) to generate Ab, used for detection and quantification
 CC of UTR especially for monitoring progress of cancer therapy. SON inhibit
 CC tumorigenicity of neoplastic cells, particularly where these are
 CC resistant to hydroxyurea

SQ Sequence 20 BP; 17 A; 1 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 9.6e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4463 CTTTTTTTTTTTTTTT 4482
 Db 20 CGTTTTTTTCTTTTTT 1

RESULT 1419
 AAV52748/c
 ID AAV52748 standard; DNA; 20 BP.
 XX AAV52748;
 AC XX
 XX 02-NOV-1998 (first entry)
 DT XX
 XX Angiotensin-converting enzyme PCR 5'-primer SEQ ID NO:1.
 DE XX
 XX Angiotensin-converting enzyme; ACE; human; heart; PCR primer; detection;
 KM screening; cardiovascular disease; ss.
 OS XX
 OS Synthetic.
 OS Homo sapiens.
 XX XX
 PN US5800990-A.
 PD XX
 PD 01-SEP-1998.
 PF XX
 PF 06-DEC-1995; 95US-00568271.
 XX XX
 PR 06-DEC-1995; 95US-00568271.
 XX XX
 PA (COLS) UNIV COLORADO.
 PI XX
 PI Perryman MB, Raynolds MV;
 XX XX
 DR WPI; 1998-494763/42.
 PT Detecting mutation(s) in angiotensin-converting enzyme gene - to assess
 PT cardiovascular disease risk.
 PS XX
 PS Example 1; Col 9; 12pp; English.

The following methods have been developed for detecting small deletions,
 CC insertions or point mutations in an angiotensin-converting enzyme (ACE)
 CC gene of a human patient: (1) a method comprising: (a) isolating an ACE
 CC genomic DNA sequence from the patient, where the sequence spans intron
 CC 25, using oligonucleotide primers in the 3' region of exon 25 and the 5',
 CC region of exon 26; (b) hybridising the genomic sequence with a detectable
 CC probe specific for the corresponding sequence with no mutations; and (c)
 CC detecting mismatches between the genomic sequence and the probe; (2) a
 CC method comprising: (a) isolating an ACE genomic DNA sequence as in (1);
 CC (b) amplifying the sequence; (c) hybridising the amplification products

CC with a probe as in (1); and (d) detecting mismatches between the
 CC amplification products and the probe; (3) a method comprising: (a)
 CC isolating an ACE genomic DNA sequence as in (1); (b) denaturing the
 CC genomic sequence to obtain single-stranded DNA; (c) hybridising the
 CC single-stranded DNA with a probe as in (1); and (d) detecting mismatches
 CC between the single-stranded DNA and the probe; (4) a method comprising:
 CC (a) isolating an ACE genomic DNA sequence as in (1); (b) amplifying the
 CC sequence; (c) denaturing the amplification products to obtain single-
 CC stranded DNA; (d) hybridising the single-stranded DNA with a probe as in
 CC (1); and (e) detecting mismatches between the single-stranded DNA and the
 CC probe. The methods are used for assessing the patient's risk of
 CC developing cardiovascular disease. The present sequence represents a PCR
 CC primer for ACE

SQ Sequence 20 BP; 0 A; 7 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 9.6e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7415 GCAGCAGCAGCAGCAGCAGC 7434
 Db 20 GCAGCAACAGCAGCGCAGC 1

RESULT 1420
 AAZ35086
 ID AAZ35086 standard; DNA; 20 BP.
 XX AAZ35086;
 AC XX
 XX 13-MAR-2000 (first entry)
 DT XX
 XX Herpesvirus entry protein B (HvEB) PCR primer PRR2A8.
 DE XX
 XX Herpesvirus entry protein B; HvEB; tumour necrosis factor receptor;
 KM alphaherpesvirus; infection; therapy; human; PCR; primer; ss.
 OS XX
 OS Synthetic.
 OS Homo sapiens.
 XX XX
 PN WC9963063-A1.
 PD XX
 PD 09-DEC-1999.
 PF XX
 PF 02-JUN-1999; 99WO-US012235.
 XX XX
 PR 03-JUN-1998; 98US-0087862P.
 XX XX
 PA (NOUN) UNIV NORTHWESTERN.
 PA (UYPE-) UNIV PENNSYLVANIA.
 XX XX
 PI Spear PG, Warner MS, Geraghty RG, Martinez MM, Montgomery RI;
 PI Cohen GH, Eisenberg RJ, Whitbeck CJ, Krummenacher C;
 XX XX
 DR WPI; 2000-097325/08.
 PT Novel proteins used to prevent viral infection and to identify other
 PT inhibitors.
 PS XX
 PS Example 1; Page 57; 144pp; English.

Primer PRR2A8 was used in the PCR amplification of herpesvirus entry
 CC protein B (HvEB) cDNA (see also AAZ35084). HvEB is a novel member of the
 CC human tumour necrosis factor receptor family that mediates entry of an
 CC alphaherpesvirus (aHV) into cells. Cellular herpesvirus entry proteins
 CC (1) such as HvEB, their mutants, homologues, derivatives, variants and
 CC active fragments are claimed, as are recombinant cells (especially CHO,
 CC murine melanoma, swine testes), vectors, and anti-cellular herpesvirus
 CC protein compounds (II). Suitable (II) include antisense oligonucleotides,
 CC antibodies specific for (I), peptides and peptidomimetics. Methods of
 CC identifying (II), of inhibiting entry of an aHV into a cell using (II),
 CC and of treating an aHV infection in an animal, especially a human, using

CC (II) are also claimed
 XX
 SQ Sequence 20 BP; 8 A; 6 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 9.6e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7414 AGCAGCAGCAGCAGCAGCAG 7433
 DB 1 AGAAGCAGCAGCAGCAGCAG 20

RESULT 1421
 AAD15628/c
 ID AAD15628 standard; DNA; 20 BP.

AC AAD15628;

DT 15-NOV-2001 (first entry)

XX Human Bcl-2 protein target DNA #2.

XX Human; Bcl-2 protein; genetic disease; antisense target; therapeutic; ss.

XX Homo sapiens.

XX WO200161030-A2.

XX 23-AUG-2001.

XX 14-FEB-2001; 2001WO-US004732.

XX 14-FEB-2000; 2000US-00504653.

XX (BOLL/) BOLLION A P.

XX (GRAY/) GRAY D M.

XX (JUSE/) JU-SEOG L.

XX BOLLION AP, Gray DM, Ju-Seog L;

XX WPI; 2001-529916/58.

XX Selecting optimal subsequence antisense targets for inhibition of mRNA

XX expression of target mRNA for the therapeutic treatment of genetic

XX disease.

XX Example 9; Page 28; 87pp; English.

XX The invention relates to a method for selecting optimal subsequence

XX antisense targets. The method involves preparing an antisense

XX oligonucleotide capable of inhibiting mRNA expression of target mRNA.

XX sequences, as well as antisense oligonucleotides capable of binding DNA.

XX The antisense and antigen libraries are useful for preparing therapeutic

XX agents for the treatment of genetic disease. The present DNA sequence is

XX human Bcl-2 protein target DNA related to the invention. Note: The

XX present sequence is shown as DNA in the specification; however, in vivo,

XX this target sequence would be mRNA

XX Sequence 20 BP; 0 A; 9 C; 10 G; 1 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 16.8; DB 1; Length 20;

XX Best Local Similarity 90.0%; Pred. No. 9.6e+02;

XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX AAS05713;
 AC
 XX
 DT 07-SEP-2001 (first entry)

XX Polypyrimidine Crick strand oligonucleotide.

XX reverse phase triplex forming oligonucleotide; RP-TFO;

XX protected nucleic acid sequence; PNAS; single nucleotide polymorphism;

XX SNP; short tandem repeat; cancer; Factor V Leiden SNP; ss.

XX Synthetic.

XX WO200132929-A1.

XX 10-MAY-2001.

XX 03-NOV-2000; 2000WO-US030534.

XX 03-NOV-1999; 99US-0163356P.

XX 03-NOV-1999; 99US-0163416P.

XX 21-DEC-1999; 99US-0171348P.

XX 07-UTL-2000; 2000US-0216579P.

XX (CYGE-) CYGENE INC.

XX (OSTE/) OSTE C C.

XX Oste CC, Ramberg ER;

XX WPI; 2001-343488/36.

XX Analyzing target nucleic acid sequences, useful for population genetics,

XX drug development and diagnosing cancer, comprises hybridizing triple

XX forming oligonucleotide and probe to target sequence.

XX Example 2; Page 66; 141pp; English.

XX The sequence is a polypyrimidine oligonucleotide for binding a second

XX reverse phase triplex forming oligonucleotide, RP-TFO, (3' to the SNP) to

XX the target SNP used to analyse Factor V Leiden SNP using the method of

XX the invention. The invention relates to analysing target nucleic acid

XX sequences comprising restricting isolated DNA, hybridizing at least one

XX triplex forming oligonucleotide (TFO), adding a 3' to 5' exonuclease to

XX form a protected nucleic acid sequence (PNAS) tail structure, hybridizing

XX the captured structure with a single nucleotide polymorphisms (SNP)

XX identification probe and determining the SNP score. The methods can be

XX used for analysing target nucleic acid sequences, especially genomic DNA

XX sequences, to determine if they contain SNPs or short tandem repeats

XX (STRs). The methods can be used to detect SNPs for use in population

XX genetics, drug development, forensics, cancer, genetic disease research,

XX genomic analysis, diagnostics and therapeutics in humans, plants and

XX animals

XX Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 16.8; DB 1; Length 20;

XX Best Local Similarity 90.0%; Pred. No. 9.6e+02;

XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4483
 DB 1 TTTT TTTT TTTT TTTT TTTT 20

RESULT 1423
 AAS20967/c
 ID AAS20967 standard; DNA; 20 BP.

AC AAS20967;

DT 09-APR-2002 (first entry)

XX PCR primer Snrpn-U relating to gene imprinting invention.

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XX Human; genomic imprinting; pluripotent mouse embryonic germ cell line;
 KW Eg; methylated CpG island; DNA methylation; gene imprinting;
 KW post-translational modification of histone; cancer; birth defect;
 KW diabetes; aberrant imprinting; PCR; primer; ss.
 OS Homo sapiens.
 PN W0200190313-A2.
 XX
 PD 29-NOV-2001.
 XX
 PF 22-MAY-2001; 2001WO-US016253.
 PR 22-MAY-2000; 2000US-0206158P.
 PR 22-MAY-2000; 2000US-0206161P.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Feinberg A, Strichman-Almashanu L, Jiang S;
 DR WPI; 2002-083100/11.
 XX
 PT Forming embryonic germ cells useful as model system to study imprinting
 PT involves mating genetically divergent male and female mammal of same
 PT species, dissecting and dissociating embryo obtained from pregnant
 PT mammal.
 XX
 PS Disclosure; Page 54; 125pp; English.
 XX
 CC The present invention relates to a model system for genomic imprinting
 CC using pluripotent mouse embryonic germ (EG) cell lines derived from an
 CC interspecific cross. Also disclosed is a library containing methylated
 CC CpG islands and a method for assaying methylation in one or more
 CC impritable genes. The gene imprinting assay is carried out by single-
 CC nucleotide primer extension or hot stop PCR. The assays are carried out
 CC to determine the post-translational modification of histones. The method
 CC further involves identifying a test substance as a candidate drug for
 CC treating cancer if the test substance enhances imprinting of a gene whose
 CC imprinting is lost in cancer, or if the test substance inhibits
 CC imprinting of a gene whose imprinting is gained in cancer. The methylated
 CC CpG islands are useful for providing an assessment of the risk of
 CC developing cancer, or for providing diagnostic information relative to
 CC cancer which involves determining the methylation status of the CpG
 CC island in a patient's DNA. The EG cells allow the accession of imprinted
 CC genes which are useful for detecting birth defects, diabetes and cancers
 CC associated with aberrant imprinting. The EG cell lines represent the
 CC first in vitro model system in which genomic imprinting can be followed
 CC dynamically and the two alleles can be distinguished. AAS20953-AAS20969
 CC represent PCR primers described in the present invention
 CC
 XX
 SQ Sequence 20 BP; 1 A; 5 C; 6 G; 8 T; 0 U; 0 Other;
 Query Match 0.2%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 9.6e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 7413 CAGCAGCAGCAGCAGCA 7432
 Db 20 CATGACGACGACGACGCA 1
 AC AB230367;
 AC 30-JAN-2003 (first entry)
 DT
 XX Candida albicans GRACE strain PCR primer SEQ ID NO 4518.
 DE

KW Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;
 KW signal transduction; DNA replication; cell division; growth;
 KW proliferation; Candida albicans; fungicide; antifungal; PCR; primer; ss.
 OS
 XX Candida albicans.
 PN W0200253728-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 26-DEC-2001; 2001WO-US049486.
 PR 29-DEC-2000; 2000US-0259128P.
 PR 20-FEB-2001; 2001US-00792024.
 PR 22-AUG-2001; 2001US-0314050P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;
 DR WPI; 2002-566694/60.
 XX
 PT Constructing strains for identifying gene products as effective targets
 PT for therapeutic intervention, by inactivating in the strain one allele of
 PT a gene and placing other allele of the gene under conditional expression.
 XX
 PS Claim 36; SEQ ID NO 4518; 167pp + Sequence listing; English.
 XX
 CC The invention relates to constructing (M1) a strain of diploid fungal
 CC cells in which both alleles of a gene are modified, comprising modifying
 CC one allele by insertion or replacement by a cassette having an
 CC expressible selectable marker and modifying other allele by
 CC recombination, of a promoter replacement fragment with a heterologous
 CC promoter, so that expression of the second allele is regulated by the
 CC promoter. (M1) is useful for constructing a strain of diploid fungal
 CC cells in which both alleles of a gene are modified. The diploid fungal
 CC cells having both alleles modified are useful for identifying a gene that
 CC is essential to the survival or growth of a fungus, a gene that
 CC contributes to the virulence and/or pathogenicity of a fungus, a gene
 CC that contributes to the resistance of a diploid fungus to an antifungal
 CC agent, an antifungal agent that inhibits the growth of a diploid fungus
 CC and for identifying a therapeutic agent for treatment of a mammalian
 CC disease. (M1) is useful for identifying a compound which modulates the
 CC activity of a gene product, preferably enzymatic activity, carbon
 CC compound catabolism, biosynthetic, transporter, transcriptional,
 CC translational, signal transduction, DNA replication and cell division
 CC activity. The method is useful for identifying a compound having the
 CC ability to inhibit growth or proliferation of C. albicans cells and for
 CC treating infection by C. albicans. The present sequence is that of a PCR
 CC primer used in the method of the invention. Note: The sequence data for
 CC this patent is not represented in the printed specification but is based
 CC on sequence information supplied to Derwent by the European Patent Office
 CC
 XX
 SQ Sequence 20 BP; 3 A; 4 C; 7 G; 6 T; 0 U; 0 Other;
 Query Match 0.2%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 90.0%; Pred. No. 9.6e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 7410 CATCAGCAGCAGCAGCA 7429
 Db 20 CATCAGCTTCAGCAGCAGCA 1
 AC AAD33499;
 AC AAD33499;
 AC 01-JUL-2002 (first entry)
 DT
 XX TTT18Apad_PS27-20-0003 probe for calibration of molecular array data.
 DE

```

XX Molecular array; probe; ss.
XX Unidentified.
OS EPI186673-A2.
XX
XX 13-MAR-2002.
PD
XX 10-SEP-2001; 2001EP-00307665.
PF
XX 11-SEP-2000; 2000US-00659173.
PR
XX (AGIL-) AGILENT TECHNOLOGIES INC.
PA
XX Wobler PK, Delenattarr GC;
PI
XX WPI; 2002-282886/33.
DR
XX Calibration of molecular array data by employing calibration probes that
PT generate signals proportional to total concentrations of labeled target
PT molecules, and molecular arrays incorporating sets of calibration probes.
XX
XX Disclosure; Page 14; 32pp; English.
PS
XX The invention relates to a method for calibrating data scanned from a
CC molecular array. The method involves employing calibration probes that
CC generate signals proportional to the total concentrations of labeled
CC target molecules to which the molecular array probes are directed over an
CC entire range of sample solutions and molecular arrays incorporating sets
CC of calibration probes. Method is useful for calibrating different types
CC of signals scanned from a molecular array, or calibrating signals scanned
CC from different molecular arrays. The present sequence is poly (A)
CC normalisation probe used in calibration of molecular array data
XX
SQ Sequence 20 BP; 16 A; 2 C; 0 G; 2 T; 0 U; 0 Other;
Query Match 0.2%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 9.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4461 GACTTTTTTTTTTTTTTTTT 4480
DB 20 GAGATTTTTTTTTTTTTTTT 1
RESULT 1426
AB286069/C
ID AB286069 standard; DNA; 20 BP.
XX
XX AB286069;
AC
XX
XX 17-OCT-2003 (first entry)
DT
XX
XX Human oligonucleotide sequence.
DE
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XX antiaesthetic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
OS
XX WO200285308-A2.
PN
XX 31-OCT-2002.
PD
XX 23-APR-2002; 2002MO-US013135.
PF
XX 24-APR-2001; 2001US-0286137P.
PR
XX

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PA (EPIC-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-229219/22.
DR
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(e) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX Claim 15; SEQ ID NO 1311; 872pp; English.
PS
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiaesthetic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 0 A; 8 C; 7 G; 5 T; 0 U; 0 Other;
Query Match 0.2%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 9.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 7413 CAGCAGCAGCAGCAGCAGCA 7432
DB 20 CAGCGCGCGCAGCAGCAGCA 1
RESULT 1427
AB289676/C
ID AB289676 standard; DNA; 20 BP.
XX
XX AB289676;
AC
XX
XX 17-OCT-2003 (first entry)
DT
XX
XX Human oligonucleotide sequence.
DE
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XX antiaesthetic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
OS
XX WO200285308-A2.
PN
XX 31-OCT-2002.
PD
XX 23-APR-2002; 2002MO-US013135.
PF
XX 24-APR-2001; 2001US-0286137P.
PR
XX

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PA (EPIG-) EPIGENESIS PHARM INC.
XX
XX NYCE JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI, 2003-229219/22.
XX
XX PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAe, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX PS Claim 15; SEQ ID NO 1312; 872pp; English.
XX
XX CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cyostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 20 BP; 0 A; 8 C; 7 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 9.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 7413 CAGCAGCAGCAGCAGCAGCA 7432
DB 20 CAGCAGCAGCAGCGCGCAGCA 1
XX
XX RESULT 1430
AB285669
ID AB285669 standard; DNA; 20 BP.
XX
XX AC AB285669;
XX
XX DT 17-OCT-2003 (first entry)
XX
XX DE Human oligonucleotide sequence.
XX
XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cyostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
XX OS Homo sapiens.
XX
XX PN WO200285308-A2.
XX
XX PD 31-OCT-2002.
XX
XX PF 23-APR-2002; 2002MO-US013135.
XX
XX PR 24-APR-2001; 2001US-0286137P.
XX

PA (EPIG-) EPIGENESIS PHARM INC.
XX
XX NYCE JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI, 2003-229219/22.
XX
XX PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAe, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX PS Claim 15; SEQ ID NO 911; 872pp; English.
XX
XX CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cyostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 20 BP; 0 A; 2 C; 0 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 9.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4483
DB 1 TTTT TTTT TTTT TTTT TTTT TTTT 20
XX
XX RESULT 1431
AB285353/C
ID AB285353 standard; DNA; 20 BP.
XX
XX AC AB285353;
XX
XX DT 17-OCT-2003 (first entry)
XX
XX DE Human oligonucleotide sequence.
XX
XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cyostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
XX OS Homo sapiens.
XX
XX PN WO200285308-A2.
XX
XX PD 31-OCT-2002.
XX
XX PF 23-APR-2002; 2002MO-US013135.
XX
XX PR 24-APR-2001; 2001US-0286137P.
XX

PA	(EPICG-) EPIGENEESIS PHARM INC.
XX	
P1	Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
P1	Miller S, Tang L, Shahabuddin S;
XX	
DR	WPI; 2003-229219/22.
XX	
PT	Pharmaceutical composition for treating ailments associated with impaired
PT	respiration, has oligo(s) antisense to specific gene(s) or its
PT	corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT	ubiquinone.
PS	Claim 15; SEQ ID NO 777; 872pp; English.
XX	
CC	The invention relates to a novel pharmaceutical composition, which has a
CC	first active agent comprising an oligonucleotide antisense to the
CC	initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC	5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC	junctions of genes encoding a polypeptide associated with lung and/or
CC	nasal airway dysfunction and a second active agent comprising an
CC	antiinflammatory steroid and ubiquinone. A composition of the invention
CC	has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC	immunosuppressive, and cyostatic activity. The composition may have a
CC	use in antisense gene therapy. The composition is useful for treating or
CC	preventing a respiratory, lung or malignant disease or condition, also
CC	for enhancing the prophylactic or therapeutic respiratory effect of an
CC	antiinflammatory steroid in a subject, for reducing or depleting levels
CC	of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC	receptor, producing bronchodilation, increasing levels of ubiquinone or
CC	lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC	lung inflammation, lung allergies, or a respiratory disease or condition.
CC	Note: The sequence data for this patent is not represented in the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences
XX	
SQ	Sequence 20 BP; 18 A; 0 C; 2 G; 0 T; 0 U; 0 Other;
	Query Match 0.2%; Score 16.8; DB 1; Length 20;
	Best Local Similarity 90.0%; Pred. No. 9.6e+02;
	Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY	4464 TTTTTTTTTTTTTTTTTTTT 4483
Db	20 TTTTTCTTTCTTTT 1
RESULT 1432	
ID ACC70568/c	
ACC70568 standard; DNA; 20 BP.	
XX	
AC	ACC70568;
XX	
DT	13-AUG-2003 (first entry)
XX	
DE	Sphingosine-1-phosphate lyase antisense oligonucleotide, SEQ ID 61.
XX	
KM	Cytostatic; antimicrobial; antiinflammatory; tumour; infection;
KM	sphingosine-1-phosphatase lyase; developmental disorder; apoptosis;
KW	inflammation; antisense; phosphorothioate; ss.
XX	
OS	Synthetic.
XX	
FH	Key
FT	modified_base
FT	Location/Qualifiers
FT	1..20
FT	/tag= a
FT	/mod_base= OTHER
FT	/note= "This oligonucleotide has a phosphorothioate
FT	backbone and 2'-methoxyethyl (2'-MOE) wings at the 5'
FT	and 3' ends, which are 5 nucleotides in length. Also all
FT	cytidine residues are 5-methylcytidines"
XX	
PN	WO2003028637-A2.
XX	

BD	10-APR-2003.
XX	
PF	26-SEP-2002; 2002W0-US030575.
XX	
PR	28-SEP-2001; 2001US-00967669.
XX	
PA	(ISIS-) ISIS PHARM INC.
PI	Bennett FC, Freier SM;
XX	
DR	WPI; 2003-381581/36.
XX	
PT	New antisense oligonucleotides for modulating sphingosine-1-phosphate
PT	lyase gene expression, useful for preventing or treating a developmental
PT	disorder or aberrant apoptosis, e.g. infection, inflammation or tumor
PT	formation.
XX	
PS	Example 15; Page 73; 118pp; English.
XX	
CC	The present invention relates to novel antisense oligonucleotides
CC	(ACC70520-ACC70597) which are targeted to a sphingosine-1-phosphate lyase
CC	DNA sequence, and specifically hybridizes with the nucleic acid and
CC	inhibits the expression of sphingosine-1-phosphate lyase. The antisense
CC	oligonucleotides are useful for treating an animal having a disease or
CC	condition associated with sphingosine-1-phosphate lyase, particularly a
CC	developmental disorder, or a disease or condition arising from aberrant
CC	apoptosis, e.g. infection, inflammation or tumour formation
XX	
SQ	Sequence 20 BP; 6 A; 7 C; 4 G; 3 T; 0 U; 0 Other;
	Query Match 0.2%; Score 16.8; DB 1; Length 20;
	Best Local Similarity 90.0%; Pred. No. 9.6e+02;
	Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
CY	4680 CTATCCTGATTCGTGATGA 4639
DB	20 CTATCCTGGCGTGTGATGA 1
	RESULT 1433
ID	ADB65928
XX	ADB65928 standard; DNA; 20 BP.
AC	
XX	ADB65928;
XX	
DT	04-DEC-2003 (first entry)
XX	
DE	Clone specific PCR primer #129.
XX	
KW	Pharmaceutical; diagnostic; gene therapy; tissue regeneration;
KW	cell regeneration; membrane protein; signal transduction-related protein;
KW	transcription-related protein; osteoporosis; neurological disease;
XX	cancer; tumour; primer; PCR; ss.
XX	
OS	Homo sapiens.
XX	
PN	EP1308459-A2.
XX	
PD	07-MAY-2003.
XX	
PF	28-MAR-2002; 2002EP-00007401.
XX	
PR	05-NOV-2001; 2001JP-00379298.
XX	
PR	25-JAN-2002; 2002US-00350578.
XX	
PA	(HELI-) HELIX RGS INST.
XX	(REAS-) RES ASSOC BIOTECHNOLOGY.
XX	
PI	Isegai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI	Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI	Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuno Y;
XX	
DR	WPI; 2003-450961/43.

XX New polynucleotides and polypeptides, useful for developing a diagnostic
PT marker or medicines for regulation of their expression and activity, or
PT as targets of gene therapy.
XX
XX
XX Example 8; Page 129; 222pp; English.
XX
CC The invention discloses a polynucleotide comprising a sequence selected
CC from 1970 fully defined nucleotide sequences which encode novel
CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
CC or its partial peptide, an antibody binding to the polypeptide or peptide
CC of the polynucleotide, immunologically assaying the polypeptide or
CC peptide of the polynucleotide by contacting the polypeptide or peptide
CC with the antibody of the encoded protein, and observing the binding
CC between the two, a transformant carrying the polynucleotide in an
CC expressible manner and an antisense polynucleotide. The oligonucleotide
CC is useful as a primer for synthesizing the polynucleotide, or as a probe
CC for detecting the polynucleotide. The polynucleotides and encoded
CC proteins are useful as pharmaceutical agents and many disease-related
CC genes may be included in them, for developing a diagnostic marker or
CC medicines for regulation of their expression and activity, or as targets
CC of gene therapy. The genes are involved in tissue and/or cell
CC regeneration. Membrane proteins, signal transduction-related proteins,
CC transcription-related proteins, disease-related proteins and genes
CC encoding them can be used as indicators for diseases (e.g. osteoporosis,
CC neurological diseases, cancer, tumours. The cDNA may be used to regulate
CC the activity or expression of the encoded protein to treat diseases. The
CC sequence presented is clone specific PCR primer which was used in the
CC expression analysis of the genes of the invention. Note: Some of the
CC sequence data for this patent is not represented in the printed
CC specification, but is based on sequence information supplied by the
CC European Patent Office.
XX
SQ Sequence 20 BP; 2 A; 9 C; 0 G; 9 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 9.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3443 CCACCTTACTTCTCTCCCT 3462

DB 1 CCACCTTATTCTCTCCCT 20

RESULT 1434

ABX81537
ID ABX81537 standard; DNA; 21 BP.

XX AC ABX81537;

XX DT 22-APR-2003 (first entry)

DE DNA encoding an RGD-containing peptide.

XX Targeting ligand; bioactive agent; polymer matrix; cancer; cytoskeletal;

KM cathepsin-D substrate; peptides; neuroreceptor; adrenal receptor;

KM fibronectin; vitronectin; integrin; RGD motif; angiogenic endothelium;

KM tumour; cationic cancer-targeting peptide; ds; bFGF;

KW basic fibroblast growth factor.

XX Synthetic.

OS US2002041898-A1.

XX PN 11-APR-2002.

XX PF 25-JUL-2001; 2001US-00912609.

XX PR 05-JAN-2000; 2000US-00478124.

XX PR 31-OCT-2000; 2000US-00703474.

XX PA (UNGE/) UNGER E C.

XX PA (MATS/) MATSUNAGA T O.

PA (RAMA/) RAMASWAMI V.
PA (ROMA/) ROMANOWSKI M J.
PI Unger EC, Matsunaga TO, Ramaswami V, Romanowski MJ;
XX
XX MPI; 2003-208921/20.
DR P-PSDB; ABUS9647.

PT Targeted delivery system comprising a bioactive agent homogeneously
PT dispersed in a targeted matrix is especially useful in cancer therapy.

XX Example 10; Page 30; 46pp; English.

CC The invention relates to a composition comprising a bioactive agent
CC homogeneously dispersed in a targeted matrix (polymer and targeting
CC ligand). Also included are a targeted matrix for use as a delivery
CC vehicle comprising a polymer associated with a targeting ligand,
CC enhancing the bioavailability of an agent comprising administration of
CC the composition and treating cancer comprising administration of the
CC novel composition. The method is useful for targeted delivery of a drug,
CC especially in cancer therapy. The targeting ligand may be a peptide.
CC Examples of targeting peptides are disclosed including cathepsin-D,
CC substrate peptides, peptides targeting receptors in the brain and kidney,
CC peptides recognising fibronectin- and vitronectin-binding integrins,
CC peptides targeting the RGD (Arg-Gly-Asp)-motif in, e.g., antibodies,
CC peptides targeting the angiogenic endothelium of solid tumours, tissue
CC specific peptides (e.g. of lung, skin, pancreas, intestine, uterus,
CC adrenal gland and retina), and cationic cancer-targeting peptides. In an
CC experiment disclosed in the invention a DNA sequence encoding human bFGF
CC (basic fibroblast growth factor) is mutated to express bFGF protein with
CC C-terminal cysteines. The mutated bFGF can be conjugated to PEG
CC (polyethylene glycol) in a bioconjugate. The present sequence encodes a
CC synthetic peptide (GGGRGDS) disclosed in the same experiment, but the use
CC of the peptide is not explained
XX
SQ Sequence 21 BP; 5 A; 1 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3627 GGGGGTGGAGAGAGAGTAG 3646

DB 1 GGGGGTGGAGAGAGAGTAG 20

RESULT 1435

ACC90647
ID ACC90647 standard; DNA; 21 BP.

XX AC ACC90647;

XX DT 13-AUG-2003 (first entry)

XX DE Human CYP1A2 PCR primer SEQ ID NO:13.

XX CYP1A2; cytochrome P450; cytosolic; hepatotropic; dermatological;

KM cerebroprotective; gene therapy; cancer; congenital jaundice;

KM porphyria cutanea tarda; tardive dyskinesia; schizophrania; human; PCR;

KW primer; ss.

XX Homo sapiens.

OS WO2003014387-A2.

XX PN 20-FEB-2003.

XX PF 08-AUG-2002; 2002WO-EP008893.

XX PR 08-AUG-2001; 2001EP-00118770.

XX PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.

PI Wojnowski L, Presecan-Siedel E;
 XX WPI; 2003-256599/25.
 DR
 XX New CYP1A2 polynucleotide and polypeptide, useful for the preparation of
 PT a diagnostic or therapeutic composition for cancer, congenital jaundice,
 PT porphyria cutanea tarda or tardive dyskinesia in schizophrenia.
 XX
 PS Example 1; Page 38, 117pp; English.
 XX
 CC The invention relates to a novel polynucleotide comprising any of 37 11-
 CC 761 base pair sequences, given in the specification, encoding a
 CC polypeptide with any of 4 28-31 residue amino acid sequences, in the
 CC specification, hybridising to a CYP1A2 gene, or encoding a CYP1A2
 CC polypeptide or fragment comprising an amino acid substitution at position
 CC 6, 298, 401 or 438. A polypeptide of the invention has cytostatic,
 CC hepatotropic, dermatological, and cerebroprotective activity. A
 CC polynucleotide of the invention may act as a CYP1A2-antagonist or CYP1A2-
 CC agonist, and may have a use in gene therapy. The methods and compositions
 CC of the present invention are useful for the preparation of a diagnostic
 CC or therapeutic composition for a disease, in particular cancer,
 CC congenital jaundice, porphyria cutanea tarda or tardive dyskinesia in
 CC schizophrenia. The sequences shown in ACC90635-ACC90686 represent PCR
 CC primer used in the invention to screen for polymorphisms within CYP1A2
 XX
 SQ Sequence 21 BP; 8 A; 3 C; 10 G; 0 T; 0 U; 0 Other;
 Query Match 0.2%; Score 16.8; DB 1; Length 21;
 Best Local Similarity 90.0%; Pred. No. 1e+03;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2861 AGGAGCGAAGAGGAGGAG 2880
 DB 2 AGGAGCGAAGAGGAGGAG 21
 RESULT 1436
 AAZ37995
 ID AAZ37995 standard; DNA; 22 BP.
 XX
 AC AAZ37995;
 XX
 DT 07-FEB-2000 (first entry)
 XX
 DE Human GLC1A gene exon 3 specific forward primer.
 XX
 KM Glaucoma; PCR amplification; primary open wide angle glaucoma;
 KM GLC1A gene; human; PCR primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN MO9951779-A2.
 XX
 PD 14-OCT-1999.
 XX
 PF 07-APR-1999; 99WO-US007671.
 XX
 PR 07-APR-1998; 98US-00056285.
 XX
 PA (IOWA) UNIV IOWA RES FOUND.
 XX
 PI Stone EM, Sheffield VC, Alward WLM, Fingert J;
 DR WPI; 2000-022956/02.
 XX
 PT Determination of a predisposition to glaucoma by analysing mutations in
 PT the GLC1A gene.
 XX
 PS Claim 1; Page 132; 137pp; English.
 XX
 CC The invention relates to a method for the determination of a
 CC predisposition to glaucoma. The method comprises amplifying a GLC1A gene

CC with a primer pair selected from the sequences shown in AAZ37981-238008.
 CC The primers are used to determine whether a subject has or has the
 CC potential to develop primary open wide angle glaucoma. Sequences AAZ37981
 CC -238008 represent primer pairs specific for human GLC1A gene exon
 CC sequences. These primers were used for the GLC1A assay to identify
 CC patients having a predisposition to glaucoma
 XX
 SQ Sequence 22 BP; 4 A; 2 C; 7 G; 9 T; 0 U; 0 Other;
 Query Match 0.2%; Score 16.8; DB 1; Length 22;
 Best Local Similarity 90.0%; Pred. No. 1.1e+03;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 5597 TTTGGTTAAGCGGCTTC 5616
 DB 2 TATGATTAAGCGGCTTC 21
 RESULT 1437
 AAF76808
 ID AAF76808 standard; DNA; 22 BP.
 XX
 AC AAF76808;
 XX
 DT 14-MAY-2001 (first entry)
 XX
 DE Codon-optimised HPV6 E2 fragment 6PM.
 XX
 KM Human papillomavirus; HPV; HPV16; HPV6a; HPV18; L1; E2; E7; E1;
 KM antiviral; immunostimulant; vaccine; immunogen; infection; ss.
 XX
 OS Synthetic.
 OS Human papillomavirus.
 XX
 PN WO200114416-A2.
 XX
 PD 01-MAR-2001.
 XX
 PF 21-AUG-2000; 2000WO-US022932.
 XX
 PR 25-AUG-1999; 99US-0150728P.
 PR 07-JUN-2000; 2000US-0210143P.
 XX
 PA (MERT) MERCK & CO INC.
 XX
 PI Neepert MP, McClements WL, Jansen KU, Schultz LD, Chen L, Wang X;
 XX
 DR WPI; 2001-218428/22.
 XX
 PT Novel synthetic polynucleotide encoding human papillomavirus (HPV)
 PT protein or mutated HPV protein useful as anti-HPV vaccines, comprises
 PT optimized-codons for expression of the viral proteins in human host
 PT cells.
 XX
 PS Example 6; Fig 23; 119pp; English.
 XX
 CC The present sequence is an oligomer which was used in the assembly of one
 CC of a number of synthetic polynucleotides that encode a human
 CC papillomavirus (HPV) protein, or a mutated form of a HPV protein. The
 CC mutated HPV proteins have reduced protein function as compared to wild
 CC type proteins but maintain immunogenicity. The proteins comprise codons
 CC for optimised expression in humans. The polynucleotides are useful as a
 CC vaccine which provides effective immunoprophylaxis against papillomavirus
 CC infection through stimulation of neutralising antibody and cell-mediated
 CC immunity
 XX
 SQ Sequence 22 BP; 9 A; 9 C; 4 G; 0 T; 0 U; 0 Other;
 Query Match 0.2%; Score 16.8; DB 1; Length 22;
 Best Local Similarity 90.0%; Pred. No. 1.1e+03;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 7406 GCAACATCAGCAGCAGCAGC 7425

Db 3 GCACACACAGCAGCAGCAGC 22

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RESULT 1438
AAF76807/c
XX AAF76807 standard; DNA; 23 BP.
XX
AC AAF76807;
XX
DT 14-MAY-2001 (first entry)
XX
DE Codon-optimised HPV6 E2 fragment 6PL.
XX
KM Human papillomavirus; HPV; HPV16; HPV6a; HPV18; L1; E2; E7; E1;
KM antiviral; immunostimulant; vaccine; immunogen; infection; ss.
XX
OS Human papillomavirus.
OS Synthetic.
XX
PN WO200114416-A2.
XX
PD 01-MAR-2001.
XX
PF 21-AUG-2000; 2000WO-US022932.
XX
PR 25-AUG-1999; 99US-0150728P.
PR 07-JUN-2000; 2000US-0210143P.
XX
PA (MERI ) MERCK & CO INC.
XX
PI Neoper MP, McClements WL, Jansen KU, Schultz LD, Chen L, Wang X;
XX
DR WPI; 2001-218428/22.
XX
PT Novel synthetic polynucleotide encoding human papillomavirus (HPV)
PT protein or mutated HPV protein useful as anti-HPV vaccines, comprises
PT optimized-codons for expression of the viral proteins in human host
PT cells.
XX
PS Example 6; Fig 23; 119pp; English.
XX
XX The present sequence is an oligomer which was used in the assembly of one
CC of a number of synthetic polynucleotides that encode a human
CC papillomavirus (HPV) protein, or a mutated form of a HPV protein. The
CC mutated HPV proteins have reduced protein function as compared to wild
CC type proteins but maintain immunogenicity. The proteins comprise codons
CC for optimised expression in humans. The polynucleotides are useful as a
CC vaccine which provides effective immunoprophylaxis against papillomavirus
CC infection through stimulation of neutralising antibody and cell-mediated
CC immunity
XX
SQ Sequence 23 BP; 0 A; 5 C; 9 G; 9 T; 0 U; 0 Other;
Query Match 0.2%; Score 16.8; DB 1; Length 23;
Best Local Similarity 90.0%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 7406 GCACACTCAGCAGCAGCAGC 7425
DB 23 GCACACACAGCAGCAGCAGC 4
RESULT 1439
ABA05571
ID ABA05571 standard; DNA; 23 BP.
XX
AC ABA05571;
XX
XX 26-FEB-2002 (first entry)
XX
DE PCR primer GSH2R7.
XX

```

```

KM Glutathione synthase; Saccharomyces cerevisiae; yeast; cysteine;
KM gamma-glutamylcysteine; food industry; flavour enhancer; PCR primer; ss.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200190310-A1.
XX
PD 29-NOV-2001.
XX
PF 24-MAY-2001; 2001WO-JP004366.
XX
PR 25-MAY-2000; 2000JP-00155121.
XX
PA (AJIN ) AJINOMOTO CO INC.
XX
PI Nishituchi H, Sano K, Sugimoto R, Ueda Y;
XX
DR WPI; 2002-083099/11.
XX
PT A novel glutathione synthase-lacking Saccharomyces cerevisiae useful for
PT producing gamma-glutamylcysteine and then cysteine for application in
PT food industry to improve flavor.
XX
PS Disclosure; Page 27; 31pp; Japanese.
XX
XX The invention relates to a glutathione synthase-lacking Saccharomyces
CC cerevisiae strain that grows slower than its wild-type in a medium
CC containing not less than 1 wt.% gamma-glutamylcysteine in the logarithmic
CC growth phase with 0.004-0.1 wt.% glutathione when cultured. The method is
CC useful for production of gamma-glutamylcysteine and cysteine for use in
CC the food industry to improve flavour. The present sequence is a PCR
CC primer provided in the specification
XX
SQ Sequence 23 BP; 11 A; 4 C; 6 G; 2 T; 0 U; 0 Other;
Query Match 0.2%; Score 16.8; DB 1; Length 23;
Best Local Similarity 90.0%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6964 GAAGGAAATGAGCTAAACA 6983
DB 2 GAAGGAAATGAGCTAAACA 21
RESULT 1440
AAL57112
ID AAL57112 standard; DNA; 23 BP.
XX
XX AAL57112;
XX
AC AAL57112;
XX
DT 17-SEP-2003 (first entry)
XX
DE Human epithelial cadherine PCR primer 2 (from primer pair A).
XX
KM Human epithelial cadherine; E cadherine; gastric carcinoma; PCR; primer;
KM ss.
XX
OS Homo sapiens.
XX
PN WO2003042409-A2.
XX
PD 22-MAY-2003.
XX
PF 15-NOV-2002; 2002WO-IT000729.
XX
PR 16-NOV-2001; 2001IT-TO001077.
XX
PA (UYUR-) UNIV URBINO.
XX
PI Magnani M, Graziano F, Ruzzo A;
XX
DR WPI; 2003-449579/42.
XX

```

PT Identifying greater susceptibility to gastric carcinoma by searching for
PT polymorphisms in the promoter of the E-cadherine gene.
XX
XX Claim 11; Page 12; 17pp; English.
CC This invention relates to a novel method for the diagnosis of greater
CC susceptibility to gastric carcinoma, comprising searching for a possible
CC polymorphism in the promoter of the epithelial cadherine (E-cadherine)
CC gene. The method is useful for identifying a genetic polymorphism that
CC leads to a greater predisposition to the onset of gastric carcinoma. The
CC method is relatively simple, quick, accurate and reliable. The present
CC sequence is that of E-cadherine PCR primer 2 (from primer pair A) used
CC during a method to identify the genotype of an individual for a C to A
CC polymorphism at nucleotide -160 of the E-cadherine gene and claimed in
CC claim 11 of the specification
XX
XX Sequence 23 BP; 6 A; 7 C; 8 G; 2 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 16.8; DB 1; Length 23;
Best Local Similarity 90.0%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 7411 ATCAGCAGCAGCAGCAGCAG 7430
Db 4 ACCTGCGACGACGACGACGACG 23
RESULT 1441
ADC81375
ID ADC81375 standard; DNA; 23 BP.
XX
XX ADC81375;
AC
XX 01-JAN-2004 (first entry)
XX
XX PCR primer R1 #SEQ ID 2.
XX
XX
XX Yeast; N-methyl-N'-nitro-N-nitrosoguanidine; MNNG;
KM gamma-glutamyl cysteine; Food; drink; alcohol; bread; yeast extract;
KM glutathione synthetase; PCR; primer; ss.
XX
XX Saccharomyces cerevisiae.
XX
XX JP2003159048-A.
XX
XX 03-JUN-2003.
XX
XX 26-NOV-2001; 2001JP-00359781.
XX
XX 26-NOV-2001; 2001JP-00359781.
XX
XX (AJIN) AJINOMOTO KK.
XX
XX WPI; 2003-818671/77.
XX
XX Novel yeast strain having N-Methyl-N'-nitro-N-nitrosoguanidine resistance
PT and producing gamma-glutamyl cysteine, useful for manufacturing cysteine
PT containing food stuffs.
XX
XX Example 1; SEQ ID NO 2; 30pp; Japanese.
XX
XX The invention relates to a yeast strain having N-methyl-N'-nitro-N-
CC nitrosoguanidine (MNNG) resistance and produces gamma-glutamyl cysteine.
CC The yeast strain of the invention is useful in producing food/beverage
CC products such as alcohol, bread or fermented-foods. It is also useful in
CC manufacturing yeast extract and in the manufacturing of gamma-glutamyl
CC cysteine or cysteine containing foodstuffs. The current sequence
CC represents a PCR primer used in an example from the invention for
CC amplifying the glutathione synthetase gene.
XX
SQ Sequence 23 BP; 11 A; 4 C; 6 G; 2 T; 0 U; 0 Other;
Query Match 0.2%; Score 16.8; DB 1; Length 23;

Best Local Similarity 90.0%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6964 GAGGAGTACGCTAAACCA 6983
Db 2 GAGGAGTACGCTAAACCA 21
RESULT 1442
ADD43540
ID ADD43540 standard; DNA; 23 BP.
XX
XX ADD43540;
AC
XX 15-JUN-2004 (first entry)
XX
XX Human PAPSS2 PCR primer #11.
XX
XX Human; ss; PCR; PAPSS2;
KM 3'-phosphoadenosine-5'-phosphosulphate synthetase 2;
KM spondyloepimetaphyseal dysplasia; SEMD; gene therapy;
KM osteoarthritis disorder; Stickler syndrome; spondyloepiphyseal dysplasia;
KM achondrogenesis; achondroplasia; chondrodysplasia; diastrophic dysplasia;
KM pseudoachondroplasia; multiple epiphyseal dysplasia; chromosome 10q23-24;
KM primer.
XX
XX Homo sapiens.
XX
XX US2003195162-A1.
XX
XX 16-OCT-2003.
XX
XX 02-JUL-2001; 2001US-00896200.
XX
XX 17-SEP-1999; 99US-00399212.
XX
XX (COHN/) COHN D H.
PA (PATY/) PATYAZ-UL-HAQUE M.
PA (KING/) KING L.
PA (KRAK/) KRAKOW D.
XX
XX Cohn DH, Patyaz-UL-Haque M, King L, Krakow D;
DR WPI; 2003-844479/78.
XX
XX New polynucleotide comprising a nucleic acid encoding a human or murine
PT 3'-phosphoadenosine-5'-phosphosulfate synthetase, useful in diagnosing or
PT treating osteoarthritis disorder e.g. spondyloepimetaphyseal dysplasia.
XX
XX Claim 28; SEQ ID NO 17; 39pp; English.
XX
XX The invention relates to an isolated polynucleotide (1) comprises a
CC nucleic acid segment encoding a human or a murine 3'-phosphoadenosine-5'-
CC phosphosulphate synthetase (PAPSS2) having a nucleotide sequence (S1 or
CC S2) appearing as AAD43524 and AAD43525, a nucleotide sequence
CC complementary to S1 or S2, a degenerate coding sequence of S1 or S2 or a
CC gene-specific fragment of any of these. Also included are a nucleic acid
CC construct comprising a nucleic acid segment comprising (1) or encoding a
CC human PAPSS2 protein appearing as AAD43530 and AAD43531 (designated as P1
CC and P2, respectively), an oligonucleotide primer for amplifying a PAPSS2-
CC specific nucleic acid segment, a genetically modified vertebrate cell
CC comprising the nucleic acid construct of (1), a non-human vertebrate
CC comprising the cell, an isolated PAPS synthetase protein comprising P1 or
CC P2 or an antibody binding fragment least 6 amino acids long, diagnosing
CC spondyloepimetaphyseal dysplasia (SEMD) in a human subject, identifying a
CC human carrier of an heritable allele associated with SEMD, a gene therapy
CC method for treating a human subject having an osteoarthritis disorder, a
CC genetic testing kit for diagnosing SEMD in a human subject or for
CC identifying a human carrier of SEMD comprising primers, an isolated
CC antibody or antibody fragment (comprising an antibody or antibody
CC fragment that selectively binds a PAPS synthetase protein or selectively
CC binds an antibody binding fragment of either of these at least 6 amino
CC acids long), a protein therapy method for treating a human subject having

CC	an osteoarthritic disorder, and a kit for the treatment of osteoarthritis.
CC	disorders caused or aggravated by deficient enzymatic sulphation activity
CC	(comprising: a fusion protein comprising a first PAPSS2 polypeptide
CC	segment comprising PI or an enzymatically active fragment, and a second
CC	polypeptide segment capable of infiltrating the cell; and instructions
CC	for using the fusion protein for treating osteoarthritic disorder(s)
CC	caused or aggravated by deficient enzymatic sulphation activity). The
CC	PAPSS2 DNA is useful in treating or diagnosing osteoarthritic disorders
CC	including spondyloepiphyseal dysplasia, Stickler syndrome,
CC	spondyloepiphyseal dysplasia, achondrogenesis, achondroplasia,
CC	chondrodysplasia, diastrophic dysplasia, pseudochondroplasia, or
CC	multiple epiphyseal dysplasia. The human PAPSS2 gene is located on
CC	chromosome 10q33-24. The present sequence is a human PAPSS2 PCR primer of
CC	the invention.
XX	
SQ	Sequence 23 BP; 6 A; 5 C; 6 G; 6 T; 0 U; 0 Other;
Query Match	0.2%; Score 16.8; DB 1; Length 23;
Best Local Similarity	90.0%; Pred. No. 1.2e+03;
Matches 18; Conservative	0; Mismatches 2; Indels 0; Gaps 0
OY	1012 GTACCCACTGTGGACAGAT 1031
DB	 1 GTCACTCCTGTGGACAAT 20
RESULT 1443	
ID	AAV82670 standard; DNA; 24 BP.
AC	AAV82670;
XX	
DT	16-FEB-1999 (first entry)
XX	
DE	Primer used to identify cDNA encoding ST38.2.
KM	Rat; chemokine; ST38.2; chemotaxis; leucocyte-activating; inflammation;
KW	immune response; brain injury; trauma; ischaemia;
KW	autoimmune inflammation; multiple sclerosis; stroke;
KW	rheumatoid arthritis; meningitis; encephalitis; PCR primer; ss.
XX	
OS	Synthetic.
OS	Rattus sp.
PN	MO9849309-A1.
PD	05-NOV-1998.
XX	
PE	23-APR-1998; 98WO-BP002405.
XX	
PR	30-APR-1997; 97EP-00107135.
PA	(HOFF) HOFFMANN LA ROCHE & CO AG F.
PI	Leselauer W, Utanschnetz U;
DR	WPI, 1999-009430/01.
XX	
PT	New chemokine ST38.2 with chemotactic and leucocyte-activating properties
PT	- used to treat inflammation and immune responses and to identify
PT	specific modulators.
XX	
PS	Example 3; Page 28; 64pp; English.
XX	
CC	PCR primers AAV82670-71 were used to amplify cDNA encoding a novel rat
CC	chemokine designated ST38.2. In addition, primer AAV82670 was used to
CC	reverse transcribe rat RNA. The protein has chemotactic and leucocyte-
CC	activating properties. ST38.2 is involved in inflammation and immune
CC	responses, particularly inflammatory response to brain injury (trauma,
CC	ischaemia or autoimmune inflammation) but also in multiple sclerosis,
CC	stroke, rheumatoid arthritis and infections (particularly meningitis and
CC	encephalitis)
XX	

Seq	Sequence	24 BP; 2 A; 2 C; 2 G; 18 T; 0 U; 0 Other;
QY	Query Match	0.2%; Score 16.8; DB 1; Length 24;
DB	Best Local Similarity	90.0%; Fred. No. 1.2e+03;
XX	Matches 18; Conservative	0; Mismatches 2; Indels 0; Gaps 0
QY	4459 TGGACCTTTTCTTTTCTTTT 4478	
DB	5 TAGATTTTCTTTTCTTTTCTTTT 24	
RESULT 1444	AAA64343/C	
ID	AAA64343 standard; DNA; 24 BP.	
XX	AAA64343;	
AC	20-DEC-2000 (first entry)	
DT	Reverse PCR primer used to amplify cDNA encoding Erk2.	
XX		
DE	Conformational state; post-translational modification; enzyme activity;	
XX	Erk2; protein kinase; PCR primer; ss.	
KW	Rattus sp.	
XX	WO200050901-A1.	
PN	31-AUG-2000.	
XX	25-FEB-2000; 2000WO-GB000668.	
PF	25-FEB-1999; 99GB-00004395.	
XX	(FLUO-) FLUORESCENCE LTD.	
PA	Colyer J, Craig RK;	
XX	WPI; 2000-565475/52.	
DR	Determining the conformational state of a protein, comprises contacting	
PT	the protein with a labeled binding protein and assessing the labeling of	
PT	the protein.	
PI	Example 4; Page 39; 56pp; English.	
XX	The specification describes a method for determining the conformational	
PS	state of a protein. The method uses at least one labelled binding partner	
XX	capable of binding to the protein in a manner dependent on the	
CC	conformational state of the protein. The method is for detecting the	
CC	modifications of proteins, and for determining the activity of an enzyme.	
CC	PCR primers AAA64342-43 were used to amplify cDNA encoding full length	
CC	rat Erk2 protein kinase. Erk2 is used in the method of the invention,	
CC	which is used for detection of conformation change of Erk2 protein kinase	
CC	due to phosphorylation	
SQ	Sequence 24 BP; 4 A; 7 C; 5 G; 8 T; 0 U; 0 Other;	
QY	Query Match	0.2%; Score 16.8; DB 1; Length 24;
DB	Best Local Similarity	90.0%; Fred. No. 1.2e+03;
XX	Matches 18; Conservative	0; Mismatches 2; Indels 0; Gaps 0
QY	1523 GGAAACAGTTCTACATGGG 1542	
DB	20 GGATACAGATCTACATGGG 1	
RESULT 1445	AAH75510	
ID	AAH75510 standard; DNA; 24 BP.	
XX	AAH75510;	

[illegible]

```

FT      /tag= a
FT      24
FT      modified_base
FT      ,
FT      /*tag= c
FT      /mod_base= OTHER
FT      /note= "3, linker joined to an amine-reactive
FT      fluorophore"
FT
XX      WO200218951-A2.
XX      PN
XX      07-MAR-2002.
XX      PD
XX      29-AUG-2001; 2001WO-US041941.
XX      PF
XX      29-AUG-2000; 2000US-0228728P.
XX      PR
XX      30-MAR-2001; 2001US-0280350P.
XX      PA
XX      (UVRQ ) UNIV ROCKEFELLER.
XX      PI
XX      Dubertret B, Calame M, Libchaber A;
XX      DR
XX      WPI; 2002-404569/43.
XX      PT
XX      Sensitive detecting proximity changes in a system that utilizes an
XX      interacting fluorophore and quencher, for high sensitivity applications,
XX      PT
XX      involves utilizing a metal surface as quencher.
XX
XX      Example 5; Page 33; 62pp; English.
XX
CC      The present sequence is an oligonucleotide probe that was used in a
CC      molecular beacon in an example from the invention. The probe forms a
CC      hairpin structure in the native state. The 5' end of the probe is
CC      covalently joined via a linker to a disulfide or primary amine. The 3'
CC      end of the probe is covalently joined to an amine-reactive fluorescent
CC      dye such as fluorescein. A gold surface or other metal film surface is
CC      attached to the disulfide or amine group to form the molecular beacon. In
CC      the native state with hybridised terminl, the proximity of the
CC      fluorophore and quencher (gold surface) in the molecular beacon is such
CC      that little or no fluorescence is detectable. Upon hybridisation of the
CC      central complementary stretch of the probe to a target sequence (e.g. the
CC      sequence in ABL51070), the hairpin undergoes a conformational change
CC      resulting in an increase in fluorescence, the extent of which is
CC      proportional to the amount of binding partner present. The invention
CC      relates generally to the use of metal surface quenchers such as particles
CC      or films for high sensitivity applications in, for example, detection and
CC      diagnostic systems
CC      CC
SQ      Sequence 24 BP; 1 A; 3 C; 4 G; 16 T; 0 U; 0 Other;
SQ
Query Match      0.2%; Score 16.8; DB 1; Length 24;
Best Local Similarity 90.0%; Pred.No.1.2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      4461 GACCTTTTCTTTTCTTTTCTT 4480
DB      |||||||
DB      3 GAGTTTCTTTTCTTTTCTTCT 22
DB
RESULT 1447
ABX15065
ID      ABX15065 standard; DNA; 24 BP.
XX
XX      ABX15065;
XX      AC
XX      12-MAR-2003 (first entry)
XX      DT
XX      DE
XX      Homeotic domain transcription factor 38.72 RT-PCR primer #2.
XX      DE
XX      Homeotic transcription factor 38.72; primer; ss; HIV infection;
XX      immunological disease; homeotic domain; tumour; haemopathy;
XX      human immunodeficiency virus; inflammation; tumour; RT-PCR;
XX      reverse transcription.
XX
OS      Unidentified.

```

XX	CN1358744-A.
PN	17-JUL-2002.
PD	13-DEC-2000; 2000CN-00127899.
PF	13-DEC-2000; 2000CN-00127899.
PP	(SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
PR	Mao Y, Xie Y;
PX	WPI: 2002-73353/80.
PA	Novel polypeptide-humoeotic regional transcription factor 38.72 and
PI	polynucleotide for encoding said polypeptide.
PT	Example 3; Page 17 (disclosure); 34pp; Chinese.
PS	The present invention discloses a novel polypeptide-homeotic domain
SS	transcription factor 38.72, a polynucleotide for coding the polypeptide
CC	and method for producing this polypeptide by using DNA recombination
CC	technology. The invention also discloses the method for curing several
CC	diseases, such as malignant tumour, haemopathy, human immunodeficiency
CC	virus (HIV) infection, immunological disease and various inflammations
CC	using the polypeptide. The invention also discloses an antagonist for
CC	resisting the polypeptide and a method for its use, and also the
CC	application of polynucleotide coding this novel homeotic domain
CC	transcription factor 38.72. The present sequence represents a reverse
CC	transcriptase (RT) PCR primer used to isolate the homeotic domain
CC	transcription factor cDNA 38.72 of the invention
SQ	Sequence 24 BP; 2 A; 5 C; 2 G; 15 T; 0 U; 0 Other;
	Query Match 0.2%; Score 16.8; DB 1; Length 24;
	Best Local Similarity 90.0%; Pred.No.1.2e+03;
	Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0
OY	4461 GACCTTTTTCCTTTTTTTT 4480 Db 3 GACATGTTTTTTTTTTTTT 22
	RESULT 1448
ID	ABQ77543
XX	ABQ77543 standard; DNA; 24 BP.
AC	ABQ77543;
DT	01-OCT-2002 (first entry)
DE	Human red blood cell cytoplasmic protein 15.29 RT-PCR primer, SEQ ID:3.
KM	Human; red blood cell cytoplasmic protein 15.29; erythrocyte;
KM	recombinant production; gene therapy; cerebral anoxia;
KM	respiratory dyspnea; arrhythmia; intestinal palsy; anaemia; haemostatic;
KM	cardiac; reverse transcription-PCR; RT-PCR; primer; ss.
OS	Homo sapiens.
FN	CN139497-A.
PD	13-MAR-2002.
PF	23-AUG-2000; 2000CN-00119732.
PR	23-AUG-2000; 2000CN-00119732.
PA	(BODE-) BODE GENE DEV CO LTD SHANGHAI.
PI	Mao Y, Xie Y;

```

DR      WPI; 2002-472206/51.
XX
XX      New polypeptide-human red blood cell cytoplasmic protein 15.29 for
PT      treating anaerobic cerebral disease, respiratory adynamia, arrythmia,
PT      intestinal palsy, and anemia.
XX
XX      Example 2; Page 16 (Disclosure); 32pp; Chinese.
XX
XX      The invention relates to human red blood cell cytoplasmic protein 15.29
CC      (AA098161) and nucleic acids encoding it (AB077542). The protein has a
CC      molecular weight of 15 kD. The invention also relates to a method for the
CC      recombinant production of the protein, an antagonist of the protein, and
CC      the use of the protein, gene and antagonist in therapeutic applications.
CC      Red blood cell cytoplasmic protein 15.29 can be used in the treatment of
CC      a variety of diseases such as cerebral anoxia, respiratory adynamia,
CC      arrhythmia, intestinal palsy and anaemia. Sequences AB077543- AB077544
CC      represent reverse transcription-PCR (RT-PCR) primers used in an
CC      exemplification of the invention to isolate human red blood cell
CC      cytoplasmic protein 15.29 cDNA
XX
XX      Sequence 24 BP; 3 A; 3 G; 17 T; 0 U; 0 Other:
SQ
XX
XX      Query Match      0.2%; Score 16.8; DB 1; Length 24;
XX      Best Local Similarity 90.0%; Pred. No. 1.2e+03;
XX      Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0
XX
XX      4465 TTTTTCCTTTTTCCTTTTGG 4484
XX      4 TTTTTCCTTTTTCCTTTTGG 23
XX
XX      RESULT 1449
XX      AA098161
XX      ID AA098161 standard; DNA; 25 BP.
XX
XX      AA098161:
XX      05-FEB-1996 (first entry)
XX      DE Hind III primer/adaptor.
XX
XX      Hind III primer/adaptor; random oligonucleotide identification;
KM      beta-galactosidase gene; E. coli; infectious diseases;
KM      herpes simplex virus; ss.
XX
XX      Synthetic.
XX
XX      WO9516054-A1.
XX      PN 15-JUN-1995.
XX
XX      02-DEC-1994; 94WO-US013884.
XX      PF 02-DEC-1993; 93US-00161281.
XX      PR
XX      (MIRA/) MIRABELLI C K.
PA      (ECKE/) ECKER D J.
PA      (VICK/) VICKERS T A.
PA      (ROBE/) ROBERTSON D L.
PI      Mirabelli CK, Ecker DJ, Vickers TA, Robertson DL;
XX      WPI; 1995-224334/29.
XX
XX      Identification of oligo:nucleotide(s) with a desired activity, e.g.
PT      activity against an infectious agent - by cloning vectors contg. randomly
PT      sequenced oligo:nucleotide(s) into cells and assaying for the desired
PT      phenotype.
XX
XX      Claim 25; Page 25; 53pp; English.
XX
XX      AA098161 is a random oligonucleotide Hind III primer/adaptor used in a
CC      new method for the identification of random oligonucleotides which

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CC inhibit the expression of a target gene, e.g. the beta-galactosidase gene
CC in E. coli. Such random oligonucleotides may be used in the treatment of
CC infectious diseases, pref. herpes simplex virus infection
XX
SQ Sequence 25 BP; 2 A; 3 C; 3 G; 17 T; 0 U; 0 Other;
Query Match 0.2%; Score 16.8; DB 1; Length 25;
Best Local Similarity 90.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4463 CTTTCTTTTCTTTTCTTTT 4482
Db 6 CTTCGTTTCTTTTCTTTT 25
RESULT 1450
AAV13056
ID AAV13056 standard; DNA; 25 BP.
XX
AC AAV13056;
XX
DT 18-MAY-1998 (first entry)
XX
DE Oligonucleotide target Bsp-CYP2D7 SEQ ID NO:4 from WO9743450.
XX
KM Hybridisation; oligonucleotide array; high-density; substrate-bound;
KM target; genetic variant; infectious disease; HIV; ss.
XX
OS Synthetic.
XX
PN WO9743450-A1.
XX
PD 20-NOV-1997.
XX
PF 16-MAY-1997; 97MO-US008446.
XX
PR 16-MAY-1996; 96US-00648709.
XX
PA (AEFY-) AEFYMETRIX INC.
XX
PI Cronin MT, Miyada CG, Trulsson M, Gingeras TR, Mcgall G;
PI Robinson C, Oval M;
XX
DR WPI; 1998-008909/01.
XX
PT New hybridisation assay on high density oligo:nucleotide arrays - is
PT carried out in the presence of a hybridisation optimising agent, such as
PT an iso:stabilising agent, denaturing agent or renaturation accelerant.
XX
PS Example; Page 15; 30pp; English.
XX
CC The present sequence represents an oligonucleotide target used in the
CC example of the present invention. The present invention describes methods
CC for performing a hybridisation assay between a target nucleic acid
CC molecule and an oligonucleotide array (which comprises a surface to
CC which, at discrete, known locations, oligonucleotide probes with
CC different, known sequences, are covalently attached). The method
CC comprises: (a) incubating the array with a hybridisation mixture
CC comprising the target and at least one hybridisation optimising agent
CC (which is not a lower alkyllammonium salt) to allow hybridisation; and (b)
CC determining the identity of probes to which the target has hybridised.
CC The array has a density of at least 500 features per square centimetre,
CC where a feature is defined as an area of substrate having a collection of
CC same-sequence, surface-immobilised oligonucleotide molecules. The process
CC may be used for identifying genetic variants of infectious diseases (such
CC as HIV) or genetic diseases (such as cystic fibrosis). Addition of the
CC hybridisation optimisation agent improves signal resolution. The
CC improvement is manifested as fewer total signals from the substrate due
CC to decreases in the number of hybrids between mis-matched sequences, and
CC normalisation of signal strength among detectable hybrids
XX
SQ Sequence 25 BP; 4 A; 5 C; 7 G; 9 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.8; DB 1; Length 25;
Best Local Similarity 90.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3547 TGTGGGTAAACGAGCCCTT 3566
Db 6 TGTGGGTAAACCTGTTCTT 25
RESULT 1451
AAK8480/C
ID AAK8480 standard; DNA; 25 BP.
XX
AC AAK8480;
XX
DT 01-OCT-1999 (first entry)
XX
DE Human MIP-1 beta primer PIC.
XX
KM RANTES; chemokine; detection; primer; probe; amplification; MIP-1 alpha;
KM regulated upon activation normal T expressed and secreted; MIP-1 beta;
KM macrophage inflammatory protein; CD4+ T-cell; inhibitor; prognosis;
KM primary non-syncytium-inducing HIV-1 strain; therapy; ss.
XX
OS Synthetic.
XX
OS Homo sapiens.
XX
PN WO937815-A1.
XX
PD 29-JUL-1999.
XX
PF 22-JAN-1999; 99MO-US001327.
XX
PR 22-JAN-1998; 98US-00010641.
XX
PA (ALKU) AKZO NOBEL NV.
XX
PI Romano JW, Shurtliff R, Williams KG;
XX
DR WPI; 1999-469145/39.
XX
PT Detection of expression levels of the cytokines RANTES, MIP-1alpha and
PT MIP-1beta used as prognostic markers of HIV-infected patients.
XX
PS Claim 1; Page 43; 48pp; English.
XX
CC This invention describes novel oligonucleotides which are used for
CC detecting the chemokines RANTES (regulated upon activation normal T
CC expressed and secreted), macrophage inflammatory protein (MIP)-1 alpha or
CC MIP-1 beta by (a) obtaining a sample possible containing RANTES or MIP-1
CC alpha or MIP-1 beta RNA, (b) performing an isothermal transcriptional
CC amplification on the sample with 2 oligonucleotide primers, (c) detecting
CC the product of step (b) where detection of a product indicates the
CC presence of RANTES, MIP-1 alpha or MIP-1 beta in the sample. The assay is
CC used to determine the levels of the chemokines RANTES, MIP-1 alpha and
CC MIP-1 beta in samples, especially cells. These chemokines have been shown
CC to be inhibitors of CD4+ T-cells by primary non-syncytium-inducing HIV-1
CC strains. Thus the level of expression of these genes can be used as
CC prognostic markers for direct therapeutic management of HIV-infected
CC patients. By being isothermal, the assay requires less manipulation by
CC the experimenter. Also, 'spiking' the sample with a known amount of
CC control RNA allows quantitation and qualification of the products in a
CC single assay. AAK8447-X88491 represent the primers and probes used in the
CC method of the invention
XX
SQ Sequence 25 BP; 3 A; 5 C; 13 G; 4 T; 0 U; 0 Other;
Query Match 0.2%; Score 16.8; DB 1; Length 25;
Best Local Similarity 90.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 5286 GCAGCCTTATCCTCCGCA 5305
|||||||

DB 22 GCAGCCTCTGCTCCAGCCA 3

RESULT 1452

AAA97402
ID AAA97402 standard; DNA; 25 BP.

AC AAA97402;

DT 29-JAN-2001 (first entry)

DE Pea pra2 light-repressible promoter clone PL8 PCR primer, SEQ ID NO:20.

KW GTP-binding protein pra2; pea; light-repressible promoter;

KW photoinhibitory; expression cassette; transgenic plant;

XX deterioration prevention; storage; PCR primer; ss.

OS Pisum sativum.

PN WO200055313-A1.

PD 21-SEP-2000.

PF 03-MAR-2000; 2000WO-UP001269.

PR 12-MAR-1999; 99JP-0006551.

PA (SUNR) SUNTORY LTD.

PI Sasaki Y, Nagano Y, Inaba T;

XX WPI; 2000-587526/55.

PT New DNA fragment or promoter for expressing a target gene, specifically

PS under photoinhibitory conditions, and for transforming a plant cell or

CC plant to improve quality and prevent deterioration during storage.

CC Example 3; Page 14; 49pp; Japanese.

CC The invention relates to a light-repressible promoter (AAA97385), or

CC pea GTP-binding protein pra2. The invention also relates to an expression

CC cassette containing the pra2 promoter or its active fragments for the

CC expression of a gene under photoinhibitory or dark conditions in a plant,

CC and to transgenic plants, their descendants and plant tissues comprising

CC the expression cassette. The expression cassette of the invention can be

CC used to generate transgenic plants in which deterioration during storage

CC in the dark is prevented. This is particularly useful for agricultural

CC products. Sequences AAA97387-A97392 and AAA97398-A97410 represent PCR

CC primers used in an exemplification of the invention to amplify the pea

CC pra2 promoter for cloning

XX SQ Sequence 25 BP; 12 A; 8 C; 2 G; 3 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 16.8; DB 1; Length 25;

XX Best Local Similarity 90.0%; Pred. No. 1.3e+03;

XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX QY 3743 AAAAGTCAACCTTACA 3762

DB 3 AAAACATCAACCTCTAGA 22

RESULT 1453

AAC96751

ID AAC96751 standard; DNA; 25 BP.

XX AAC96751;

AC AAC96751;

XX 26-FEB-2001 (first entry)

XX HLA HLA-A gene PCR primer #128.

XX DE

KW DNA sequence analysis; sequencing; protein sequence; protein structure;

KW gene typing; organ donation; bacteria identification; 16S rRNA; HLA;

XX human leukocyte antigen; PCR primer; ss.

OS Homo sapiens.

PN WO200065088-A2.

PD 02-NOV-2000.

PF 20-APR-2000; 2000WO-EP003636.

PR 26-APR-1999; 99EP-00303215.

PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.

PI Ulfendahl P, Wong K;

XX WPI; 2000-679677/66.

PT Identifying extendible primers for use in identification, or

PT classification of a nucleic acid of an organism, allele or gene such as

PT class 1/2 HLA comprises identifying all possible nucleotide sequences of

PT specific length.

PS Claim 14; Page 56; 66pp; English.

XX The present invention provides a method for identifying a set of

CC extendible primers which can be used in the identification, typing and

CC classification of genes. This can then be used to predict protein

CC sequence and structure, in organ donation to match the organ with the

CC receiver, and to identify bacteria in a sample. The method can be used to

CC type the human leukocyte antigen genes (HLA) and 16S rRNA genes in

CC particular

XX SQ Sequence 25 BP; 2 A; 4 C; 4 G; 15 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 16.8; DB 1; Length 25;

XX Best Local Similarity 90.0%; Pred. No. 1.3e+03;

XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX QY 4472 TTTTCTTTTCTGCTGAG 4491

DB 1 TTTTCTTTTCTGCTGAG 20

RESULT 1454

AAC95870

ID AAC95870 standard; DNA; 25 BP.

AC AAC95870;

XX 26-FEB-2001 (first entry)

XX HLA HLA-A gene PCR primer #50.

XX DNA sequence analysis; sequencing; protein sequence; protein structure;

XX gene typing; organ donation; bacteria identification; 16S rRNA; HLA;

XX human leukocyte antigen; PCR primer; ss.

XX Homo sapiens.

XX WO200065088-A2.

XX 02-NOV-2000.

XX 20-APR-2000; 2000WO-EP003636.

XX 26-APR-1999; 99EP-00303215.

XX (AMSH) AMERSHAM PHARMACIA BIOTECH AB.

XX Ulfendahl P, Wong K;

XX PI

XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 41; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16S rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 0 A; 2 C; 8 G; 15 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 16.8; DB 1; Length 25;
Best Local Similarity 90.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 4472 TTTTCTTTTGTCTGTGAG 4491
DB 1 TTTTCTTTTGTCTGTGAG 20
XX
RESULT 1455
AAC96649
ID AAC96649 standard; DNA; 25 BP.
XX
AC AAC96649;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA HLA-A gene PCR primer #26.
XX
KM DNA sequence analysis; sequencing; protein sequence; protein structure;
KM gene typing; organ donation; bacteria identification; 16S rRNA; HLA;
KM human leukocyte antigen; PCR primer; 6S.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 55; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16S rRNA genes in
CC particular

XX
SQ Sequence 25 BP; 0 A; 2 C; 8 G; 15 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 16.8; DB 1; Length 25;
Best Local Similarity 90.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 4472 TTTTCTTTTGTCTGTGAG 4491
DB 1 TTTTCTTTTGTCTGTGAG 20
XX
RESULT 1456
AA77454/C
ID AA77454 standard; DNA; 25 BP.
XX
AC AA77454;
XX
DT 15-JUN-2001 (first entry)
XX
DE Intron II fragment 4 of the goat beta-casein gene.
XX
KM Goat; beta-casein; ds.
XX
OS Capra hircus.
XX
FH Key Location/Qualifiers
FT conflict replace(12..14,TC)
FT /tag= a
FT /note= "Conflict occurs at this location when compared to
FT beta-casein gene given by Roberts et al (1992)"
XX
PN TW413702-A.
XX
PD 01-DEC-2000.
XX
PF 28-MAY-1997; 97TW-00107261.
XX
PR 28-MAY-1997; 97TW-00107261.
XX
PA (NASC-) NAT SCI COUNCIL.
XX
PI Huang M, Lin J;
XX
DR WPI; 2001-264857/27.
XX
PT DNA molecules containing goat beta-casein gene - .
XX
PS Disclosure; Page 34; 41pp; Chinese.
XX
CC This invention relates to the goat beta-casein gene, represented by
CC AAF77439. There are 18 positions in the 5'-flanking region, 21 positions
CC in intron sequences and 1 position in exon VII that conflict with the
CC sequence reported for this gene by Roberts et al (1992). The present
CC sequence represents a fragment of the casein gene in which a conflict
CC occurs when compared to the Roberts et al (1992) sequence for the same
CC gene
XX
SQ Sequence 25 BP; 0 A; 4 C; 2 G; 19 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 16.8; DB 1; Length 25;
Best Local Similarity 90.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 4020 AAAAAGAGAGAAAACAAA 4039
DB 24 AAAAGAGAGAGAAAACAAA 5
XX
RESULT 1457
ABN13921
ID ABN13921 standard; DNA; 25 BP.
XX

AC ABLN13921;
 XX
 DT 29-MAY-2002 (first entry)
 XX
 DE Human GDMLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:13913.
 XX
 KM Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
 KM muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KM skeletal muscle disorder; amplicon; screening; ss.
 OS Homo sapiens.
 XX
 PN WO200192524-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 25-MAY-2001; 2001WO-US016981.
 XX
 PR 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 05-FEB-2001; 2001US-0266860P.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX
 DR WPI; 2002-179446/23.
 XX
 PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
 XX
 PS Disclosure; SEQ ID NO 13913; 214pp; English.

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 5546 GTGCATGCAGCTGAGACT 5565
 DB 1 GTGCATGCAGCTGAGACT 20
 RESULT 1458
 ABL57069
 ID ABL57069 standard; DNA; 25 BP.
 XX
 AC ABL57069;
 XX
 DT 22-JUL-2002 (first entry)
 XX
 DE Molecular beacon oligonucleotide probe.
 XX
 KM Molecular beacon; probe; fluorophore; nanoparticle;
 KM nucleic acid detection; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT stem_loop 1..25
 FT /tag= a
 FT 1..21
 FT misc_binding /tag= e
 FT /bound_moiety= "Target oligonucleotide"
 FT /note= "Forms double-stranded region with bases 1-21 of
 sequence in ABL57071"
 FT 1..20
 FT /tag= d
 FT /bound_moiety= "Target oligonucleotide"
 FT /note= "Forms double-stranded region with bases 1-20 of
 sequence in ABL57070"
 FT modified_base 1
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "5' disulfide group"
 FT modified_base 25
 FT /tag= C
 FT /mod_base= OTHER
 FT /note= "3' amino group"
 XX
 PN WO200218951-A2.
 XX
 PD 07-MAR-2002.
 XX
 PF 29-AUG-2001; 2001WO-US041941.
 XX
 PR 29-AUG-2000; 2000US-0228728P.
 PR 30-MAR-2001; 2001US-0280350P.
 XX
 PA (UYRQ) UNIV ROCKEFELLER.
 PI Dubertret B, Calame M, Liebhaber A;
 XX
 DR WPI; 2002-404569/43.
 XX
 PT Sensitive detecting proximity changes in a system that utilizes an
 PT interacting fluorophore and quencher, for high sensitivity applications,
 PT involves utilizing a metal surface as quencher.
 XX
 PS Example 1; Page 22; 62pp; English.

XX The present sequence is an oligonucleotide probe that was used in a
 CC molecular beacon in examples from the invention. The probe has a hairpin
 CC structure in the native state. The disulfide group at the 5' end of the
 CC probe was covalently linked to the 5' phosphate via a (CH2)6 spacer, and
 CC the primary amino group at the 3' was attached to the 3' hydroxyl via a
 CC (CH2)7 spacer. An amino-reactive dye, such as fluorescein, rhodamine 6G
 CC or Texas Red, was covalently linked to the 3'-amino group. A
 CC monomaleimido-gold nanoparticle was then covalently linked to the 5'

Query Match 0.2%; Score 16.8; DB 1; Length 25;
 Best Local Similarity 90.0%; Pred. No. 1.3e+03;

CC sulfhydryl group to form the molecular beacon. In the native state with
CC hybridised termini, the proximity of the fluorophore and quencher (gold
CC nanoparticle) in the molecular beacon is such that little or no
CC fluorescence is detectable. Upon hybridisation of the central
CC complementary stretch of the probe to a target sequence (e.g. the
CC sequence in ABL57070 or ABL57071), the hairpin undergoes a conformational
CC change resulting in an increase in fluorescence, the extent of which is
CC proportional to the amount of binding partner present. Single mismatch
CC detection was demonstrated. The invention relates generally to the use of
CC metal surface quenchers such as particles or films for high sensitivity
CC applications in, for example, detection and diagnostic systems

XX
SQ Sequence 25 BP; 1 A; 4 C; 4 G; 16 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.8; DB 1; Length 25;
Best Local Similarity 90.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4461 GACTTTTCTTTTCTTTTCT 4480
Db 3 GAGTTTCTTTTCTTTTCT 22

RESULT 1459
ABL57077
ID ABL57077 standard; DNA; 25 BP.
XX
AC ABL57077;
XX
DT 22-JUL-2002 (first entry)
XX
DE Molecular beacon oligonucleotide probe.
XX
KW Molecular beacon; probe; fluorophore; nanoparticle;
KM nucleic acid detection; ss.
XX
OS Synthetic.

XX
FH Key Location/Qualifiers
FT stem_loop 1..22
FT /*tag= a
FT modified_base 1
FT /*tag= b
FT /*mod_base= OTHER
FT /*note= "5' amine"
FT 6..21
FT /*tag= d
FT /*bound_molety= "Target oligonucleotide"
FT /*note= "Forms double-stranded region with bases 1-16 of
FT sequence in ABL57075"
FT 25
FT /*tag= c
FT /*mod_base= OTHER
FT /*note= "3' DABCYL"

XX
PN WO200218951-A2.
XX
PD 07-MAR-2002.
XX
PF 29-AUG-2001; 2001WO-US041941.
XX
PR 29-AUG-2000; 2000US-0228728P.
PR 30-MAR-2001; 2001US-0280350P.
XX
PA (UVRQ) UNIV ROCKEFELLER.
XX
PI Dubertret B, Calame M, Libhaber A;
XX
DR WPI; 2002-404569/43.
XX
PT Sensitive detecting proximity changes in a system that utilizes an
PT interacting fluorophore and quencher, for high sensitivity applications,
PT involves utilizing a metal surface as quencher.

XX
XX Example 3; Page 30; 62pp; English.

CC The present sequence is an oligonucleotide probe that was used in a
CC molecular beacon in an example from the invention. A rhodamine 6G dye was
CC attached to the primary amine at the 5' end of the oligonucleotide, which
CC had DABCYL attached to its 3' end. A rhodamine-DNA-gold conjugate
CC molecular beacon (see ABL57069) was also used. In the native state with
CC hybridised termini, the proximity of the fluorophore and quencher (gold
CC nanoparticle) in the molecular beacon is such that little or no
CC fluorescence is detectable. Upon hybridisation of the central
CC complementary stretch of the probe to a target sequence, the hairpin
CC undergoes a conformational change resulting in an increase in
CC fluorescence, the extent of which is proportional to the amount of
CC binding partner present. Single mismatch detection was demonstrated. The
CC invention relates generally to the use of metal surface quenchers such as
CC particles or films for high sensitivity applications in, for example,
CC detection and diagnostic systems

XX
SQ Sequence 25 BP; 1 A; 4 C; 4 G; 16 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.8; DB 1; Length 25;
Best Local Similarity 90.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4461 GACTTTTCTTTTCTTTTCT 4480
Db 3 GAGTTTCTTTTCTTTTCT 22

RESULT 1460
AA170776/C
ID AA170776 standard; DNA; 25 BP.
XX
AC AA170776;
XX
DT 18-FEB-2002 (first entry)
XX
DE ETEC csad gene PCR primer CS4D3.
XX
KW CS4 plus; enterotoxigenic; ETEC; LT gene; csad gene; fimbriae; vaccine;
KM diarrhoea; antibacterial; antidiarrhetic; PCR primer; ss.
XX
OS Escherichia coli.
XX
PN WO200181582-A2.
XX
PD 01-NOV-2001.
XX
PF 20-APR-2001; 2001WO-US012914.
XX
PR 20-APR-2000; 2000US-0198686P.
XX
PA (UYMA-) UNIV MARYLAND BALTIMORE.
XX
PI Altboun Z, Levine MM, Barry EM;
XX
DR WPI; 2002-049280/06.
XX
PT New nucleotide sequence, useful as immunogenic agent for generating
PT immune response against recombinant product of the operon, comprises csa
PT operon which encodes enterotoxigenic Escherichia coli-CS4 pili.
XX
XX Example 1; Page 29; 81pp; English.

CC The present sequence is that of PCR primer CS4D3, which corresponds to bp
CC 5540-5564 of the enterotoxigenic Escherichia coli (ETEC) strain E11881A
CC csa operon (see AA170780). In order to determine whether strain E11881A
CC contained a complete csad gene, PCR assays were performed with primers
CC that are homologous to csad' gene, i.e. CS4D2 (see AA170777) and CS4D3,
CC and with primer CS4D1 (see AA170778), which is homologous to cfaD and rns
CC genes. PCR amplifications indicated that strain E11881A does not contain
CC the complete csad gene. Primers CS4D2/CS4D3 amplified the expected 476 bp

CC fragment, while primers CS4D1/CS4D3 did not amplify the expected 646 bp
CC fragment. Strains E11881E, DS9-1, H10407 and C91f all contained the
CC complete gene. The csa operon encodes the CS4 pili. It is useful in the
CC production of recombinant CsaA-CsaE polypeptides (see AAM0338-43) that
CC are used in claimed immunogenic compositions to prevent ETEC
CC colonisation, and hence to protect against diarrhoea

XX Sequence 25 BP; 7 A; 3 C; 5 G; 10 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.8; DB 1; Length 25;
Best Local Similarity 90.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2970 CCAGAAATCTGTGATATCAA 2989

DB 25 CCGATATCTCAGATATCAA 6

RESULT 1461

ADB04565
ADB04565 standard; DNA; 25 BP.

XX ADB04565;

DT 20-NOV-2003 (first entry)

XX Human MD27 scanning oligonucleotide SEQ ID 5551.

XX Cytostatic; immunostimulant; gene therapy; vaccine; human;

KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

KM chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;

KW developmental disorder; ss.

XX Homo sapiens.

XX EPI281758-A2.

XX 05-FEB-2003.

XX 30-JUL-2002; 2002EP-00016874.

XX 02-AUG-2001; 2001US-00922181.

XX (AEOM-) AEOMICA INC.

XX Shannon M, Gu Y, Nguyen C;

XX WPI; 2003-423107/40.

XX New zinc finger-containing proteins and nucleic acids, useful in

XX manufacturing a medicament for treating or preventing a disorder

XX associated with decreased or increased expression or activity of MD23,

XX MD24, MD27 or MD212, e.g. cancer.

XX Example 8; SEQ ID NO 5551; 103bp; English.

XX The present invention relates to novel human zinc finger-containing

XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is

XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,

XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome

XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,

XX or in manufacturing a medicament for treating or preventing a disorder

XX associated with decreased or increased expression or activity of MD23,

XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic

XX acids and proteins are also useful for diagnosing or monitoring a disease

XX caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic

XX alterations can also be used as probes to detect and characterize gross

XX alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are

XX useful in constructing microarrays for measuring gene expression. The

XX proteins are useful as therapeutic agents for gene therapy or as

XX vaccines. The present sequence was used to illustrate the invention.

XX Sequence 25 BP; 2 A; 3 C; 4 G; 16 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.8; DB 1; Length 25;
Best Local Similarity 90.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4460 GGACTTTTTTTTTTTTTTTT 4479

DB 6 GGATTCCTTTTTTTTTTTTTT 25

RESULT 1462

ADB04578
ADB04578 standard; DNA; 25 BP.

XX ADB04578;

DT 20-NOV-2003 (first entry)

XX Human MD27 scanning oligonucleotide SEQ ID 5564.

XX Cytostatic; immunostimulant; gene therapy; vaccine; human;

KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

KM chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;

KW developmental disorder; ss.

XX Homo sapiens.

XX EPI281758-A2.

XX 05-FEB-2003.

XX 30-JUL-2002; 2002EP-00016874.

XX 02-AUG-2001; 2001US-00922181.

XX (AEOM-) AEOMICA INC.

XX Shannon M, Gu Y, Nguyen C;

XX WPI; 2003-423107/40.

XX New zinc finger-containing proteins and nucleic acids, useful in

XX manufacturing a medicament for treating or preventing a disorder

XX associated with decreased or increased expression or activity of MD23,

XX MD24, MD27 or MD212, e.g. cancer.

XX Example 8; SEQ ID NO 5564; 103bp; English.

XX The present invention relates to novel human zinc finger-containing

XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is

XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,

XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome

XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,

XX or in manufacturing a medicament for treating or preventing a disorder

XX associated with decreased or increased expression or activity of MD23,

XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic

XX acids and proteins are also useful for diagnosing or monitoring a disease

XX caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic

XX alterations can also be used as probes to detect and characterize gross

XX alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are

XX useful in constructing microarrays for measuring gene expression. The

XX proteins are useful as therapeutic agents for gene therapy or as

XX vaccines. The present sequence was used to illustrate the invention.

XX Sequence 25 BP; 4 A; 2 C; 4 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.8; DB 1; Length 25;

Best Local Similarity 90.0%; Pred. No. 1.3e+03;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4475 TTTTCTTTTCTGTGAGACA 4494

DB 1 TTTTCTTTTCTGTGAGACA 20

RESULT 1463

ID ABX93770/c
AC ABX93770 standard; DNA; 25 BP.

XX ABX93770;

DT 16-JUN-2003 (first entry)

DE cfad gene PCR primer CS4D2.

XX PCR; ss: csa operon; CS4 plus; bacterial pili protein; ETEC; CS4; CS4D2;
KM enterotoxigenic Escherichia coli; multivalent Shigella-ETEC; diarrhoea;
KM Shigella; antibacterial; primer; cfad gene.

XX Unidentified.

PN US2002176868-A1.

PD 28-NOV-2002.

PF 20-APR-2001; 2001US-00839894.

PR 20-APR-2000; 2000US-0198626P.

XX (ALT/) ALTBOWM Z.
PA (LEVI/) LEVINE M M.
PA (BARR/) BARRY E M.

PI Altbouw Z, Levine MM, Barry EM;

DR WPI; 2003-352604/33.

PT Novel isolated nucleic acid comprising csa operon encoding proteins
PT required for producing CS4 pili, useful for generating immune response in
PT vertebrate against the enterotoxigenic Escherichia coli.

XX Example 1; Page 16; 58pp; English.

XX The invention relates to an isolated nucleotide sequence comprising a csa
CC operon (encoding proteins required for producing CS4 pili) or its
CC functional fragment. An immunogenic composition comprising a recombinant
CC product of a csa operon and a carrier, is useful for generating an immune
CC response in a subject, which involves contacting the subject with the
CC immunogenic composition. The recombinant product of the composition is
CC the CS4 antigen (bacterial pili protein) and is provided in an acellular
CC or cellular composition. The nucleic acid is useful for producing a
CC polypeptide product from a csa operon or functional fragment, which
CC involves providing a nucleic acid, introducing the csa operon in an
CC expression vector, such that a recombinant host cell is produced and
CC subjecting the recombinant host cell to conditions such that a protein
CC from the csa operon is expressed. The nucleic acid encoding at least an
CC immunogenic portion of the csa operon or a polypeptide encoded by the
CC nucleic acid is useful for generating an immune response in a vertebrate
CC against ETEC (enterotoxigenic Escherichia coli). The nucleic acid is also
CC useful for identifying polynucleotides encoding other proteins with
CC biological functions similar to that of the csa operon and for creating a
CC multivalent Shigella-ETEC immunogenic composition that will protect from
CC diarrhoea caused by either Shigella or CS4 expressing ETEC strains. This
CC sequence represents a PCR primer used in the scope of the invention

XX Sequence 25 BP; 7 A; 3 C; 5 G; 10 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.8; DB 1; Length 25;

Best Local Similarity 90.0%; Pred. No. 1.3e+03;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2970 CCGAATCTCTGATATCAA 2989
DB 25 CCAGATATCTCAGATATCAA 6

RESULT 1464

ID AC158350
AC AC158350 standard; DNA; 25 BP.

XX AC158350;

DT 13-OCT-2003 (first entry)

DE Human microarray DNA oligonucleotide SEQ ID NO 58341.

XX EST; ss: probe; expressed sequence tag; microarray; gene expression;
KM genetic variation; biallelic marker; polymorphism; human;
KM cross-species comparison.

XX Homo sapiens.

PN US2003104410-A1.

PD 05-JUN-2003.

PF 15-MAR-2002; 2002US-00098263.

PR 16-MAR-2001; 2001US-0276759P.

PA (AFFY-) AFFYMETRIX INC.

XX Miltmann MP;
PI WPI; 2003-567953/53.

PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.

XX Claim 1; SEQ ID NO 58341; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridization to a DNA library,
CC in analysis of genetic variation or in hybridization of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridizing at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridization. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in situ hybridization, in Southern, Northern or dot-
CC blot hybridization to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html

XX Sequence 25 BP; 9 A; 7 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.8; DB 1; Length 25;

Best Local Similarity 90.0%; Pred. No. 1.3e+03;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3093 GTGACTCAGACAGTCCTAAAGA 3112
DB 2 GTGACCCACAGTCCTAAAGA 21

RESULT 1465
AC119412

DT 13-OCT-2003 (first entry)
XX Human microarray DNA oligonucleotide SEQ ID NO 49701.
DE EST, ss; probe; expressed sequence tag; microarray; gene expression;
XX genetic variation; biallelic marker; polymorphism; human;
KM cross-species comparison.
XX Homo sapiens.
OS
PN US2003104410-A1.
XX
PD 05-JUN-2003.
XX
PF 15-MAR-2002; 2002US-00098263.
XX
PR 16-MAR-2001; 2001US-0276759P.
XX
PA (AFY-) AFFYMETRIX INC.
PI Miltmann MP;
XX
DR WPI; 2003-567953/53.
XX
PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
PS Claim 1; SEQ ID NO 49701; 9pp; English.
XX
XX The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 25 BP; 7 A; 7 C; 4 G; 7 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 16.8; DB 1; Length 25;
Best Local Similarity 90.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6612 TTCCCATCAGGGTAGAAA 6631
DB 4 TTCTCTCTCAGGGTAGAAA 23
RESULT 1468
ACI46333/c
ID ACI46333 standard; DNA; 25 BP.
XX
XX ACI46333;
AC
XX
DT 13-OCT-2003 (first entry)
XX

DE Human microarray DNA oligonucleotide SEQ ID NO 46324.
XX
XX EST, ss; probe; expressed sequence tag; microarray; gene expression;
KM genetic variation; biallelic marker; polymorphism; human;
XX cross-species comparison.
XX Homo sapiens.
OS
PN US2003104410-A1.
XX
PD 05-JUN-2003.
XX
PF 15-MAR-2002; 2002US-00098263.
XX
PR 16-MAR-2001; 2001US-0276759P.
XX
PA (AFY-) AFFYMETRIX INC.
PI Miltmann MP;
XX
DR WPI; 2003-567953/53.
XX
PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
PS Claim 1; SEQ ID NO 46324; 9pp; English.
XX
XX The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 25 BP; 6 A; 9 C; 7 G; 3 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 16.8; DB 1; Length 25;
Best Local Similarity 90.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1650 GGGGATGCTTATCCAGGCTC 1669
DB 24 GGGGATCCTTTCAGGGCTC 5
RESULT 1469
ACK08071
ID ACK08071 standard; DNA; 25 BP.
XX
XX ACK08071;
AC
XX
DT 14-OCT-2003 (first entry)
XX
XX Human microarray DNA oligonucleotide SEQ ID NO 108052.
DE

KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
 KW genetic variation; biallelic marker; polymorphism; human;
 KW cross-species comparison.
 XX
 OS Homo sapiens.
 XX
 PN US2003104410-A1.
 XX
 PD 05-JUN-2003.
 XX
 PF 15-MAR-2002; 2002US-00098263.
 XX
 PR 16-MAR-2001; 2001US-0276759P.
 XX
 PA (AFEX-) AFFYMETRIX INC.
 XX
 PI Miltmann MP;
 XX
 DR WPI; 2003-567953/53.
 XX
 PT New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.
 PS
 PS Claim 1; SEQ ID NO 108052; 9pp; English.
 XX
 CC The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridization to a DNA library,
 CC in analysis of genetic variation or in hybridization of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridizing at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridization. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying biallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in in situ hybridization, in Southern, Northern or dot-
 CC blot hybridization to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html
 CC
 SQ Sequence 25 BP; 8 A; 7 C; 8 G; 2 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 16.8; DB 1; Length 25;
 Best Local Similarity 90.0%; Pred. No. 1.3e+03;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 2944 ACAGGCGCCAGACAGAC 2963
 Db 4 ACAGGCGCTGCAAGACAGAC 23
 RESULT 1470
 ACH55887/c
 ID ACH55887 standard; DNA; 25 BP.
 XX
 AC ACH55887;
 XX
 DT 16-OCT-2003 (first entry)
 XX
 DE DNA target sequence #5023 useful in array for genetic analyses.
 XX
 KW Gene expression analysis; array; hybridization; genetic variation;
 KW tag-labelled compound; gene family; in situ hybridization;

KW library screening; Southern hybridization; northern hybridization;
 KW dot-blot hybridization; gene sequence; mutation detection;
 KW target sequence; probe; PCR; primer; ss.
 XX
 OS Unidentified.
 XX
 PN US2003082596-A1.
 XX
 PD 01-MAY-2003.
 XX
 PF 08-AUG-2002; 2002US-00215112.
 XX
 PR 08-AUG-2001; 2001US-0311040P.
 XX
 PA (MITT/) MITTMANN M.
 XX
 PI Miltmann M;
 XX
 DR WPI; 2003-576608/54.
 XX
 PT New probe array useful e.g. for monitoring gene expression levels, for
 PT analyzing genetic variations, or for hybridizing tag-labelled compounds,
 PT comprises multiple nucleic acid probes.
 PS
 PS Claim 1; SEQ ID NO 5023; 9pp; English.
 XX
 CC The present invention relates to nucleic acid sequences that are
 CC complementary to particular genes, and can be used as probes for a
 CC variety of analyses such as gene expression analysis. Each probe
 CC comprises 9 or more consecutive nucleotides from at least one of 14936
 CC nucleotide sequences defined in the patent, or their perfect sense match,
 CC sense mismatch, antisense match or antisense mismatch oligonucleotides.
 CC The probes may be used in an array comprising at least 10 distinct
 CC nucleic acid probes. The array is useful in monitoring gene expression
 CC levels by hybridization to a DNA library, in analysing genetic
 CC variations, and in hybridizing tag-labelled compounds. The probes are
 CC useful for identifying family members of a gene. The probes are also
 CC useful in in situ hybridizations, in screening cDNA or genomic libraries
 CC (or derived subclones) for additional clones containing segments of DNA
 CC that have been previously isolated and sequenced, in Southern, northern,
 CC or dot-blot hybridization of genomic DNA to identify or detect the
 CC sequence of any gene or detect specific mutations in any gene, and in
 CC mapping the 5' termini of mRNA molecules by primer extensions. The
 CC nucleic acid sequences of the invention are also useful as PCR primers.
 CC The invention provides a large collection of nucleic acid sequences.
 CC Complementary to particular genes with a wide range of analytical uses.
 CC ACH50885-ACH63260 represent the target sequences of the invention. Note:
 CC The sequence data for this patent was obtained in electronic format
 CC directly from the USPTO web site at seqdata.uspto.gov/patseqid.html
 CC
 SQ Sequence 25 BP; 6 A; 9 C; 5 G; 5 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 16.8; DB 1; Length 25;
 Best Local Similarity 90.0%; Pred. No. 1.3e+03;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 836 TGTGGAAGATGATGCTCAAC 855
 Db 25 TGTGGAAGATGCTGCTGAC 6
 RESULT 1471
 ACH56009/c
 ID ACH56009 standard; DNA; 25 BP.
 XX
 AC ACH56009;
 XX
 DT 16-OCT-2003 (first entry)
 XX
 DE DNA target sequence #5145 useful in array for genetic analyses.
 XX
 KW Gene expression analysis; array; hybridization; genetic variation;
 KW tag-labelled compound; gene family; in situ hybridization;

KM	library screening; Southern hybridisation; northern hybridisation;
KW	dot-blot hybridisation; gene sequence; mutation detection;
KW	target sequence; probe; PCR; primer; ss.
OS	unidentified.
XX	
XX	US2003082596-A1.
XX	
PD	01-MAY-2003.
XX	
PE	08-AUG-2002; 2002US-00215112.
FR	08-AUG-2001; 2001US-0311040P.
PA	(MITT/) MITTMANN M.
XX	
PI	Miltmann M;
XX	
DR	WPI; 2003-576608/54.
XX	
PT	New probe array useful e.g. for monitoring gene expression levels, for analyzing genetic variations, or for hybridizing tag-labeled compounds, comprises multiple nucleic acid probes.
PT	
PS	Claim 1; SEQ ID NO 5145; 9pp; English.
XX	
CC	The present invention relates to nucleic acid sequences that are complementary to particular genes, and can be used as probes for a variety of analyses such as gene expression analysis. Each probe comprises 9 or more consecutive nucleotides from at least one of 14936 nucleotide sequences defined in the patent, or their perfect sense match, sense mismatch, antisense match or antisense mismatch oligonucleotides. The probes may be used in an array comprising at least 10 distinct nucleic acid probes. The array is useful in monitoring gene expression levels by hybridisation to a DNA library, in analysing genetic variations, and in hybridising tag-labelled compounds. The probes are useful for identifying family members of a gene. The probes are also useful in situ hybridisations, in screening cDNA or genomic libraries (or derived subclones) for additional clones containing segments of DNA that have been previously isolated and sequenced, in Southern, northern, or dot-blot hybridisation of genomic DNA to identify or detect the sequence of any gene or detect specific mutations in any gene, and in mapping the 5' terminal of mRNA molecules by primer extensions. The nucleic acid sequences of the invention are also useful as PCR primers. The invention provides a large collection of nucleic acid sequences complementary to particular genes with a wide range of analytical uses. ACH50865-ACH65260 represent the target sequences of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at segdata.uspto.gov/patidsidentity.html
CC	
CC	
SQ	Sequence 25 BP; 8 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
	Query Match 0.2%; Score 16.8; DB 1; Length 25;
	Best Local Similarity 90.0%; Pred. No. 1.3e+03;
	Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY	836 TGTGGAAGATGATGCTCAAC 855
DB	24 TATGGAAAGTAGTGCTTAAC 5
RESULT 1472	
ID	ADA14835
AD	ADA14835 standard; DNA; 25 BP.
XX	
AC	ADA14835;
XX	
DT	06-NOV-2003 (first entry)
XX	
DE	Hairpin oligonucleotide, #1, used in an example of the invention.
XX	
KW	Hairpin sensor; hairpin loop; complementary probe; inverse repeat arm; quencher fluorescent agent; microarray; semiconductor; nanocrystal;
KW	quencher fluorescent agent; microarray; semiconductor; nanocrystal;

XX	rhodamine B-labelled dye; detection; gold support; ss.
XX	Synthetic.
PH	Key
FT	modified_base
FT	1
FT	/tag= a
FT	/mod_base= OTHER
FT	/note= "OTHER= thiol group"
FT	6. .20
FT	/tag= b
FT	/bound_moiety= "Target sequence #1"
FT	/note= "Forms a double-stranded region with the target sequence shown in example 2"
FT	25
FT	/tag= c
FT	/mod_base= OTHER
FT	/note= "OTHER= amino group"
PN	US2003013109-A1.
PD	16-JAN-2003.
XX	
XX	21-JUN-2002; 2002US-00176055.
PR	21-JUN-2001; 2001US-0299460P.
XX	
PA	(BALL/) BALLINGER C T.
PA	(LOCA/) LOCCASIO M.
PA	(LAND/) LANDRY D P.
PI	Ballinger CT, Loccasio M, Landry DP,
XX	
XX	WPI; 2003-596312/56.
PT	Haipin sensor useful for detecting a target nucleotide sequence in a
PT	sample, comprises a haipin loop assembly including a complementary probe
PT	and a quenchable fluorescing agent.
XX	
PS	Example 2; Page 11; 16pp; English.
XX	
CC	The invention discloses a haipin sensor comprising a haipin loop
CC	assembly including a complementary probe positioned between a first
CC	inverse repeat arm and a second inverse repeat arm, and a quenchable
CC	fluorescing agent joined, directly or indirectly, to the end of the
CC	second inverse repeat arm of the haipin loop assembly opposite the
CC	complementary probe. Also claimed is a microarray comprising the haipin
CC	sensor, where the end of the first inverse repeat arm opposite the
CC	complementary probe is bound, directly or indirectly, to a support, a kit
CC	for detecting a target nucleotide sequence in a sample comprising the
CC	haipin sensor, and a support, and a haipin sensor system, in which the
CC	particle is conductive or semi-conductive, including at least one of the
CC	above haipin sensor assemblies. The haipin sensor further comprises a
CC	functional group joined to the end of the first inverse repeat arm
CC	opposite the complementary probe, or first spacer opposite the first
CC	inverse repeat arm, the functional group selected from amino, carboxyl,
CC	thiol and hydroxyl. Further, the sensor comprises a ligand positioned
CC	between the second inverse repeat arm and the quenchable fluorescing
CC	agent, where the ligand is selected from mercapto, hydroxyl, amino,
CC	nitrile and carboxyl, carboxylic acid, organic acid and amino acid. The
CC	second spacer is positioned between the second inverse repeat arm and the
CC	quenchable fluorescing agent which comprises a semiconductor nanocrystal
CC	or rhodamine B-labelled dye. Within the microarray the support is capable
CC	of accepting a charge. At least one haipin sensor comprises two or more
CC	haipin sensors. The two or more haipin sensors include complementary
CC	probes that are the same or different and respective quenchable
CC	fluorescing agents that are the same or different. The two or more
CC	haipin sensors are arranged in a spatially-defined pattern. The sensor
CC	and system are useful for detecting a target nucleotide sequence in a
CC	sample. Further, the method involves identifying the target nucleotide
CC	sequence by the location of the complementary probe to which the target
CC	nucleotide sequence binds. The two or more haipin sensors include
CC	complementary probes or quenchable fluorescing agents, that are

CC different. The sequence presented is the hairpin oligonucleotide, #1,
 CC used in an example of the invention.

XX Sequence 25 BP; 1 A; 4 C; 4 G; 16 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.8; DB 1; Length 25;
 Best Local Similarity 90.0%; Pred. No. 1.3e+03;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4461 GACCTTTTTTTTTTTT 4480
 |||
 DB 3 GAGTTTTTTTTTTTCT 22

RESULT 1473

AAD57902
 ID AAD57902 standard; DNA; 25 BP.

XX AAD57902;

XX 20-NOV-2003 (first entry)

XX Oligonucleotide used in nonlinear optical technique.

XX Nonlinear optical technique; screening; ss.

XX Unidentified.

XX Key Location/Qualifiers

FT modified_base 1

FT /tag= a

FT /mod_base= OTHER

FT /note= "linked to Au particle"

FT modified_base 25

FT /tag= b

FT /mod_base= OTHER

FT /note= "linked to Dye"

PN WO2003064991-A2.

XX 07-AUG-2003.

XX 17-JUL-2002; 2002WO-US022681.

XX 17-JUL-2001; 2001US-0306040P.

XX 23-OCT-2001; 2001US-0347821P.

XX 06-FEB-2002; 2002US-0354668P.

XX (SALA/) SALAFSKY J S.

XX Salafsky JS;

XX MPI; 2003-646172/61.

XX Screening candidate binding partner(s) for binding to test molecule by

XX applying external force field to sample in homogeneous phase,

XX illuminating sample with light beam(s) at fundamental frequencies, and

XX measuring physical properties.

XX Disclosure; Fig 20B; 146pp; English.

XX The present invention relates to a method for detecting interactions

XX between biological components using a nonlinear optical technique. The

XX invention is used for screening candidate binding partner(s) for binding

XX to test molecule. It can also be used to detect changes in orientation or

XX conformation of the probe and/or target. The present sequence is an

XX oligonucleotide used in nonlinear optical technique

XX Sequence 25 BP; 1 A; 4 C; 4 G; 16 T; 0 U; 0 Other;

SQ Query Match 0.2%; Score 16.8; DB 1; Length 25;

Best Local Similarity 90.0%; Pred. No. 1.3e+03;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4461 GACCTTTTTTTTTTTT 4480
 |||
 DB 3 GAGTTTTTTTTTTTCT 22

RESULT 1474
 AAQ05003/C
 ID AAQ05003 standard; DNA; 29 BP.

XX AAQ05003;

XX 25-MAR-2003 (revised)

XX 31-OCT-1990 (first entry)

XX Sequence binding to and inhibiting the GSTpi gene.

XX C-myc; cancer; HIV-1; AIDS; collagenase; Alzheimer's disease; EGF;

XX epidermal growth factor; GSTpi; HMGCoA; thalassemia;

XX Herpes simplex virus; nerve growth factor receptor; globin; ss.

XX Synthetic.

XX EP375408-A.

XX 27-JUN-1990.

XX 20-DEC-1989; 89BP-00313391.

XX 20-DEC-1988; 88US-00287359.

XX (BAYU) BAYLOR COLLEGE MEDICINE.

XX (HOGA/) HOGAN M E.

XX Hogan ME, Kessler DJ;

XX MPI; 1990-195509/26.

XX Synthetic oligo-nucleotide(s) which bind target duplex DNA - forming co-

XX linear triplex to control transcription process in gene-specific fashion.

XX Claim 39; Page 30; 40pp; English.

XX Sequence forms triplex with the double stranded target sequence with G

XX binding to G-C and T to A-T. The strand runs 3' to 5' in an antiparallel

XX orientation and when targeted to a specific sequence will deactivate it.

XX This allows for growth inhibition in cancerous cells; manipulation of

XX cellular structural protein content; inhibition of IL-2 chain receptor;

XX disrupting plaque formation in Alzheimer's disease; inhibiting EGF gene;

XX CC modulating cholesterol synthesis through the HMGCoA gene; suppressing NGF

XX CC gene expression; arresting HSV-1 replication and suppressing Beta-globin

XX CC expression in thalassemia and sickle cell anemia patients. (Updated on

XX 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA

XX field.)

XX Sequence 29 BP; 0 A; 0 C; 0 G; 29 T; 0 U; 0 Other;

SQ Query Match 0.2%; Score 16.8; DB 1; Length 29;

Best Local Similarity 75.0%; Pred. No. 1.5e+03;

Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAAGAGAGAAAAACAAA 4039

DB 29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 1475

AAAN70277/C
 ID AAAN70277 standard; DNA; 30 BP.

XX AAAN70277;

XX 03-OCT-2002 (revised)

```
DT 26-MAY-1991 (first entry)
XX Sequence of scissile link probe MRCO64 (HL).
XX Hybridisation; probe; ss.
XX Synthetic.
OS
PN EP227976-A.
XX
PD 08-JUL-1987.
XX
PF 04-DEC-1986; 86EP-00116906.
XX
PR 05-DEC-1985; 85US-00805279.
XX
PA (MEIO-) MEIOGENICS INC.
XX
PI Duck P, Bender R, Crosby W, Robertson JG;
XX
DR WPI; 1987-186567/27.
XX
PT Synthetic nucleic acid probes - comprising two nucleic acid sequences
XX linked by a scissile linkage.
PS
XX Example; p29; 46pp; English.
XX
CC The patent claims a new molecule of formula (NA1)----S----(NA2)n. NA1 and
CC NA2 are noncomplementary nucleic acid sequences; ---S--- = a scissile
CC linkage; n = 1 or 1,000, which is used for the detection of specific DNA
CC or RNA sequences in a test soln. The scissile link probes may be PL
CC (Permanent Linkage to Solid Support) or HL (Hydrolysable Linkage to Solid
CC Support). The differential liability of DNA and RNA may be exploited in a
CC heterogeneous system when the scissile linkage is an RNA molecule. In the
CC examples, counter probe molecules 9 through 16 were used to determine
CC suitable hybridisation conditions. (Updated on 03-OCT-2002 to add missing
CC OS field.)
XX
SQ Sequence 30 BP; 0 A; 0 C; 0 G; 22 T; 8 U; 0 Other;
XX
Query Match 0.2%; Score 16.8; DB 1; Length 30;
Best Local Similarity 75.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 4012 AAAATGAGAAAAAGAGAGAAACAAA 4039
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAA 3
RESULT 1476
AAN92243/c
ID AAN92243 standard; DNA; 30 BP.
XX
AC AAN92243;
XX
DT 25-MAR-2003 (revised)
DT 31-OCT-2002 (revised)
DT 25-APR-1990 (first entry)
XX
DE SS probe MRCO64.
XX
KM Probe MRCO64; solid support; ribonuclease.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT 1..12
FT /*tag= a
FT /notes= "deoxyribonucleotides."
FT 13..20
FT /*tag= b
FT /notes= "ribonucleotides."
FT misc_feature 21..30
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FT /*tag= C
FT /notes= "deoxyribonucleotides."
PN WO8910415-A.
XX
PD 02-NOV-1989.
XX
PF 29-APR-1988; 88US-00187814.
XX
PR 29-APR-1988; 88US-00187814.
XX
PA (MEIO-) MEIOGENICS INC.
XX
PI Duck P, Bender R;
XX
DR WPI; 1989-339977/46.
XX
PT Detecting target nucleic acid molecules - using excess complementary
XX nucleic acid probes and nicking to complete a cycling sequence.
PS Disclosure; Page 24; 34pp; English.
XX
CC Probe MRCO64 is bound by a hydrolysable linkage to a solid support at its
CC 3' end. It is used by reacting excess probe with a target nucleic acid;
CC nicking hybridised probe at least once within a predetermined sequence to
CC form 2 or more probe fragments hybridised to the target sequence, which
CC results in the probe fragments becoming hybridised to another probe; and
CC identifying probe fragments, so detecting the target sequence. The probe
CC can react with target sequence to complete a cycling sequence. Using this
CC system, sensitivity of 10 exp. -19 to 10 exp. -20 molecules of target can
CC be obt'd. The probe is cleavable at the ribonucleotides by a ds RNase, eg
CC RNase H or ExoIII. (Updated on 31-OCT-2002 to add missing OS field.)
XX
SQ Sequence 30 BP; 0 A; 0 C; 0 G; 22 T; 8 U; 0 Other;
XX
Query Match 0.2%; Score 16.8; DB 1; Length 30;
Best Local Similarity 75.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 4012 AAAATGAGAAAAAGAGAGAAACAAA 4039
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAA 3
RESULT 1477
AAQ36302/c
ID AAQ36302 standard; DNA; 30 BP.
XX
AC AAQ36302;
XX
DT 25-MAR-2003 (revised)
DT 07-JUN-1993 (first entry)
XX
DE GST3ant1, for GSTpi gene target sequence.
XX
KM Glutathione-s-transferase pi; cancer; drug resistance; chemotherapy;
KM sensitisation; triplex; target; duplex; ss.
XX
OS Synthetic.
XX
PN US5176996-A.
XX
PD 05-JAN-1993.
XX
PF 22-DEC-1989; 89US-00453532.
XX
PR 20-DEC-1988; 88US-00287359.
XX
PA (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI Hogan ME, Kessler DJ;
XX
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DR  WPI; 1993-035718/04.
XX
XX  Synthetic oligo-nucleotide(s), prodn. useful e.g. for HIV-1 inhibition -
PT  which bind to target sequence in duplex DNA forming colinear triplex by
PT  binding to major groove.
XX
XX  Example 8; Col 27; 23pp; English.
XX
CC  Overexpression of the enzyme glutathione-S-transferase pi has been
CC  implicated as being responsible for the broad range drug resistance which
CC  develops in a variety of cancers. Expression of the gene may be prevented
CC  by the formation of a triplex between the duplex target DNA sequence and
CC  an anti parallel or parallel synthetic oligonucleotide. A suitable target
CC  sequence is that from base -499 to -410 of GSTpi, an unusual repetitive
CC  DNA segment within the control domain. Oligonucleotides targeted against
CC  this sequence will repress GSTpi transcription. See also AAQ36219-362.
CC  (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ  Sequence 30 BP; 0 A; 0 C; 0 G; 30 T; 0 U; 0 Other;

Query Match      0.2%; Score 16.8; DB 1; Length 30;
Best Local Similarity 75.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy      4012 AAAATGAGAAAAAGAGAGAAACAAA 4039
Db      30 AAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 1478
AAQ36301/C
ID  AAQ36301 standard; DNA; 30 BP.
XX
XX  AAQ36301;
XX
XX  25-MAR-2003 (revised)
DT  07-JUN-1993 (first entry)
XX
XX  GST3par, for GSTpi gene target sequence.
XX
XX  Glutathione-S-transferase pi; cancer; drug resistance; chemotherapy;
KM  sensitisation; triplex; target; duplex; ss.
XX
OS  Synthetic.
XX
XX  US5176996-A.
XX
XX  05-JAN-1993.
PD
XX
XX  22-DEC-1989; 89US-00453532.
PF
XX
XX  20-DEC-1988; 88US-00287359.
PR
XX
XX  (BAYU ) BAYLOR COLLEGE MEDICINE.
PA
XX
XX  Hogan ME, Kessler DJ;
PI
XX
XX  WPI; 1993-035718/04.
DR
XX
XX  Synthetic oligo-nucleotide(s), prodn. useful e.g. for HIV-1 inhibition -
PT  which bind to target sequence in duplex DNA forming colinear triplex by
PT  binding to major groove.
XX
XX  Example 8; Col 27; 23pp; English.
XX
CC  Overexpression of the enzyme glutathione-S-transferase pi has been
CC  implicated as being responsible for the broad range drug resistance which
CC  develops in a variety of cancers. Expression of the gene may be prevented
CC  by the formation of a triplex between the duplex target DNA sequence and
CC  an anti parallel or parallel synthetic oligonucleotide. A suitable target
CC  sequence is that from base -499 to -410 of GSTpi, an unusual repetitive
CC  DNA segment within the control domain. Oligonucleotides targeted against
CC  this sequence will repress GSTpi transcription. See also AAQ36219-362.

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CC  (Updated on 25-MAR-2003 to correct PF field.)
XX
XX  Sequence 30 BP; 0 A; 0 C; 0 G; 30 T; 0 U; 0 Other;
SQ
Query Match      0.2%; Score 16.8; DB 1; Length 30;
Best Local Similarity 75.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy      4012 AAAATGAGAAAAAGAGAGAAACAAA 4039
Db      30 AAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 1479
AAK57020/C
ID  AAK57020 standard; DNA; 30 BP.
XX
XX  AAK57020;
XX
XX  19-JUL-1999 (first entry)
DT
XX
XX  WO9923258 oligonucleotide primer 2.
DE
XX
XX  Visual; nucleic acid detection; target; hybridisation; probe; primer;
KM  agglutination; bridging molecule; ss.
XX
OS  Synthetic.
XX
XX  WO9923258-A1.
XX
XX  14-MAY-1999.
PD
XX
XX  30-OCT-1998; 98WO-US023267.
PF
XX
XX  31-OCT-1997; 97US-0063969P.
PR
XX
XX  (GENP-) GEN-PROBE INC.
PA
XX
XX  Weiburg WC, Stull PD, Reshatoff MR;
PI
XX
XX  WPI; 1999-326994/27.
DR
XX
XX  Optical detection of hybridization complexes for specific target nucleic
PT  acid sequences.
XX
XX  Example 1; Page 40; 46pp; English.
XX
XX  This invention describes a novel method for the visual detection of
CC  target nucleic acid presence in a sample. A preferred target is a
CC  Mycobacterium complex nucleic acid sequence. The detection method uses
CC  visual detection of a change in the hybridization without aid of
CC  instrumentation. Multiple copies of a target nucleic acid sequence are
CC  mixed with first and second detectable probes under hybridizing
CC  conditions favouring particle agglutination via a bridging molecule
CC  allowing for visual detection of the target nucleic acid sequence. The
CC  bridging molecule enhances or inhibits formation of a hybridization
CC  complex
XX
SQ  Sequence 30 BP; 0 A; 0 C; 0 G; 30 T; 0 U; 0 Other;

Query Match      0.2%; Score 16.8; DB 1; Length 30;
Best Local Similarity 75.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy      4012 AAAATGAGAAAAAGAGAGAAACAAA 4039
Db      30 AAAAAAAAAAAAAAAAAAAAAAAAAA 3

RESULT 1480
AAF99889
ID  AAF99889 standard; DNA; 30 BP.
XX

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AC  AAF9889;
XX
DT  12-JUN-2001 (first entry)
XX
DE  Immunostimulatory nucleic acid #1005.
XX
XX  Vaccine; cytostatic; virocidal; bactericidal; fungicidal; anti-parasitic;
KM  immunostimulatory; tumour; viral infection; bacterial infection;
KM  fungal infection; parasitic infection; cancer; asthma;
XX  infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS  Synthetic.
XX
PN  WO200122972-A2.
XX
PD  05-APR-2001.
XX
PF  25-SEP-2000; 2000WO-US026383.
XX
PR  25-SEP-1999; 99US-0156113P.
PR  27-SEP-1999; 99US-0156135P.
PR  23-AUG-2000; 2000US-0227436P.
XX
XX  (IOWA ) UNIV IOWA RES FOUND.
PA  (COLE-) COLEY PHARM GMBH.
XX
PI  Krieg AM, Schetter C, Vollmer J;
XX
DR  WPI; 2001-273485/28.
XX
PT  Vaccinating against tumors, infectious diseases, allergies and asthma
PT  using immunostimulatory Py-rich and TG nucleic acids.
XX
PS  Example 6; Page 60; 338pp; English.
XX
XX  The present invention relates to a method for stimulating an immune
CC  response. The method comprises administering an immunostimulatory nucleic
CC  acid to a non-rodent subject in sufficient quantity to stimulate an
CC  immune response. The present sequence is one such immunostimulatory
CC  nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC  (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC  against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC  and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC  haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC  staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC  also useful for preventing cancer, asthma, infectious disease, allergy or
CC  immune deficiency. The present sequence can also be used to redirect a
CC  Th2 to a Th1 immune response and to activate immune cells. Note: the
CC  present sequence may have a phosphorothioate backbone
XX
SQ  Sequence 30 BP; 30 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
XX  Query Match 0.2%; Score 16.8; DB 1; Length 30;
XX  Best Local Similarity 75.0%; Pred. No. 1.6e+03;
XX  Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
XX
QY  4012 AAAATGAGAAAAAGAGAGAAACAAA 4039
Db  1 AAAAAAAAAAAAAAAAAAAAAAAAAA 28

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KM  fungal infection; parasitic infection; cancer; asthma;
KM  infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS  Synthetic.
XX
PN  WO200122972-A2.
XX
PD  05-APR-2001.
XX
PF  25-SEP-2000; 2000WO-US026383.
XX
PR  25-SEP-1999; 99US-0156113P.
PR  27-SEP-1999; 99US-0156135P.
PR  23-AUG-2000; 2000US-0227436P.
XX
XX  (IOWA ) UNIV IOWA RES FOUND.
PA  (COLE-) COLEY PHARM GMBH.
XX
PI  Krieg AM, Schetter C, Vollmer J;
XX
DR  WPI; 2001-273485/28.
XX
PT  Vaccinating against tumors, infectious diseases, allergies and asthma
PT  using immunostimulatory Py-rich and TG nucleic acids.
XX
PS  Example 6; Page 60; 338pp; English.
XX
XX  The present invention relates to a method for stimulating an immune
CC  response. The method comprises administering an immunostimulatory nucleic
CC  acid to a non-rodent subject in sufficient quantity to stimulate an
CC  immune response. The present sequence is one such immunostimulatory
CC  nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC  (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC  against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC  and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC  haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC  staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC  also useful for preventing cancer, asthma, infectious disease, allergy or
CC  immune deficiency. The present sequence can also be used to redirect a
CC  Th2 to a Th1 immune response and to activate immune cells. Note: the
CC  present sequence may have a phosphorothioate backbone
XX
SQ  Sequence 30 BP; 0 A; 0 C; 0 G; 30 T; 0 U; 0 Other;
XX
XX  Query Match 0.2%; Score 16.8; DB 1; Length 30;
XX  Best Local Similarity 75.0%; Pred. No. 1.6e+03;
XX  Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
XX
QY  4012 AAAATGAGAAAAAGAGAGAAACAAA 4039
Db  30 AAAAAAAAAAAAAAAAAAAAAAAAAA 3

```

```

RESULT 1481
AAF9888/c
ID  AAF9888 standard; DNA; 30 BP.
XX
AC  AAF9888;
XX
DT  12-JUN-2001 (first entry)
XX
DE  Immunostimulatory nucleic acid #1004.
XX
DE  Vaccine; cytostatic; virocidal; bactericidal; fungicidal; anti-parasitic;
KM  immunostimulatory; tumour; viral infection; bacterial infection;

```

```

RESULT 1482
ABK10416
ID  ABK10416 standard; DNA; 30 BP.
XX
AC  ABK10416;
XX
DT  21-MAY-2002 (first entry)
XX
DE  Synthetic primer sequence 5'-A30-3'.
XX
KM  ss; 5'-A30-3'; double stranded DNA generation; promiscuous base;
KM  target molecule; primer.
XX
OS  Synthetic.
XX
PN  US6326143-B1.
XX
PD  04-DEC-2001.
XX
PF  22-MAY-1998; 98US-00083123.

```

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XX PR 22-NOV-1996; 96MO-EP005149.
XX XX (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX PA Orum H, Seeger C;
XX PI WPI; 2002-214947/27.
XX DR
XX PT Determining an analyte in a sample, for generating multiple double
XX PT stranded nucleic acids, comprises employing a single primer sequence with
XX PT a nucleobase sequence having affinity to the sequence contained in a
XX PT target nucleic acid.
XX PS
XX PS Example 1; Col 14; 25pp; English.
XX CC
XX CC The invention relates to determining an analyte in a sample comprising
XX CC (a) providing a target nucleic acid comprising a region A, a nucleobase
XX CC sequence B, and a sequence I linked to the 5' terminus of the nucleobase
XX CC sequence B, where the nucleobase sequence B is not specific for the
XX CC analyte, and the region A specifically binds to the analyte, (b) binding
XX CC the target nucleic acid to the analyte, separating the analyte bound to
XX CC the target nucleic acid from the remaining part of the sample, (d)
XX CC hybridising a primer to the target nucleic acid, where the primer
XX CC comprises a nucleobase sequence B', and the nucleobase sequence B'
XX CC hybridises to the nucleobase sequence B, (e) elongating the hybridised
XX CC primer to produce an elongation product E using the target nucleic acid
XX CC as a template and using nucleotides, where at least 30 % of the
XX CC nucleotides contain at least one promiscuous base which is capable of
XX CC base pairing with each of adenine, guanine, cytosine, and thymine, (f)
XX CC separating the target nucleic acid from the elongation product E, (g)
XX CC hybridising a further primer which comprises the nucleobase sequence B'
XX CC to the elongation product E, where the elongation product E is capable of
XX CC acting as a template for the elongation of the further primer, (h)
XX CC elongating the hybridised further primer of step (g) to produce an
XX CC elongation product E' using the elongation product E as a template and
XX CC using nucleotides, where at least 30 % of the nucleotides contain at
XX CC least one promiscuous base, (i) separating the elongation product E from
XX CC the elongation product E', (j) hybridising a further primer comprising a
XX CC nucleobase sequence B' to the target nucleic acid or the elongation
XX CC product E, (k) elongating the further primer of step (j) to produce
XX CC another elongation product E using the target nucleic acid or elongation
XX CC product E as a template and using nucleotides, where at least 30 % of the
XX CC nucleotides contain at least one promiscuous base, (l) separating product
XX CC E of step (k) from the target nucleic acid or elongation product E, (m)
XX CC optionally repeating steps (g) - (l) a sufficient number of times to
XX CC generate a desired amount of double stranded nucleic acids and (n)
XX CC determining the elongation product E and/or elongation product E' as a
XX CC measure of the presence or amount of the analyte, where the lengths of
XX CC the sequence I and the nucleobase sequence B are chosen such that, when
XX CC the further primer hybridises to the elongation product E in step (g),
XX CC the further primer spans a sequence formed by elongation of the
XX CC hybridised primer of step (e) and overlaps at least a part of the 3'
XX CC region of the hybridized primer of step (e) by an overlap length. The
XX CC method is useful for determining an analyte in a sample. In particular, the
XX CC method is useful for generating multiple double stranded nucleic acids.
XX CC The present sequence is a primer molecule used to exemplify the method of
XX CC the invention
XX XX
XX SQ Sequence 30 BP; 30 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 16.8; DB 1; Length 30;
XX Best Local Similarity 75.0%; Pred. No. 1.6e+03;
XX Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
XX
XX 4012 AAAATGAGAAAAAGAGAGAAAAAAGAAAA 4039
XX ||||| ||||| ||||| ||||| |||||
XX 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 28
XX
XX RESULT 1483
XX ABRK10412/C
XX ID ABRK10412 standard; DNA; 30 BP.

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XX AC ABRK10412;
XX XX
XX DT 21-MAY-2002 (first entry)
XX DE Synthetic primer sequence 5'-T30-3'.
XX XX
XX KM ss; 5'-T30-3'; double stranded DNA generation; promiscuous base;
XX KM target molecule; primer.
XX OS Synthetic.
XX PN US6326143-B1.
XX PD 04-DEC-2001.
XX XX
XX PF 22-MAY-1998; 98US-00083123.
XX XX
XX PR 22-NOV-1996; 96MO-EP005149.
XX XX (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX PA Orum H, Seeger C;
XX PI WPI; 2002-214947/27.
XX DR
XX PT Determining an analyte in a sample, for generating multiple double
XX PT stranded nucleic acids, comprises employing a single primer sequence with
XX PT a nucleobase sequence having affinity to the sequence contained in a
XX PT target nucleic acid.
XX PS
XX PS Example 1; Col 14; 25pp; English.
XX CC
XX CC The invention relates to determining an analyte in a sample comprising
XX CC (a) providing a target nucleic acid comprising a region A, a nucleobase
XX CC sequence B, and a sequence I linked to the 5' terminus of the nucleobase
XX CC sequence B, where the nucleobase sequence B is not specific for the
XX CC analyte, and the region A specifically binds to the analyte, (b) binding
XX CC the target nucleic acid to the analyte, separating the analyte bound to
XX CC the target nucleic acid from the remaining part of the sample, (d)
XX CC hybridising a primer to the target nucleic acid, where the primer
XX CC comprises a nucleobase sequence B', and the nucleobase sequence B'
XX CC hybridises to the nucleobase sequence B, (e) elongating the hybridised
XX CC primer to produce an elongation product E using the target nucleic acid
XX CC as a template and using nucleotides, where at least 30 % of the
XX CC nucleotides contain at least one promiscuous base which is capable of
XX CC base pairing with each of adenine, guanine, cytosine, and thymine, (f)
XX CC separating the target nucleic acid from the elongation product E, (g)
XX CC hybridising a further primer which comprises the nucleobase sequence B'
XX CC to the elongation product E, where the elongation product E is capable of
XX CC acting as a template for the elongation of the further primer, (h)
XX CC elongating the hybridised further primer of step (g) to produce an
XX CC elongation product E' using the elongation product E as a template and
XX CC using nucleotides, where at least 30 % of the nucleotides contain at
XX CC least one promiscuous base, (i) separating the elongation product E from
XX CC the elongation product E', (j) hybridising a further primer comprising a
XX CC nucleobase sequence B' to the target nucleic acid or the elongation
XX CC product E, (k) elongating the further primer of step (j) to produce
XX CC another elongation product E using the target nucleic acid or elongation
XX CC product E as a template and using nucleotides, where at least 30 % of the
XX CC nucleotides contain at least one promiscuous base, (l) separating product
XX CC E of step (k) from the target nucleic acid or elongation product E, (m)
XX CC optionally repeating steps (g) - (l) a sufficient number of times to
XX CC generate a desired amount of double stranded nucleic acids and (n)
XX CC determining the elongation product E and/or elongation product E' as a
XX CC measure of the presence or amount of the analyte, where the lengths of
XX CC the sequence I and the nucleobase sequence B are chosen such that, when
XX CC the further primer hybridises to the elongation product E in step (g),
XX CC the further primer spans a sequence formed by elongation of the
XX CC hybridised primer of step (e) and overlaps at least a part of the 3'
XX CC region of the hybridized primer of step (e) by an overlap length. The
XX CC method is useful for determining an analyte in a sample. In particular, the
XX CC method is useful for generating multiple double stranded nucleic acids.

```


CC The present sequence is a primer molecule used to exemplify the method of
CC the invention
XX
SQ Sequence 30 BP; 0 A; 0 C; 0 G; 30 T; 0 U; 0 Other;
Query Match 0.2%; Score 16.8; DB 1; Length 30;
Best Local Similarity 75.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 4012 AAAATGAGAAAAAGAGAGAAACAAA 4039
DB 30 AAAAAAAAAAAAAAAAAAAAAAAA 3
RESULT 1484
ABK70490/c
ID ABK70490 standard; DNA; 30 BP.
XX
AC ABK70490;
XX
DT 15-JUL-2002 (first entry)
XX
DE In-situ analysis synthetic probe #58.
XX
KM Human; oligonucleotide label-domain; CMV; cytomegalovirus; EBV;
KM Epstein-Barr virus; lambda-immunoglobulin light chain; hapten;
KM kappa-immunoglobulin light chain; repetitive Alu sequence; EBER;
KM Epstein-Barr early RNA; probe; ss.
XX
OS Synthetic.
XX
PN WO200222874-A2.
XX
PD 21-MAR-2002.
XX
PF 06-SEP-2001; 2001WO-US028014.
XX
PR 15-SEP-2000; 2000US-0233177P.
XX
PA (VENT-) VENTANA MEDICAL SYSTEMS INC.
XX
PI Utermohlen JG, Connaughton J;
XX
DR WPI; 2002-371972/40.
XX
PT Novel oligonucleotide label-domain for incorporation into oligonucleotide
PT probes useful for detecting or localizing nucleic acid target genes
XX within a cell or tissue sample.
XX
PS Disclosure; Page 69; 71pp; English.
XX
CC The present invention relates to a new oligonucleotide label-domain
CC comprising the sequence (CTATTY) n and its complement (AAATYG) n, where
CC n is 1. The probe sets of the invention are useful for detecting kappa or
CC lambda-immunoglobulin light chain mRNA or corresponding heteronuclear
CC RNA, CMV (cytomegalovirus) immediate early RNA, EBV (Epstein-Barr virus)
CC early RNA 1 and RNA 2, and human Alu repetitive satellite genomic
CC sequences. The invention is a useful generic sequence for incorporation
CC into oligonucleotide probes for detecting gene-specific sequences within
CC cells or tissue samples in in situ hybridisation analysis and for
CC attaching a label to immunoglobulins or other proteins for detecting
CC haptens and antigens in immunohistochemical analyses. The present nucleic
CC acid sequence represents one of a collection (ABK70376-ABK70501) of
CC oligonucleotide probes that were used in the invention for detecting or
CC localising a plurality nucleic acid target gene or antigen within a cell
CC or tissue sample
XX
SQ Sequence 30 BP; 0 A; 0 C; 0 G; 30 T; 0 U; 0 Other;
Query Match 0.2%; Score 16.8; DB 1; Length 30;
Best Local Similarity 75.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAAGAGAGAAACAAA 4039
DB 30 AAAAAAAAAAAAAAAAAAAAAAAA 3
RESULT 1485
ABSS3961/c
ID ABSS3961 standard; DNA; 30 BP.
XX
AC ABSS3961;
XX
DT 26-NOV-2002 (first entry)
XX
DE Method of measuring nucleic acid related oligonucleotide dt30mer.
XX
KM Fluorescent intercalative dye; nucleic acid detection; gene diagnosis;
KM clinical diagnostics; Stokes shift; ds.
XX
OS Synthetic.
XX
PN EP123226-A2.
XX
PD 17-JUL-2002.
XX
PF 11-JAN-2002; 2002EP-00000723.
XX
PR 11-JAN-2001; 2001JP-00003432.
XX
PA (TOYO) TOSOH CORP.
XX
PI Tokunaga T, Ishiguro T, Horie R;
XX
DR WPI; 2002-645688/70.
XX
PT Fluorescent dye or its salt, hydrate, solvate or stereoisomer for nucleic
PT acid probe for measuring nucleic acid(s) containing specific nucleic acid
PT sequence in sample, has specific formula.
XX
PS Example 5; Page 33; 40pp; English.
XX
CC The invention describes a novel fluorescent dye and method of detecting
CC nucleic acid. The dye and method are useful for nucleic acid probes for
CC measuring nucleic acid(s) containing a specific nucleic acid sequence in
CC a sample, and for qualitative/quantitative assay of target RNA containing
CC specific base sequence anticipated in gene mixture. The assay is useful
CC in gene diagnosis and other areas of clinical diagnostics and in
CC identification/quantification microorganisms in biological samples such
CC as serum, plasma and urine, microbially contaminated samples from food,
CC rooms, soil, rivers and sea. The fluorescent intercalative dye shows a
CC large fluorescent enhancement upon intercalation into double-stranded
CC nucleic acid, and shows a great difference between excitation and
CC emission wavelengths (has a large Stokes shift) and does not have a
CC fluorescent spectrum that overlaps with those of conventionally known
CC fluorescent intercalation dyes. Viruses, microbial RNAs, specific
CC sequences in one RNA, are detected or quantified in a short time, hence
CC the detection method is applicable to clinical diagnosis which requires
CC high reliability. Amplification and extraction efficiencies of the target
CC nucleic acid, are checked. This sequence represents a synthetic DNA used
CC as the target in an assay to detect double stranded DNA
XX
SQ Sequence 30 BP; 0 A; 0 C; 0 G; 30 T; 0 U; 0 Other;
Query Match 0.2%; Score 16.8; DB 1; Length 30;
Best Local Similarity 75.0%; Pred. No. 1.6e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 4012 AAAATGAGAAAAAGAGAGAAACAAA 4039
DB 30 AAAAAAAAAAAAAAAAAAAAAAAA 3
RESULT 1486
ABSS5182

```
ID  ABS55182 standard; DNA; 31 BP.
XX
XX  ABS55182;
AC
XX  12-DEC-2002 (first entry)
DT
XX  Tumour-suppressor gene associated oligonucleotide.
DE
XX  Tumour-suppressor; cancer; ss.
KM
XX  Unidentified.
OS
XX  KR2001061173-A.
PN
XX  07-JUL-2001.
PD
XX  28-DEC-1999; 99KR-00063661.
PF
XX  28-DEC-1999; 99KR-00063661.
PR
XX  28-DEC-1999; 99KR-00063661.
PA  (CHAE/) CHAE J H.
PA  (CHOI/) CHOI W H.
PA  (CHUN/) CHUNG T J.
PA  (JUNG/) JUNG H J.
PA  (KIMC/) KIM C G.
PA  (KIMH/) KIM H G.
PA  (PARK/) PARK C I.
PA  (PARK/) PARK J H.
XX
XX  Chae JH, Choi WH, Chung TJ, Jung HJ, Kim CG, Kim HG, Park CI;
PI  Park JH;
XX
XX  WPI; 2002-016333/02.
DR
XX
XX  Vector containing polymerase chain reaction primers of tumor-suppressor
PT  gene, useful for diagnosis of cancer.
XX
XX  Disclosure; Page 11; 19pp; Korean.
PS
XX
XX  The present invention relates to a new vector comprising polymerase chain
CC  reaction (PCR) primers of tumour-suppressor gene. The invention can be
CC  useful for the diagnosis of cancer. The present nucleic acid sequence
CC  represents an oligonucleotide as described in the invention
XX
XX  Sequence 31 BP; 22 A; 0 C; 4 G; 5 T; 0 U; 0 Other;
SQ
XX
XX  Query Match 0.2%; Score 16.8; DB 1; Length 31;
XX  Best Local Similarity 75.0%; Pred. No. 1.6e+03;
XX  Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY  4007 GGTCTAAATGAGAAAAAGAGAAAA 4034
DB  3 GGTGAATATGAAAAAAGAAAAA 30
RESULT 1487
AAN70278/c
ID  AAN70278 standard; DNA; 32 BP.
XX
XX  AAN70278;
AC
XX  03-OCT-2002 (revised)
DT  26-MAY-1991 (first entry)
XX
XX  Sequence of scissile link probe MRC068 (HL).
DE
XX  Hybridisation; probe; ss.
XX
XX  Synthetic.
OS
XX  EP227976-A.
PN
XX  08-JUL-1987.
PD
```

```
XX  04-DEC-1986; 86EP-00116906.
PF
XX  05-DEC-1985; 85US-00805279.
PR
XX  (MEIO-) MEIOGENICS INC.
XX
XX  Duck P, Bender R, Crosby W, Robertson JG;
PI  WPI; 1987-186567/27.
DR
XX
XX  Synthetic nucleic acid probes - comprising two nucleic acid sequences
PT  linked by a scissile linkage.
XX
XX  Example; p29; 46pp; English.
XX
XX  The patent claims a new molecule of formula (NA1---S---NA2)n. NA1 and
CC  NA2 are noncomplementary nucleic acid sequences; ---S--- = a scissile
CC  linkage; n = 1 or 1,000, which is used for the detection of specific DNA
CC  or RNA sequences in a test soln. The scissile link probes may be PL
CC  (Permanent Linkage to Solid Support) or HL (Hydrolysable Linkage to Solid
CC  Support). The differential liability of DNA and RNA may be exploited in a
CC  heterogeneous system when the scissile linkage is an RNA molecule. In the
CC  examples, counter probe molecules 9 through 16 were used to determine
CC  suitable hybridisation conditions. (Updated on 03-OCT-2002 to add missing
CC  OS field.)
XX
XX  Sequence 32 BP; 0 A; 0 C; 0 G; 24 T; 8 U; 0 Other;
SQ
XX
XX  Query Match 0.2%; Score 16.8; DB 1; Length 32;
XX  Best Local Similarity 75.0%; Pred. No. 1.7e+03;
XX  Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY  4012 AAAATGAGAAAAAGAGAAAAACAAA 4039
DB  32 AAAAAAAAAAAAAAAAAAAAAAAAAA 5
RESULT 1488
AAN92244/c
ID  AAN92244 standard; DNA; 32 BP.
XX
XX  AAN92244;
AC
XX  25-MAR-2003 (revised)
DT  31-OCT-2002 (revised)
DT  25-APR-1990 (first entry)
XX
XX  SS probe MRC068.
DE
XX
XX  Probe MRC068; solid support; ribonuclease.
KM
XX  Synthetic.
OS
XX
XX  Key Location/Qualifiers
XX  misc_feature 1..14
XX  FT /tag= a
XX  FT /note= "deoxyribonucleotides."
XX  FT 15..22
XX  FT /tag= b
XX  FT /note= "ribonucleotides."
XX  FT 23..32
XX  FT /tag= c
XX  FT /note= "deoxyribonucleotides."
XX
XX  WO8910415-A.
PN
XX  02-NOV-1989.
PD
XX  29-APR-1988; 88US-00187814.
PF
XX  29-APR-1988; 88US-00187814.
PR
XX  29-APR-1988; 88US-00187814.
PD
```

PA (MEIO-) MEIOGENICS INC.
XX
PI Duck P, Bender R;
XX
DR WPI; 1989-339977/46.
XX
PT Detecting target nucleic acid molecules - using excess complementary
XX nucleic acid probes and nicking to complete a cycling sequence.
PS Disclosure, Page 24; 34pp; English.
XX
CC Probe MRCO68 is bound by a hydrolysable linkage to a solid support at its
CC 3' end. It is used by reacting excess probe with a target nucleic acid;
CC nicking hybridised probe at least once within a predetermined sequence to
CC form 2 or more probe fragments hybridised to the target sequence, which
CC results in the probe fragments becoming hybridised to another probe; and
CC identifying probe fragments, so detecting the target sequence. The probe
CC can react with target sequence to complete a cycling sequence. Using this
CC system, sensitivity of 10 exp. -19 to 10 exp. -20 molecules of target can
CC be obt'd. The probe is cleavable at the ribonucleotides by a de RNase, eg
CC RNase H or ExoIII. (Updated on 31-OCT-2002 to add missing OS field.)
CC (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 32 BP; 0 A; 0 C; 0 G; 24 T; 8 U; 0 Other;
XX
Query Match 0.2%; Score 16.8; DB 1; Length 32;
Best Local Similarity 75.0%; Pred. No. 1.7e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
XX
QY 4012 AAAATGAGAAAAAGAGAGAAAAACAAA 4039
DB 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5
XX
RESULT 1489
ADC33445/c
ID ADC33445 standard; DNA; 32 BP.
XX
AC ADC33445;
XX
DT 18-DEC-2003 (first entry)
XX
DE Template oligonucleotide #SEQ ID 2.
XX
KM Binding; tandem repeat; label; analyte detection; ss.
XX
OS Synthetic.
XX
PN WO2003072721-A2.
XX
PD 04-SEP-2003.
XX
PF 20-FEB-2003; 2003WO-US005301.
XX
PR 21-FEB-2002; 2002US-0359223P.
XX
PR 08-MAY-2002; 2002US-0379360P.
XX
PA (DISC-) DISCOVERX INC.
XX
PI Wu M, Ullman E;
XX
DR WPI; 2003-712717/67.
XX
XX Detecting a label comprising employing (as the label) a reagent having a
XX 3' extendable terminus hybridized to a tandem repeat template in
XX combination with a DNA polymerase and dNTPs necessary for repetitively
XX replicating the tandem repeat.
PS Example; SEQ ID NO 2; 38pp; English.
XX
CC The invention relates to a method for detecting a label, comprising
CC employing (as the label) a reagent having a 3' extendable terminus
CC hybridised to a tandem repeat template in combination with a DNA

CC polymerase and dNTPs necessary for repetitively replicating the tandem
CC repeat. The method involves detecting a binding event between first and
CC second binding members, employing a label to determine the occurrence of
CC the binding event. The tandem repeating units are polyT. The method of
CC the invention is useful in detecting an analyte using repetitive
CC extension along a tandem repeat. The extended nucleic acid may be used
CC for detecting a moiety, particularly involved in a binding event
CC employing a reagent. The current sequence represents a template member
CC oligonucleotide containing a polyT tandem repeat that binds to the
CC extendable oligonucleotide given in ADC33444.
XX
SQ Sequence 32 BP; 0 A; 0 C; 0 G; 32 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 16.8; DB 1; Length 32;
Best Local Similarity 75.0%; Pred. No. 1.7e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
XX
QY 4012 AAAATGAGAAAAAGAGAGAAAAACAAA 4039
DB 32 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5
XX
RESULT 1490
AAF29153/c
ID AAF29153 standard; DNA; 33 BP.
XX
AC AAF29153;
XX
DT 04-APR-2001 (first entry)
XX
DE PCR primer SEQ ID 24 used to amplify SRSV specific cDNA.
XX
KM Small round structured virus; SRSV; food poisoning; PCR primer; ss.
XX
OS Small round structured virus.
XX
PN WO200079280-A1.
XX
PD 28-DEC-2000.
XX
PF 22-JUN-2000; 2000WO-JP004095.
XX
PR 22-JUN-1999; 99JP-00175928.
XX
PA (NINA-) JAPAN NAT INST INFECTIOUS DISEASES.
XX
PA (DENK-) DENKA SEIKEN KK.
XX
PI Takeda N, Natori K, Miyamura T, Kamata K, Sato T, Sato S;
XX
DR WPI; 2001-080848/09.
XX
XX Kit for the detection and typing of small round-structured virus (SRSV)
XX PT strains for investigation of food poisoning outbreaks, contains
XX PT antibodies.
XX
PS Example 1; Page 75; 84pp; Japanese.
XX
CC This invention relates to a kit for the detection and typing of small
CC round structured virus (SRSV) strains. The kit contains antibodies
CC directed against peptides represented in sequences AAB49700 - AAB49710,
CC which are each SRSV strain specific. Polynucleotide sequences AAF20141 -
CC AAF20151 represent cDNA encoding the strain specific proteins. The kit is
CC used for detecting and typing strains of SRSV in order to prevent the
CC spread of infection and to examine the epidemiology of outbreaks. PCR
CC primers AAF29152 - AAF29163 are used to amplify SRSV strain specific cDNA
CC sequences
XX
SQ Sequence 33 BP; 0 A; 0 C; 0 G; 33 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 16.8; DB 1; Length 33;
Best Local Similarity 75.0%; Pred. No. 1.7e+03;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAAGAGAAAAACAAA 4039
 |||||
 DB 33 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 1491
 AAA07787/c
 ID AAA07787 standard; DNA; 23 BP.
 XX
 XX AAA07787;
 AC
 XX 23-JUN-2000 (first entry)
 DT
 XX Structure of a fragment of duplex A target strand.
 DE
 XX Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
 KW viral infection; inflammatory response; cellular proliferation;
 KM psoriasis; duplex; ss.
 XX
 XX Synthetic.
 OS
 XX WO200011013-A1.
 PN
 XX 02-MAR-2000.
 PD
 XX 20-AUG-1999; 99WO-US019029.
 PF
 XX 22-AUG-1998; 98US-0097712P.
 PR
 XX (UYNE-) UNIV NEBRASKA.
 PA
 XX Gold B;
 PI
 XX WPI; 2000-246530/21.
 DR
 XX Modified nucleomonomers, used in physiologically stable, non-toxic
 PT oligomers used to inhibit expression of nucleic acids and in gene
 PR regulation, antisense technology and diagnostics.
 XX
 PS Disclosure; Page 20; 42pp; English.
 CC The invention provides modified nucleomonomers of specified formula and
 CC their pharmaceutically acceptable salts. The nucleomonomers are used as
 CC monomers in oligomers, which are used in pharmaceutical compositions to
 CC inhibit expression of nucleic acid molecules including DNA and RNA in
 CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
 CC infected cells. They are used in oligomers for gene regulation, antisense
 CC technology, diagnostic applications to detect target sequences in
 CC biological samples such as those containing pathogenic bacteria, fungi
 CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
 CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
 CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
 CC interleukins associated with pathological conditions such as inflammatory
 CC conditions, cardiovascular disorders, immune reactions, cancer, viral
 CC infections and bacterial infections (see AAA07786 for details of other
 CC uses for which the oligomers are suitable for). Oligomers comprising the
 CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to
 CC target nucleic acid sequences, are physiologically stable, non-toxic and
 CC able to penetrate into cells while maintaining stringent base pair
 CC fidelity for target DNA sequences. The oligomers demonstrate significant
 CC single- or double-stranded target nucleic acid binding activity to form
 CC duplexes, triplexes or other forms of stable association
 CC
 SQ Sequence 23 BP; 1 A; 2 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.6; DB 1; Length 23;
 Best Local Similarity 82.6%; Pred. No. 1.2e+03;
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4016 TGAAGAAAAAGAGAAAAACAAA 4038
 |||||
 DB 23 TGAAGAAAAAGAGAAAAACAAA 1

RESULT 1492
 AAA07786
 ID AAA07786 standard; DNA; 23 BP.
 XX
 XX AAA07786;
 AC
 XX 23-JUN-2000 (first entry)
 DT
 XX Structure of a fragment of duplex A target strand.
 DE
 XX Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
 KW viral infection; inflammatory response; cellular proliferation;
 KM psoriasis; duplex; ss.
 XX
 XX Synthetic.
 OS
 XX WO200011013-A1.
 PN
 XX 02-MAR-2000.
 PD
 XX 20-AUG-1999; 99WO-US019029.
 PF
 XX 22-AUG-1998; 98US-0097712P.
 PR
 XX (UYNE-) UNIV NEBRASKA.
 PA
 XX Gold B;
 PI
 XX WPI; 2000-246530/21.
 DR
 XX Modified nucleomonomers, used in physiologically stable, non-toxic
 PT oligomers used to inhibit expression of nucleic acids and in gene
 PR regulation, antisense technology and diagnostics.
 XX
 PS Disclosure; Page 20; 42pp; English.
 CC The invention provides modified nucleomonomers of specified formula and
 CC their pharmaceutically acceptable salts. The nucleomonomers are used as
 CC monomers in oligomers, which are used in pharmaceutical compositions to
 CC inhibit expression of nucleic acid molecules including DNA and RNA in
 CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
 CC infected cells. They are used in oligomers for gene regulation, antisense
 CC technology, diagnostic applications to detect target sequences in
 CC biological samples such as those containing pathogenic bacteria, fungi
 CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
 CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
 CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
 CC interleukins associated with pathological conditions such as inflammatory
 CC conditions, cardiovascular disorders, immune reactions, cancer, viral
 CC infections and bacterial infections. The oligomers are suitable for use
 CC in both in vivo and ex vivo therapeutic applications including treatment
 CC of cells such as bone marrow or peripheral blood in conditions such as
 CC leukemia or viral infections, genes as target for cancer treatments
 CC including oncogenes such as ras, k-ras, bcl-2, c-myc, bcr, c-abl
 CC or overexpressed sequences such as mdm2, oncostatin M, interleukin 6
 CC (Kaposi's sarcoma), HER-2 and translocations such as bcr/abl or RNAs
 CC encoded by such genes, as well as viral gene sequences such as polymerase
 CC or reverse transcriptase genes of cytomegalovirus, herpes simplex virus-1
 CC or -2, HTLV-1, human immunodeficiency virus-1 or -2, hepatitis B virus,
 CC human papilloma virus, varicella zoster virus, influenza virus or
 CC rhinovirus. They can also be used to modulate inflammatory responses by
 CC modulating expression of genes such as IL-1 receptor, IL-1, TGM-1 or B-
 CC selectin in mediating inflammation and modulation of cellular
 CC proliferation in conditions such as arterial occlusion (restenosis) after
 CC angioplasty by modulating the expression of growth or mitogenic factors
 CC such as non-muscle myosin, myc, fos, PCNA, platelet-derived growth factor
 CC or fibroblast growth factor or their receptors or cell proliferation
 CC factor such as c-myc, other extracellular proliferation factors such as
 CC transforming growth factor alpha, IL-6, approx.g-interferon, protein
 CC kinase C for treatment of psoriasis or other conditions, and epithelial
 CC growth factor, transforming growth factor or MHC alleles in autoimmune
 CC disease. Oligomers comprising the nucleomonomers exhibit increased duplex

CC DNA stability when hybridizing to target nucleic acid sequences, are
 CC physiologically stable, non-toxic and able to penetrate into cells while
 CC maintaining stringent base pair fidelity for target DNA sequences. The
 CC oligomers demonstrate significant single- or double-stranded target
 CC nucleic acid binding activity to form duplexes, triplexes or other forms
 CC of stable association

XX Sequence 23 BP; 18 A; 2 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.6; DB 1; Length 23;

Best Local Similarity 82.6%; Pred. No. 1.2e+03;

Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4016 TGAGAAAAAGAGAGAAACAA 4038

Db 1 TGAGAAAAAGAGAGAAACCA 23

RESULT 1493

AAT99645/c

AAAT99645 standard; DNA; 23 BP.

AC AAT99645;

DT 06-JUL-1998 (first entry)

XX Human SCA2 gene PCR primer 65B6.

XX SCA2 gene; spinocerebellar ataxia-2; ataxin-2; human; diagnosis;

KM olivoponto-cerebellar atrophy; PCR; primer; ss.

XX Synthetic.

OS Homo sapiens.

XX WO9742314-A1.

PD 13-NOV-1997.

XX 08-MAY-1997; 97WO-US007725.

XX 08-MAY-1996; 96US-0017388P.

PR 19-JUL-1996; 96US-0022207P.

PR 08-OCT-1996; 96US-00727084.

XX (CEDA-) CEDARS SINAI MEDICAL CENT.

XX Pulst S;

XX WPI; 1998-086523/08.

PT Nucleic acids encoding human and mouse ataxin 2 - a product of the

XX spinocerebellar ataxia 2 gene, SCA2; useful in the diagnosis of ataxia

XX type 2.

PS Example 4; Page 46; 98pp; English.

XX Primers 65B6 and 65A6 (see AAT99644) were used to generate a probe

CC sequence from plasmid P65122B (see AAV06551), which comprises human

CC genomic DNA from the CAG repeat region of the novel spinocerebellar

CC ataxin-2 (SCA2) gene. A second repeat region was generated from P65122B using

CC primers 65A3 and 65B5 (see AAT99642-43). The probes were labelled with

CC 3'P and used to screen a trisomy 21 foetal brain cDNA library and an

CC adult human frontal cortex cDNA library. PCR fragments were subsequently

CC used to screen the frontal cortex library. Isolated clones, plus clones

CC obtained from placental cDNA, were used to produce a composite sequence

CC (see AAV06552) for human SCA2 cDNA. Methods are provided for diagnosing

CC SCA2 based on the number of CAG repeats in a CAG repeat region of the

CC SCA2 gene

XX Sequence 23 BP; 1 A; 6 C; 9 G; 7 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 16.6; DB 1; Length 23;

XX Best Local Similarity 82.6%; Pred. No. 1.2e+03;

Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 7413 CAGACGACGACGACGACGCA 7435

Db 23 CTGAAACCCCGACGACGACGCA 1

RESULT 1494

ABK68088/c

ID ABK68088 standard; DNA; 23 BP.

AC ABK68088;

DT 02-JUL-2002 (first entry)

XX Mouse HYPLIP1 locus specific primer D3pJmg3 #1.

XX Mouse; primer; antilipemic; cardiatic; hypotensive; anorectic; HYPLIP1;

KM FCHL1; lipid disorder; familial combined hyperlipidaemia;

KM coronary artery disease; atherogenic lipoprotein phenotype; cancer;

KM hyperapobetalipoproteinaemia; hypertriglyceridaemia; obesity; ss;

KM familial dyslipidaemic hypertension; syndrome X; insulin resistance;

XX hypercholesterolaemia; chromosome 3.

XX Mus sp.

OS WO200220847-A2.

XX 14-MAR-2002.

XX 07-SEP-2001; 2001WO-US028181.

XX 08-SEP-2000; 2000US-023322P.

XX (REGC) UNIV CALIFORNIA.

XX Bodnar JS, Castellani LW, Chatterjee A, De Jong P, Luis AJ;

PI Ohmen J, Ross D, Tafuri S, Wu C;

XX WPI; 2002-339808/37.

PT Novel HYPLIP1 and FCHL1 genes and their sequence variations associated

XX with lipid disorder and cancer, useful for prognosis, diagnosis and

XX treatment of lipid disorders.

XX Claim 11; Page 72; 102pp; English.

XX This invention relates to the cDNA and protein sequences of novel

CC proteins HYPLIP1 or FCHL1 and to sequence variations within these genes

CC that have been shown to be associated with lipid disorders.

CC Oligonucleotide probes that hybridise to the cDNA sequence are useful for

CC analysing the expression of FCHL1 by detecting the expression of the mRNA

CC transcript in the sample. A host cell transformed with the cDNA of the

CC invention is useful for producing the protein by recombinant means.

CC Pharmaceutical compositions based on the sequences of the invention are

CC useful for treating or preventing a lipid disorder associated with

CC expression of FCHL1 such as familial combined hyperlipidaemia, coronary

CC artery disease, atherogenic lipoprotein phenotype,

CC hyperapobetalipoproteinaemia, hypertriglyceridaemia, familial

CC dyslipidaemic hypertension, syndrome X, obesity, insulin resistance and

CC hypercholesterolaemia. The cDNA sequence is useful in the diagnosis or

CC prognosis of predisposition to lipid disorders and cancers, and also to

CC identify a molecule which enhances or decreases the HYPLIP1 or FCHL1

CC activity. The present sequence represents an oligonucleotide primer

CC specific for the mouse HYPLIP1 locus of the invention. The mouse HYPLIP1

CC locus is situated on chromosome 3

XX Sequence 23 BP; 11 A; 4 C; 7 G; 1 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 16.6; DB 1; Length 23;

XX Best Local Similarity 82.6%; Pred. No. 1.2e+03;

XX Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5800 CTGCGCTGCTGTGCTATG 5822
 |||||
 Db 23 CTGCGCTGCTGTACTTTTG 1

RESULT 1495
 ABK70922/c
 ID ABK70992 standard; DNA; 23 BP.
 XX
 AC ABK70992;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE Mouse HYPLIPI locus PCR primer #65.
 XX
 KW Human; mouse; HYPLIPI, FCHL1; familial combined hyperlipidaemia; cancer;
 KM lipid disorder; PCR; primer; ss.
 XX
 OS Mus sp.
 XX
 PN MO200220848-A2.
 XX
 PD 14-MAR-2002.
 XX
 PF 07-SEP-2001; 2001WO-US028182.
 XX
 PR 08-SEP-2000; 2000US-0231322P.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Bodnar JS, Castellani LW, Chatterjee A, De Jong P, Lusis AJ;
 PI Ohmen J, Ross D, Tafuri S, Wu C;
 XX
 DR WPI; 2003-329882/36.
 XX
 PT New mouse HYPLIPI and human FCHL1 (familial combined hyperlipidemia)
 PT gene and their sequence variations, useful for diagnosing, treating or
 PT preventing lipid disorders and cancers.
 XX
 PS Claim 11; Page 72; 102pp; English.
 XX
 CC The invention relates to an isolated polynucleotide comprising a sequence
 CC variation of a mouse HYPLIPI cDNA or a human FCHL1 (familial combined
 CC hyperlipidemia) gene. The FCHL1 polynucleotide, the FCHL1 polypeptide or
 CC antibody immunoreactive to the FCHL1 polypeptide are useful for treating
 CC or preventing cancer associated with expression of FCHL1, as well as for
 CC treating lipid disorder. The mouse HYPLIPI cDNA or human FCHL1 gene are
 CC also useful for diagnosing or prognosing a predisposition to lipid
 CC disorder and cancer. ABK70902-ABK71303 represent mouse HYPLIPI, human
 CC FCHL1 coding sequences and PCR primers of the invention
 XX
 SQ Sequence 23 BP; 11 A; 4 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.6; DB 1; Length 23;
 Best Local Similarity 82.6%; Pred. No. 1.2e+03;
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5800 CTGCGCTGCTGTGCTATG 5822
 |||||
 Db 23 CTGCGCTGCTGTACTTTTG 1

RESULT 1496
 ADA15131/c
 ID ADA15131 standard; DNA; 23 BP.
 XX
 AC ADA15131;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Mouse HYPLIPI locus PCR primer #71.
 XX
 KW Mouse; PCR; primer; ss; HYPLIPI, FCHL1; variation; lipid disorder;
 XX

KW allele; anti-lipid disorder; anti-cancer therapy; gene therapy;
 KW familial combined hyperlipidaemia; coronary artery disease;
 KW atherogenic lipoprotein phenotype; hyperapobetalipoproteinaemia;
 KW hypertriglyceridemia; low density lipoprotein subclass B; LDL;
 KW familial dyslipidemic hypertension; syndrome X; hypercholesterolaemia;
 KW obesity; insulin resistance; cancer; cytostatic; antilipemic;
 KW hypotensive; anorectic.
 XX
 OS Mus sp.
 XX
 PN US2003064372-A1.
 XX
 PD 03-APR-2003.
 XX
 PF 07-SEP-2001; 2001US-00949428.
 XX
 PR 22-JUN-2000; 2000US-0213322P.
 XX
 PA (BODN/) BODNAR J S.
 PA (CAST/) CASTELLANI L W.
 PA (CHAT/) CHATTERJEE A.
 PA (JONG/) JONG P D.
 PA (LUSI/) LUSIS A J.
 PA (OHME/) OHMEN J.
 PA (ROSS/) ROSS D.
 PA (TAFU/) TAFURI S.
 PA (WUCC/) WU C.
 XX
 PI Bodnar JS, Castellani LW, Chatterjee A, Jong PD, Lusis AJ;
 PI Ohmen J, Ross D, Tafuri S, Wu C;
 XX
 DR WPI; 2003-540780/51.
 XX
 PT Novel isolated polynucleotide comprising a mouse or human familial
 PT combined hyperlipidemia 1 gene having a variation that is associated with
 PT a lipid disorder, useful for identifying susceptibility to the lipid
 PT disorder.
 XX
 PS Claim 11; Page 38; 63pp; English.
 XX
 CC The invention discloses isolated polynucleotides comprising mouse HYPLIPI
 CC cDNA sequence, mouse HYPLIPI genomic DNA, or the homologous human
 CC familial combined hyperlipidaemia 1 (FCHL1) gene, where a variation in
 CC the sequence is associated with a lipid disorder. Also claimed is an
 CC isolated polypeptide comprising a variant form of the mouse HYPLIPI amino
 CC acid sequence, or a variant form of a fully defined human FCHL1 amino
 CC acid sequence, where the variant is associated with the lipid disorder,
 CC an isolated polynucleotide having at least 12 contiguous nucleotides of
 CC the isolated polynucleotides, where the 12 contiguous nucleotides span
 CC the variation position, an isolated polypeptide comprising 4 contiguous
 CC amino acids of the encode polypeptides, where the 4 contiguous amino
 CC acids span the variation position, a kit for the detection of the FCHL1
 CC locus comprising, an isolated antibody, identifying susceptibility to a
 CC lipid disorder which comprises comparing the nucleotide sequence of the
 CC suspected FCHL1 allele with a wild-type FCHL1 nucleotide sequence, where
 CC the difference between the suspected allele and the wild-type sequence
 CC identifies a sequence variation of FCHL1 nucleotide sequence and a
 CC pharmaceutical composition. Also disclosed is a transgenic animal which
 CC carries an altered HYPLIPI or FCHL1 allele and a method for screening
 CC drugs for inhibition or restoration of FCHL1 gene function as an anti-
 CC lipid disorder or anti-cancer therapy. The polynucleotides, polypeptides
 CC and antibodies are useful for treating or preventing (e.g. gene therapy)
 CC a lipid disorder associated with expression of FCHL1, for diagnosis or
 CC prognosis of predisposition to lipid disorder, and cancer and for
 CC treating a lipid disorder such as familial combined hyperlipidemia,
 CC coronary artery disease, atherogenic lipoprotein phenotype,
 CC hyperapobetalipoproteinaemia, hypertriglyceridemia, low density
 CC lipoprotein (LDL) subclass B, familial dyslipidemic hypertension,
 CC syndrome X, hypercholesterolaemia, obesity, insulin resistance and
 CC cancer. The sequence presented is a PCR primer which was used to amplify
 CC part of the mouse HYPLIPI locus.
 XX
 SQ Sequence 23 BP; 11 A; 4 C; 7 G; 1 T; 0 U; 0 Other;

Query Match	0.2%	Score 16.6;	DB 1;	Length 23;
Best Local Similarity	82.6%;	Pred. No. 1.2e+03;		
Matches 19;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;

5800 CTGCTGCTGTCTGCCATATGTG 5822

Db 23 CTG CCTGCCTGTCTATCTTTTG 1

RESULT 1497
ADB95693/c
ID ADB95693 standard; DNA; 23 BP.

Query Match	0.2%	Score 16.6	DB 1	Length 23
% Best Local Similarity	82.6%	Pred. No. 1.2e+03		
Matches 19	Conservative	0	Mismatches 4	Indels 0
				Gaps 0

5800 CTGCTGCTGTCTGCCATGTG 5822

Db 23 CTGCTGCTGTCTATCTTTTG 1

RESULT 1498
AAV55825/c
ID AAV55825 standard; DNA; 24 BP.

Query Match 0.2%; Score 16.6; DB 1; Length 24;
 Best Local Similarity 82.6%; Pred. No. 1.3e+03;
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3631 GTGGAGAGAGAGTAGATGGGGA 3653
 DB 24 GTGGCCGAGAGAGTAGAGGTGGA 2

RESULT 1499

AAK18315
 ID AAK18315 standard; DNA; 24 BP.

AC AAK18315;

DT 26-JUL-1999 (first entry)

DE PCR primer for telomerase coding sequence.

XX Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukemia;
 KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
 KM smooth muscle cell hyperplasia; stem cell proliferation; Wilms tumor;
 KM stem cell differentiation; organ regeneration; organ differentiation;
 KM PCR primer; ss.

OS Synthetic.

OS Homo sapiens.

PN WO9901560-A1.

PD 14-JAN-1999.

PF 01-JUL-1998; 98WO-US013835.

PR 01-JUL-1997; 97US-0051410P.

PR 21-JUL-1997; 97US-0053018P.

PR 21-JUL-1997; 97US-0053329P.

PR 04-AUG-1997; 97US-0054642P.

PR 09-SEP-1997; 97US-0058287P.

XX (CMB-) CAMBIA BIOSYSTEMS LLC.

XX Kilian A, Bowtell D;

DR WPI; 1999-106060/09.

PT New isolated vertebrate telomerase genes - used to develop products for

PT treating cancers or for organ regeneration, nerve cell or brain cell

XX growth following injury or bone marrow transplantation.

PS Example 1; Page 42; 134pp; English.

XX This sequence is a PCR primer for DNA encoding a truncated human
 CC telomerase of the invention. Primers that amplify the telomerase coding
 CC sequence can be used in a method for diagnosing cancer in a patient. The
 CC telomerase can be used for detection, diagnosis and drug screening.
 CC Inhibitors of telomerase activity can be used to treat cancers such as
 CC melanomas, other skin cancers, neuroblastomas, breast carcinomas, colon
 CC carcinomas, leukemias, lymphomas, osteosarcomas or smooth muscle cell
 CC hyperplasias or skin growths. Enhancers of telomerase may be used to
 CC stimulate stem cell proliferation and differentiation (expansion of
 CC haematopoietic stem cells could be administered in the bone marrow
 CC transplant context). As well, many tissues have stem cells. Proliferation
 CC of these cells may be useful in wound healing, hair growth, treatment of
 CC disease such as Wilms tumor, organ regeneration or differentiation
 CC after injury or diseases, nerve cell or brain cell growth following
 CC injury
 CC
 SQ Sequence 24 BP; 6 A; 5 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.6; DB 1; Length 24;
 Best Local Similarity 82.6%; Pred. No. 1.3e+03;
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7335 TGAGCTGACCTGTTCAGTCCA 7357
 DB 2 TGAGCTGACCTGTTCAGGACA 24

RESULT 1500

AAK32836
 ID AAK32836 standard; DNA; 24 BP.

AC AAK32836;

DT 05-JUL-1999 (first entry)

DE H. felis 16S ribosomal RNA gene internal fragment primer F1A-11.

XX Haemobartonella felis; feline infectious anemia; FIA; 16S ribosomal RNA;
 KW 23S ribosomal RNA; immunisation; infection; PCR primer; ss.

OS Synthetic.

OS Mycoplasma haemofelis.

PN WO9914317-A1.

PD 25-MAR-1999.

PF 18-SEP-1998; 98WO-US019472.

PR 19-SEP-1997; 97US-0059551P.

PA (SYNB-) SYMBIOTICS CORP.

PI Steele JK, Telford DL, Cutting JA;

DR WPI; 1999-229527/19.

PT New isolated Haemobartonella felis nucleic acids used to develop products

XX for detection of Haemobartonella felis infection.

XX Claim 18; Page 13; 62pp; English.

XX The invention relates to isolated Haemobartonella felis nucleic acids
 CC that are used to develop products for detection or prevention of H. felis
 CC infection, particularly feline infectious anemia (FIA). A novel method
 CC for detecting the presence of H. felis in a mammal comprises: a)
 CC obtaining a nucleic acid sample from a body fluid of the mammal; (b)
 CC contacting the nucleic acid sample with at least one nucleic acid probe
 CC from the H. felis 16S or 23S ribosomal RNA genes, the probe being
 CC specific for H. felis; and (c) determining whether the nucleic acid probe
 CC specifically hybridises to the nucleic acid sample, where hybridisation
 CC of the probe to the sample indicates that H. felis is present in the
 CC mammal. The products and method can be used for the detection of H. felis
 CC infection, particularly FIA. They can also be used for immunisation
 CC against H. felis infection. They can also be used to monitor the course
 CC of infection or the effectiveness of treatment. Sequences AAK32836-39
 CC represent claimed PCR primers used for the amplification of a fragment
 CC internal to the H. felis 16S ribosomal RNA gene
 CC
 SQ Sequence 24 BP; 10 A; 4 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.6; DB 1; Length 24;
 Best Local Similarity 82.6%; Pred. No. 1.3e+03;
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5055 TCCTTACCAAGTGCCTTAAGAG 5077
 DB 2 TCCTTACCAAGTGCCTTAAGAG 24

RESULT 1501

AAK59342
 ID AAK59342 standard; DNA; 24 BP.

XX


```

AC AAX59342;
XX 20-SEP-1999 (first entry)
XX Dirofilaria immitis-specific DNA probe.
DE
XX
XX Heartworm; parasite; detection; diagnosis; blood; mosquito; cat; dog;
KM 5S ribosomal DNA; PCR; probe; ss.
XX
XX Synthetic.
OS Dirofilaria immitis.
XX
XX W09932504-A1.
XX
XX 01-JUL-1999.
XX
XX 18-DEC-1998; 98MO-US027063.
XX
XX 19-DEC-1997; 97US-0071792P.
XX 05-JUN-1998; 98US-0070485P.
XX 04-JUN-1998; 98US-0087956P.
XX
XX (LIZO/) LIZOTTE-MANIEWSKI M.
XX (WILL/) WILLIAMS S A.
XX
XX Lizotte-Maniewski M, Williams SA;
PI WPI; 1999-418903/35.
XX
XX Polymerase chain reaction primers specific for Dirofilaria immitis.
XX
XX Example 8; Page 28; 44pp; English.
XX
XX This oligonucleotide probe is based on the PCR product obtained from the
CC 5S ribosomal DNA spacer region of Dirofilaria immitis using a claimed
CC primer pair (see AAX59336-37). The probe was selected on the basis of its
CC hybridisation properties, i.e. a good mixture of A, G, C and T, no long
CC runs of any particular nucleotide, and no internal hybridisation to form
CC hairpins. It was used as a probe in a PCR-ELISA method of detecting D.
CC immitis. The invention discloses PCR based assays for the presence of D.
CC immitis, the heartworm parasite, prevalent in dogs and cats, as well as
CC in mosquitoes, which are the transmission vectors. The assays can detect
CC less than about one attogram of D. immitis DNA, which corresponds to less
CC than one microfilaria in 1 ml of blood, or less than one L3 larva in
CC about 50 mosquitoes, and can detect D. immitis infection for all life
CC cycle stages of the parasite
XX
XX
XX Sequence 24 BP; 7 A; 3 C; 6 G; 8 T; 0 U; 0 Other;
SO
Query Match 0.2%; Score 16.6; DB 1; Length 24;
Best Local Similarity 82.6%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 5359 TCAGCTGGGCTGAATGCATT 5381
DB 2 TCTGCTGTGGCTTGAATGAAAT 24

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OS Homo sapiens.
XX
XX W09961595-A2.
XX
XX 02-DEC-1999.
XX
XX 27-MAY-1999; 99MO-US010472.
XX
XX 27-MAY-1998; 98US-00084423.
XX
XX (CELL-) CELL GENESYS INC.
XX
XX Cohen LR, Spratt SK, Couto L;
XX WPI; 2000-062705/05.
XX
XX Producing human factor VIII activity by expressing light and heavy chains
PT from separate adeno-associated viral vectors, for treating hemophilia.
XX
XX Example; Page 24; 38pp; English.
XX
XX PCR primers AA247461-247464 are used to generate a human factor VIII
CC (F8/FVIII) light chain fragment. FVIII is a component of the coagulation
CC cascade, and is synthesised as a single chain precursor composed of a
CC signal peptide and six distinct domains. The FVIII translation product
CC consists of a heavy and light chain. The heavy and light chains are used
CC in a method for obtaining human factor VIII activity through the
CC administration of several recombinant vectors expressing one or more F8
CC domains, consisting of a light and heavy chain without the B domain.
CC Recombinant adeno-associated vectors (rAAV) are used in the method, which
CC is used to treat hemophilia A in humans or other animals. rAAVs infect a
CC wide range of non-dividing cells in many mammalian species; integrate
CC into the host chromosome; are very stable; do not cause disease and can
CC generate vectors from which all viral genes have been deleted. The
CC properties of the vectors allows them to be delivered by various routes
CC and result in high-level expression of FVIII activity in hepatic or
CC endothelial cells. The use of two vectors overcomes the difficulty of
CC cloning and packaging the very large nucleic acid encoding the FVIII
XX precursor protein
XX
XX
XX Sequence 24 BP; 6 A; 5 C; 3 G; 10 T; 0 U; 0 Other;
SO
Query Match 0.2%; Score 16.6; DB 1; Length 24;
Best Local Similarity 82.6%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 7147 AATTGGTATGTGATGTTGCATT 7169
DB 1 AATTCCATATGATGTTGCATT 23

```

PR 26-NOV-1998; 98FR-00014914.
XX
XX (INRM) INST NAT SANTE & RECH MEDICALE.
XX
XX Beauvillain J, Coulouarn Y, Jegou S, Lohrmann I, Vaudry H;
XX WPI; 2000-400075/34.
XX
XX New mammalian uroensin II polypeptide, useful for treating
PT neurodegeneration and spinal cord injury.
XX
XX Claim 8; Page 10; 42pp; French.
XX
XX PCR primers AAA46702-03 were to amplify a DNA fragment encoding a human
CC prepro-uroensin II peptide. In mammals, uroensin II promotes survival
CC and regeneration of motor neurons, and also has a hypertensive effect.
CC The uroensin II polypeptides and polynucleotides are useful for treating
CC neurodegeneration and trauma of the spinal cord (e.g. hemi-plegia, para-
CC plegia or amyotrophic lateral sclerosis). The polypeptides are also used
CC to screen for specific inhibitors, i.e. potential antihypertensive agents
XX
XX Sequence 24 BP; 9 A; 6 C; 4 G; 5 T; 0 U; 0 Other:
SQ
Query Match 0.2%; Score 16.6; DB 1; Length 24;
Best Local Similarity 82.6%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 1131 GGCACAGTATTTCACAGCAGAAAT 1153
DB 1 GACACAGTATTTCACAGCAGCAAT 23
RESULT 1504
AAH44773/C
ID AAH44773 standard; DNA; 24 BP.
XX
XX AAH44773;
XX
XX 13-DEC-2001 (first entry)
XX
XX Human DNA mismatch repair gene protein 13 PCR primer 1 SEQ ID NO:3.
XX
XX Human; DNA mismatch repair gene protein 13; cytostatic; virucidal;
XX immunomodulatory; antiinflammatory; haemostatic; anti-HIV; gene therapy;
XX diagnosis; malignant tumour; haemopathy; human immunodeficiency virus;
XX HIV infection; immunological disease; inflammation;
XX developmental disorder; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200170960-A1.
XX
XX 27-SEP-2001.
XX
XX 19-MAR-2001; 2001WO-CN000369.
XX
XX 22-MAR-2000; 2000CN-00115023.
XX
XX (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
XX Mao Y, Xie Y;
XX
XX WPI; 2001-602783/68.
XX
XX
XX New human DNA mismatch repair gene protein 13 for diagnosing and treating
PT e.g. malignant tumor, hemopathy, human immunodeficiency virus (HIV)
PT infection, immunological diseases and inflammations.
XX
XX Example 2; Page 12; 36pp; Chinese.
XX
XX The present invention represents human DNA mismatch repair gene protein
CC 13 (I). (I) has cytostatic, virucidal, immunomodulatory, haemostatic,
CC antiinflammatory and anti-HIV activities. The polynucleotide (II)

CC encoding (I) can be used in gene therapy. (I) and (II) can be used in the
CC diagnosis and treatment of malignant tumor, haemopathy, human
CC immunodeficiency virus (HIV) infection, immunological diseases, various
CC inflammations and developmental disorders. The present sequence
CC represents a PCR primer for human DNA mismatch repair gene protein 13,
CC which is used in an example from the present invention
XX
XX Sequence 24 BP; 4 A; 8 C; 6 G; 6 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 16.6; DB 1; Length 24;
Best Local Similarity 82.6%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 1238 GTACATTGTGGCTGGCAGCGC 1260
DB 23 GTACATTGTGGCTGGCAGCAGC 1
RESULT 1505
AAH75424
ID AAH75424 standard; DNA; 24 BP.
XX
XX AAH75424;
XX
XX 18-OCT-2001 (first entry)
XX
XX Human homo laminin protein 24 PCR primer 1.
XX
XX Human; homo laminin protein 24; cytostatic; virucidal; immunomodulatory;
XX antiinflammatory; haemostatic; cancer; haemopathy; HIV; phlogosis;
XX Human Immunodeficiency Virus; immunological diseases; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200155183-A1.
XX
XX 02-AUG-2001.
XX
XX 21-JAN-2001; 2001WO-CN000093.
XX
XX 28-JAN-2000; 2000CN-00111622.
XX
XX (BIOD-) BIODDOOR GENE TECHNOLOGY LTD SHANGHAI.
XX
XX Mao Y, Xie Y;
XX
XX WPI; 2001-483216/52.
XX
XX Human laminin protein 24 and encoded polynucleotide, applicable in
PT diagnosis and treatment of cancer, hemopathy, immunological diseases and
PT phlogosis.
XX
XX Example 3; Page 12; 38pp; Chinese.
XX
XX The invention relates to the human homo laminin protein 24 with
CC cytostatic, virucidal, immunomodulatory, antiinflammatory and haemostatic
CC activity. The polypeptide and encoding polynucleotide are applicable in
CC diagnosis and treatment of cancer, haemopathy, Human Immunodeficiency
CC Virus (HIV) infection, immunological diseases and phlogosis. The present
CC sequence is that of a homo laminin protein 24 PCR primer
XX
XX Sequence 24 BP; 1 A; 4 C; 3 G; 16 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 16.6; DB 1; Length 24;
Best Local Similarity 82.6%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 6459 GGATACCTTTTCTCTCTGTGT 6481
DB 2 GGATCCTTTTCTTTTCTTTTGT 24
RESULT 1506

AD46772/c
 ID AAD46772 standard; DNA; 24 BP.
 AC AAD46772;
 DT 27-JAN-2003 (first entry)
 XX
 DE Human TLR3 (Toll-like receptor) DNA specific RT-PCR primer #1.
 XX
 KW Human; TLR; Toll-like receptor; dendritic cell associated protein;
 KW autoimmune disorder; psoriasis; inflammatory bowel disease; asthma;
 KW multiple sclerosis; lupus erythematosus; rheumatoid arthritis; cancer;
 KW type I diabetes; infectious disease; gene therapy; immunosuppressive;
 KW antiinflammatory; neuroprotective; dermatological; antibacterial;
 KW virucide; cytostatic; reverse transcription; RT; PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200274921-A2.
 PD 26-SEP-2002.
 XX
 PF 19-MAR-2002; 2002MO-US008122.
 XX
 PR 19-MAR-2001; 2001US-0276474P.
 XX
 PA (CELL-) CELLULAR GENOMICS INC.
 XX
 PI Velleca MA, Mellman I;
 XX
 DR WPI; 2002-759890/82.
 XX
 PT Isolating dendritic cell associated protein using an agent which alters
 PT its expression or activity, useful in diagnosing and treating disorders
 PT with altered expression or activity of the protein, such as autoimmune
 PT disease and cancer.
 XX
 PS Example 9; Page 56; 73pp; English.
 XX
 CC The invention relates to a method for generating a dendritic cell
 CC associated protein. The invention also relates to compositions and
 CC methods for generating an antibody against a dendritic cell associated
 CC protein. The methods and compositions are useful for diagnosing and
 CC treating diseases associated with altered dendritic cell activity such as
 CC autoimmune disorders, e.g. psoriasis, inflammatory bowel disease, asthma,
 CC multiple sclerosis, lupus erythematosus, rheumatoid arthritis or type I
 CC diabetes, and cancer or infectious disease. The invention is also used in
 CC gene therapy. The present sequence is a RT (reverse transcription)-PCR
 CC primer used for amplifying human TLR (Toll-like receptor) DNA. This
 CC sequence is used to illustrate the method of the invention
 XX
 SQ Sequence 24 BP; 4 A; 5 C; 6 G; 9 T; 0 U; 0 Other;
 XX
 QY Query Match 0.2%; Score 16.6; DB 1; Length 24;
 Best Local Similarity 82.6%; Pred. No. 1.3e+03;
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 XX
 Db 3280 GAAGAAAATGAACGACCA 3302
 ||||| ||||| ||||| |||||
 23 GAAGAGAAATGTTCCGACCA 1
 XX
 RESULT 1507
 AAL42601
 ID AAL42601 standard; DNA; 24 BP.
 AC AAL42601;
 XX
 DT 11-JUL-2002 (first entry)
 XX
 DE Human serine/threonine protein kinase 10-34 PCR primer 2.
 XX
 KW Human; ss; PCR; primer; serine/threonine protein kinase 10.34;

KW embryonic developmental deformity; tumour;
 KW protein metabolism disturbance-related disease.
 XX
 OS Homo sapiens.
 XX
 PN CN1329154-A.
 XX
 PD 02-JAN-2002.
 XX
 PF 19-JUN-2000; 2000CN-00116582.
 XX
 PR 19-JUN-2000; 2000CN-00116582.
 XX
 PA (SHAN-) SHANGHAI BIODOR GENE DEV CO LTD.
 XX
 PI Mao Y, Xie Y;
 XX
 DR WPI; 2002-292822/34.
 XX
 PT New polypeptide-serine/threonine protein kinase 10.34 for treating
 PT embryonic developmental deformity, tumors and protein metabolism
 PT disturbance related disease.
 XX
 PS Example 2; Page 20 (Disclosure); 35pp; Chinese.
 XX
 CC The invention comprises the amino acid and coding sequence of the human
 CC serine/threonine protein kinase 10.34, which are useful for the treatment
 CC of embryonic developmental deformity, tumors and protein metabolism
 CC disturbance-related disease. The present DNA sequence represents a PCR
 CC primer specific for the gene sequence of the human serine/threonine
 CC protein kinase 10.34
 XX
 SQ Sequence 24 BP; 7 A; 1 C; 2 G; 14 T; 0 U; 0 Other;
 XX
 QY Query Match 0.2%; Score 16.6; DB 1; Length 24;
 Best Local Similarity 82.6%; Pred. No. 1.3e+03;
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 XX
 Db 5472 ATTTTGTGAAAAGATATTT 5494
 ||||| ||||| ||||| |||||
 2 ATTTTGTGATCTATATTT 24
 XX
 RESULT 1508
 ABK11029/c
 ID ABK11029 standard; DNA; 24 BP.
 AC ABK11029;
 XX
 DT 05-JUN-2002 (first entry)
 XX
 DE Human HPK/GCK-like kinase, reverse PCR primer.
 XX
 KW Human; HPK/GCK-like kinase; antiinflammatory; cytostatic; antimicrobial;
 KW HGK; NIK; Nck-interacting kinase; infection; inflammation; tumour;
 KW antitense gene therapy; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN US6346416-B1.
 XX
 PD 12-FEB-2002.
 XX
 PF 29-AUG-2000; 2000US-00651011.
 XX
 PR 29-AUG-2000; 2000US-00651011.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Dean NM, Cowsett LM;
 XX
 DR WPI; 2002-237091/29.
 XX

PT New antisense compound, useful for preventing or delaying infection,
PT inflammation or tumor formation, is targeted to nucleic acid molecule
PT encoding HPK/GCK-like kinase (HGK) and hybridizes and inhibits HGK
PT expression.
XX
XX Example 13; Col 42; 37pp; English.
XX
CC The invention relates to an antisense compound (I) of 8-50 nucleobases in
CC length targeted to a start codon region, coding region or 3'-untranslated
CC region of a nucleic acid molecule encoding HPK/GCK (undefined)-like
CC kinase (HGK) (also known as NIK for NCK-interacting kinase), which
CC specifically hybridizes with and inhibits expression of HGK. (I) is
CC useful for inhibiting the expression of HPK/GCK-like kinase in cells or
CC tissues in vitro. (I) is useful prophylactically e.g. to prevent or delay
CC infection, inflammation and tumor formation. (I) is also useful as a
CC diagnostic and research reagent. (I) is also useful for distinguishing
CC functions of various members of a biological pathway and in antisense
CC gene therapy. The present sequence represents a PCR primer used to
CC isolate the coding sequence of human HPK/GCK-like kinase
XX
SQ Sequence 24 BP; 6 A; 8 C; 2 G; 8 T; 0 U; 0 Other;
Query Match 0.2%; Score 16.6; DB 1; Length 24;
Best Local Similarity 82.6%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1791 GTATGCTGAGTGAACGTGTCG 1813
DB 24 GAATGCAAGAGTGAACCTGTTG 2
RESULT 1509
ABK91269
XX ID ABK91269 standard; DNA; 24 BP.
XX
XX ABK91269;
XX
DT 05-NOV-2002 (first entry)
XX
DE Leukaemia related protein 24.09 specific RT-PCR primer #2.
XX
KW Leukaemia related protein; leukaemia; lymphoma; primer; ss; haemopathy;
KW growth development disturbance disease; reverse transcription; RT-PCR.
XX
OS Unidentified.
XX
PN CN1341647-A.
XX
PD 27-MAR-2002.
XX
PF 07-SEP-2000; 2000CN-00125055.
XX
PR 07-SEP-2000; 2000CN-00125055.
XX
PA (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-520722/56.
XX
XX Novel leukemia related protein 24.09.
XX
PS Example 3; Page 17 (disclosure); 32pp; Chinese.
XX
CC This invention relates to the DNA and protein sequences of leukemia
CC related protein 24.09. The invention also comprises methods for producing
CC the protein using recombinant DNA technology and antagonists of the
CC protein which may be used for inhibiting the action of the protein. The
CC sequences of the invention may be used for treating several diseases such
CC as leukemia, lymphoma, other haemopathy and growth development
CC disturbance disease. The present sequence represents a reverse
CC transcription (RT) PCR primer used to isolate the leukemia related
CC protein cDNA 24.09 of the invention

XX
SQ Sequence 24 BP; 4 A; 1 C; 2 G; 17 T; 0 U; 0 Other;
Query Match 0.2%; Score 16.6; DB 1; Length 24;
Best Local Similarity 82.6%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4468 TTTTCTTTTCTTTTCTTGA 4490
DB 2 TCTTTTCTTTTCTTCAATTGA 24
RESULT 1510
AAQ74292/c
XX ID AAQ74292 standard; DNA; 25 BP.
XX
XX AAQ74292;
XX
AC AAQ74292;
XX
DT 25-MAR-2003 (revised)
XX
DT 12-JUN-1995 (first entry)
XX
DE Amyloid precursor protein Xist forward PCR primer.
XX
XX Amyloid precursor protein; APP; Xist PCR primer;
KW beta-amyloidosis animal models; Down's syndrome; Alzheimers disease;
KW yeast artificial chromosome; ss.
XX
OS Synthetic.
XX
PN W09423049-A2.
XX
PD 13-OCT-1994.
XX
PP 01-APR-1994; 94WO-US003619.
XX
PR 02-APR-1993; 93US-00042390.
XX
PA (UYGO) UNIV JOHNS HOPKINS.
XX
PI Gearhart JD, Lamb BT;
XX
DR WPI; 1994-333207/41.
XX
PT Introduction and expression of large genomic sequences in transgenic
PT animals - which may be used as animal models of beta-amyloidosis in
PT Alzheimer's disease and Down's syndrome.
XX
PS Example 3; Page 33; 60pp; English.
XX
CC AAQ74292 and AAQ74293 are the forward and reverse PCR primers for human
CC amyloid precursor protein (APP) Xist, these were used to screen yeast
CC artificial chromosome (YAC) libraries for APP. Isolated APP clones were
CC then injected into blastocysts, from the same species as the embryonic
CC cells which contained the YAC library. Transgenic animals which could be
CC used as models of beta-amyloidosis (prevalent in individuals with Down's
CC syndrome and Alzheimers disease), were then generated from the injected
CC blastocysts. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 25 BP; 5 A; 5 C; 7 G; 8 T; 0 U; 0 Other;
Query Match 0.2%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1298 TGATTAAGCCACAGCTAGATCC 1320
DB 24 TGATTAAGCCACAGCTAGATCC 2
RESULT 1511
AAQ67905
XX ID AAQ67905 standard; DNA; 25 BP.
XX

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AC AA067905;
XX
XX 25-MAR-2003 (revised)
DT 02-FEB-1995 (first entry)
XX
DE Primer for preparing cotton fibre cell cDNA library.
XX
XX Cotton fibre; promoter; Sea Island strain; transgenic plant;
KM bioplastic synthesis; polyester; poly(hydroxybutyrate); biodegradable;
XX thermoplastic; Gossypium; ss.
XX
XX Synthetic.
OS
XX WO9412014-A1.
PN
XX 09-JUN-1994.
PD
XX 19-NOV-1993; 93WO-US011412.
PF
XX 20-NOV-1992; 92US-00980521.
PR
XX (CETU ) AGRACETUS INC.
PA
XX Maliyakal J;
PI
XX WPI; 1994-199818/24.
DR
XX
XX New fibre producing plants expressing heterologous bio:plastic - esp
PT poly(hydroxy-alkanate), contain enzymes involved in bio:plastic synthesis
PT under control of fibre specific cotton promoter.
XX
XX Disclosure; Page 48; 68pp; English.
XX
XX Separate cDNA libraries were prepared from the mRNAs of 10-day, 15-day
CC and 23-day old cotton fibre cells. The first strand of cDNA was
CC synthesized with primer AA067905 (except for the 10-day old cDNA where an
CC oligo-dT primer is used instead). The libraries were used to identify
CC cotton fibre-specific genes and hence to isolate fibre-specific promoter
CC sequences. The promoters are useful for controlling expression of genes
CC encoding enzymes involved in production of bioplastics. Using the
CC promoter, the heterologous enzymes, e.g. ketochiolase, acetoacetyl-CoA
CC reductase and poly(hydroxybutyrate synthase, are produced only in the
CC cotton fibres of transgenic plants. The resultant fibres have altered
CC properties such as different water absorbancy, different textures or
CC better heat retention, than natural cotton. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
XX
SQ Sequence 25 BP; 2 A; 3 C; 3 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 16.6; DB 1; Length 25;
XX Best Local Similarity 82.6%; Pred. No. 1.4e+03;
XX Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 4456 GCATGACCTTTTCTTTTCTTTT 4478
DB 3 GCTGTAACCTTTTCTTTTCTTTT 25
XX
XX
RESULT 1512
AAV28811/c
ID AAV28811 standard; DNA; 25 BP.
XX
XX AAV28811;
AC
XX
XX 05-AUG-1998 (first entry)
DT
XX
XX Human immunodeficiency virus PCR primer RIT 28.
DE
XX
XX Hepatitis C virus; HCV; human immunodeficiency virus; HIV; probe;
KM primer extension product; binding; amplification; primer; detection;
KM isolation; module; diagnosis; PCR primer; ss.
XX
XX Synthetic.
OS

```

```

OS Human immunodeficiency virus 1.
XX
XX WO9813522-A1.
XX
XX 02-APR-1998.
PD
XX
XX 26-SEP-1997; 97WO-GB002629.
PF
XX 26-SEP-1996; 96GB-00020075.
PR
XX (DYNA-) DYNAL AS.
XX PA (DZIE/) DZIEGLEMSKA H E.
XX
XX Lundberg J, Uhlen M;
PI
XX WPI; 1998-230726/20.
DR
XX
XX Improving binding of series of nucleotide(s) to complementary target
PT nucleic acid - comprises use of oligo:nucleotide with at least two
PT modules providing more specific or stable binding, useful in, e.g.
PT amplification of target.
XX
XX Example 5; Page 49; 71pp; English.
XX
XX A method has been developed for improving the binding of a series of
CC consecutive nucleotides (nt) to a complementary target nucleic acid in a
CC sample. The method comprises binding a complementary modular
CC oligonucleotide, having at least 2 parts comprising nt, to adjacent
CC stretches of the target nucleic acid. The complementary modular
CC oligonucleotide has better binding than a single oligonucleotide
CC complementary to the region spanned by the complementary modular
CC oligonucleotide. The present sequence represents a PCR primer used in an
CC example of the present invention. The complementary modular
CC oligonucleotides are used as probes or primers, for replication,
CC amplification, (reverse) transcription, sequencing, isolation and/or
CC detection of the target nucleic acid. Specific applications are
CC detection/isolation of hepatitis C virus (HCV), human immunodeficiency
CC virus (HIV), e.g. for diagnosis or monitoring of infections, or
CC (universal) primer extension products, e.g. before electrophoretic
CC separation. Use of the complementary modular oligonucleotides improves
CC binding specificity, stability or ability (probably by disrupting the
CC tertiary structure of the target nucleic acid) and the method is suitable
CC for automation since pre-hybridisation, sample lysis and bead capture can
CC be combined in a single step
XX
XX
SQ Sequence 25 BP; 6 A; 3 C; 12 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 16.6; DB 1; Length 25;
XX Best Local Similarity 82.6%; Pred. No. 1.4e+03;
XX Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 4554 GCCTGAAGCAAGCATCCCCCT 4576
DB 24 GCCTTGACGACACATCCCCCTT 2
XX
XX
RESULT 1513
AAA68438/c
ID AAA68438 standard; DNA; 25 BP.
XX
XX AAA68438;
AC
XX
XX 06-AUG-2003 (revised)
DT
XX 27-OCT-2000 (first entry)
DT
XX
XX Bacteriophage 3A ORF RBS sequence 3AORF184.
DE
XX
XX Bacteriophage; antimicrobial; genome; identification; antibacterial;
KM bacterial growth inhibition; PCR primer; RBS; ribosome binding site;
KM bacterial infection; ss.
XX
XX Staphylococcus phage 3A.
OS

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PN WO200032825-A2.
XX
XX 08-JUN-2000.
XX
XX 03-DEC-1999; 99WO-IB002040.
XX
XX 03-DEC-1998; 98US-0110992P.
PR 03-JUN-1999; 99US-00326144.
PR 28-SEP-1999; 99US-00407804.
PR 30-SEP-1999; 99US-0157218P.
PR 01-DEC-1999; 99US-0168777P.
XX 02-DEC-1999; 99US-00454252.
XX
XX (PHAG-). PHAGETECH INC.
XX
XX Pelletier J, Gros P, Dubow M;
XX
XX WPI; 2000-412361/35.
XX
XX Identifying a bacteriophage coding region for treating bacterial
XX infections comprises identifying a nucleic acid encoding a product that
XX inhibits bacteria when a bacteriophage infects a bacterium.
XX
XX PS Disclosure; Page 186; 456pp; English.
XX
XX CC The present invention describes a method for identifying a bacteriophage
XX coding region encoding a product active on an essential bacterial target.
XX CC The method comprises identifying a nucleic acid sequence encoding a gene
XX CC product that provides a bacteria-inhibiting function when an
XX CC uncharacterised bacteriophage infects a pathogenic bacterium. The
XX CC compound active on a target of a bacteriophage inhibitor protein in a
XX CC bacteria is used to treat or prevent a bacterial infection in an animal.
XX CC AAA68243 to AA69442 and AAB16523 to AAB16954 represent bacteriophage
XX CC nucleotide and protein sequences which are used in the exemplification of
XX CC the present invention. (Updated on 06-AUG-2003 to correct OS field.)
XX
XX SQ Sequence 25 BP; 7 A; 3 C; 7 G; 8 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 16.6; DB 1; Length 25;
XX Best Local Similarity 82.6%; Pred. No. 1.4e+03;
XX Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 6362 GTACTAGAAATTGAACTTC 6384
XX
XX DB 24 GTTCCTGCAATCTGAACTTC 2
XX
XX RESULT 1514
XX AAA68294
XX ID AAA68294 standard; DNA; 25 BP.
XX
XX AC AAA68294;
XX
XX DT 06-AUG-2003 (revised)
XX DT 27-OCT-2000 (first entry)
XX
XX DE Bacteriophage 3A ORF RBS sequence 3AORF040.
XX
XX KW Bacteriophage; antimicrobial; genome; identification; antibacterial;
XX KW bacterial growth inhibition; PCR primer; RBS; ribosome binding site;
XX KW bacterial infection; ss.
XX
XX OS Staphylococcus phage 3A.
XX
XX PN WO200032825-A2.
XX
XX PD 08-JUN-2000.
XX
XX PF 03-DEC-1999; 99WO-IB002040.
XX
XX PR 03-DEC-1998; 98US-0110992P.
XX PR 03-JUN-1999; 99US-00326144.
XX PR 28-SEP-1999; 99US-00407804.

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PR 30-SEP-1999; 99US-0157218P.
PR 01-DEC-1999; 99US-0168777P.
PR 02-DEC-1999; 99US-00454252.
XX
XX (PHAG-). PHAGETECH INC.
XX
XX PI Pelletier J, Gros P, Dubow M;
XX
XX WPI; 2000-412361/35.
XX
XX Identifying a bacteriophage coding region for treating bacterial
XX infections comprises identifying a nucleic acid encoding a product that
XX inhibits bacteria when a bacteriophage infects a bacterium.
XX
XX PS Disclosure; Page 184; 456pp; English.
XX
XX CC The present invention describes a method for identifying a bacteriophage
XX coding region encoding a product active on an essential bacterial target.
XX CC The method comprises identifying a nucleic acid sequence encoding a gene
XX CC product that provides a bacteria-inhibiting function when an
XX CC uncharacterised bacteriophage infects a pathogenic bacterium. The
XX CC compound active on a target of a bacteriophage inhibitor protein in a
XX CC bacteria is used to treat or prevent a bacterial infection in an animal.
XX CC AAA68243 to AA69442 and AAB16523 to AAB16954 represent bacteriophage
XX CC nucleotide and protein sequences which are used in the exemplification of
XX CC the present invention. (Updated on 06-AUG-2003 to correct OS field.)
XX
XX SQ Sequence 25 BP; 7 A; 5 C; 3 G; 10 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 16.6; DB 1; Length 25;
XX Best Local Similarity 82.6%; Pred. No. 1.4e+03;
XX Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 4931 TTGACTACTCTCTCTTACTTT 4953
XX
XX DB 1 TTGATTAACCTCTCTTAAAT 23
XX
XX RESULT 1515
XX AAC96524
XX ID AAC96524 standard; DNA; 25 BP.
XX
XX AC AAC96524;
XX
XX DT 26-FEB-2001 (first entry)
XX
XX DE HLA DQB1 gene PCR primer #76.
XX
XX KW DNA sequence analysis; sequencing; protein sequence; protein structure;
XX KW gene typing; organ donation; bacteria identification; 16S rRNA; HLA;
XX KW human leukocyte antigen; PCR primer; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200065088-A2.
XX
XX PD 02-NOV-2000.
XX
XX PF 20-APR-2000; 2000WO-EP003636.
XX
XX PR 26-APR-1999; 99EP-00303215.
XX
XX PA (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
XX PI Ulfendahl P, Wong K;
XX
XX WPI; 2000-679677/66.
XX
XX Identifying extendible primers for use in identification, or
XX classification of a nucleic acid of an organism, allele or gene such as
XX class 1/2 HLA comprises identifying all possible nucleotide sequences of
XX specific length.

```

PS Claim 14; Page 52; 66pp; English.
 CC The present invention provides a method for identifying a set of
 CC extendible primers which can be used in the identification, typing and
 CC classification of genes. This can then be used to predict protein
 CC sequence and structure, in organ donation to match the organ with the
 CC receiver, and to identify bacteria in a sample. The method can be used to
 CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
 CC particular
 XX
 SQ Sequence 25 BP; 4 A; 3 C; 5 G; 13 T; 0 U; 0 Other;
 Query Match 0.2%; Score 16.6; DB 1; Length 25;
 Best Local Similarity 82.6%; Pred. No. 1.4e+03;
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 4472 TTTTCTTTTCTGCTGAGACA 4494
 DB 1 TTTTCTTTTCTGCTGAGACA 23
 RESULT 1516
 AAC96787
 ID AAC96787 standard; DNA; 25 BP.
 XX
 AC AAC96787;
 XX
 DT 26-FEB-2001 (first entry)
 XX
 DE HLA HLA-A gene PCR primer #164.
 XX
 XX DNA sequence analysis; sequencing; protein sequence; protein structure;
 KM gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
 KM human leukocyte antigen; PCR primer; ss.
 XX
 OS Homo sapiens.
 OS
 XX WO200065088-A2.
 PN
 XX 02-NOV-2000.
 PD
 XX 20-APR-2000; 2000WO-EP003636.
 PF
 XX 26-APR-1999; 99EP-00303215.
 PR
 XX (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
 PA
 XX Ulfendahl P, Wong K;
 PI
 XX WPI; 2000-679677/66.
 DR
 XX
 PT Identifying extendible primers for use in identification, or
 PT classification of a nucleic acid of an organism, allele or gene such as
 PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
 PT specific length.
 PS
 XX Claim 14; Page 57; 66pp; English.
 XX
 CC The present invention provides a method for identifying a set of
 CC extendible primers which can be used in the identification, typing and
 CC classification of genes. This can then be used to predict protein
 CC sequence and structure, in organ donation to match the organ with the
 CC receiver, and to identify bacteria in a sample. The method can be used to
 CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
 CC particular
 XX
 SQ Sequence 25 BP; 1 A; 5 C; 2 G; 17 T; 0 U; 0 Other;
 Query Match 0.2%; Score 16.6; DB 1; Length 25;
 Best Local Similarity 82.6%; Pred. No. 1.4e+03;
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 4465 TTTTCTTTTCTGCTGCT 4487

DB 1 TTTTCTTTTCTGCTGCT 23
 RESULT 1517
 AAC96291
 ID AAC96291 standard; DNA; 25 BP.
 XX
 AC AAC96291;
 XX
 DT 26-FEB-2001 (first entry)
 XX
 DE HLA DPB1 gene PCR primer #23.
 XX
 XX DNA sequence analysis; sequencing; protein sequence; protein structure;
 KM gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
 KM human leukocyte antigen; PCR primer; ss.
 XX
 OS Homo sapiens.
 OS
 XX WO200065088-A2.
 PN
 XX 02-NOV-2000.
 PD
 XX 20-APR-2000; 2000WO-EP003636.
 PF
 XX 26-APR-1999; 99EP-00303215.
 PR
 XX (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
 PA
 XX Ulfendahl P, Wong K;
 PI
 XX WPI; 2000-679677/66.
 DR
 XX
 PT Identifying extendible primers for use in identification, or
 PT classification of a nucleic acid of an organism, allele or gene such as
 PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
 PT specific length.
 PS
 XX Claim 14; Page 48; 66pp; English.
 XX
 CC The present invention provides a method for identifying a set of
 CC extendible primers which can be used in the identification, typing and
 CC classification of genes. This can then be used to predict protein
 CC sequence and structure, in organ donation to match the organ with the
 CC receiver, and to identify bacteria in a sample. The method can be used to
 CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
 CC particular
 XX
 SQ Sequence 25 BP; 1 A; 4 C; 6 G; 14 T; 0 U; 0 Other;
 Query Match 0.2%; Score 16.6; DB 1; Length 25;
 Best Local Similarity 82.6%; Pred. No. 1.4e+03;
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 4471 TTTTCTTTTCTGCTGAGAC 4493
 DB 1 TTTTCTTTTCTGCTGAGAC 23
 RESULT 1518
 AAC96418
 ID AAC96418 standard; DNA; 25 BP.
 XX
 AC AAC96418;
 XX
 DT 26-FEB-2001 (first entry)
 XX
 DE HLA DQA1 gene PCR primer #20.
 XX
 XX DNA sequence analysis; sequencing; protein sequence; protein structure;
 KM gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
 KM human leukocyte antigen; PCR primer; ss.

Query Match 0.2%; Score 16.6; DB 1; Length 25;
 Best Local Similarity 82.6%; Pred. No. 1.4e+03;
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4470 TTTTGTCTGCTGAG 4492
 |||||
 1 TTTTGTCTGCTGAG 23

Db

RESULT 1521
 AAC96026
 ID AAC96026 standard; DNA; 25 BP.
 XX
 AC AAC96026;
 XX
 DT 26-FEB-2001 (first entry)
 XX
 DE HLA HLA-C gene PCR primer #38.
 XX
 KM DNA sequence analysis; sequencing; protein sequence; protein structure;
 KM gene typing; organ donation; bacteria identification; 16S rRNA; HLA;
 KM human leukocyte antigen; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200065088-A2.
 XX
 PD 02-NOV-2000.
 XX
 PF 20-APR-2000; 2000WO-EP003636.
 XX
 PR 26-APR-1999; 99EP-00303215.
 XX
 PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
 XX
 PI Ulfendahl P, Wong K;
 XX
 DR WPI; 2000-679677/66.
 XX
 PT Identifying extendible primers for use in identification, or
 PT classification of a nucleic acid of an organism, allele or gene such as
 PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
 PT specific length.
 XX
 PS Claim 14; Page 44; 66pp; English.
 XX
 CC The present invention provides a method for identifying a set of
 CC extendible primers which can be used in the identification, typing and
 CC classification of genes. This can then be used to predict protein
 CC sequence and structure, in organ donation to match the organ with the
 CC receiver, and to identify bacteria in a sample. The method can be used to
 CC type the human leukocyte antigen genes (HLA) and 16S rRNA genes in
 CC particular
 XX
 SQ Sequence 25 BP; 3 A; 5 C; 3 G; 14 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.6; DB 1; Length 25;
 Best Local Similarity 82.6%; Pred. No. 1.4e+03;
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4472 TTTTGTCTGCTGAG 4494
 |||||
 1 TTTTGTCTGCTGAG 23

Db

RESULT 1522
 AAC95936
 ID AAC95936 standard; DNA; 25 BP.
 XX
 AC AAC95936;
 XX
 DT 26-FEB-2001 (first entry)
 XX
 PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.

DE HLA HLA-B gene PCR primer #47.
 XX
 KM DNA sequence analysis; sequencing; protein sequence; protein structure;
 KM gene typing; organ donation; bacteria identification; 16S rRNA; HLA;
 KM human leukocyte antigen; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200065088-A2.
 XX
 PD 02-NOV-2000.
 XX
 PF 20-APR-2000; 2000WO-EP003636.
 XX
 PR 26-APR-1999; 99EP-00303215.
 XX
 PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
 XX
 PI Ulfendahl P, Wong K;
 XX
 DR WPI; 2000-679677/66.
 XX
 PT Identifying extendible primers for use in identification, or
 PT classification of a nucleic acid of an organism, allele or gene such as
 PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
 PT specific length.
 XX
 PS Claim 14; Page 42; 66pp; English.
 XX
 CC The present invention provides a method for identifying a set of
 CC extendible primers which can be used in the identification, typing and
 CC classification of genes. This can then be used to predict protein
 CC sequence and structure, in organ donation to match the organ with the
 CC receiver, and to identify bacteria in a sample. The method can be used to
 CC type the human leukocyte antigen genes (HLA) and 16S rRNA genes in
 CC particular
 XX
 SQ Sequence 25 BP; 2 A; 3 C; 5 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.6; DB 1; Length 25;
 Best Local Similarity 82.6%; Pred. No. 1.4e+03;
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4469 TTTTGTCTGCTGAG 4491
 |||||
 1 TTTTGTCTGCTGAG 23

Db

RESULT 1523
 AAC96151
 ID AAC96151 standard; DNA; 25 BP.
 XX
 AC AAC96151;
 XX
 DT 26-FEB-2001 (first entry)
 XX
 DE 16S rRNA gene PCR primer #118.
 XX
 KM DNA sequence analysis; sequencing; protein sequence; protein structure;
 KM gene typing; organ donation; bacteria identification; 16S rRNA; HLA;
 KM human leukocyte antigen; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200065088-A2.
 XX
 PD 02-NOV-2000.
 XX
 PF 20-APR-2000; 2000WO-EP003636.
 XX
 PR 26-APR-1999; 99EP-00303215.
 XX
 PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.

```

XX  ULfendahl P, Wong K;
XX
XX  MPI; 2000-679677/66.
XX
XX  Identifying extendible primers for use in identification, or
XX  PT classification of a nucleic acid of an organism, allele or gene such as
XX  PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
XX  PT specific length.
XX
XX  Claim 14; Page 46; 66pp; English.
XX
XX  The present invention provides a method for identifying a set of
XX  CC extendible primers which can be used in the identification, typing and
XX  CC classification of genes. This can then be used to predict protein
XX  CC sequence and structure, in organ donation to match the organ with the
XX  CC receiver, and to identify bacteria in a sample. The method can be used to
XX  CC type the human leukocyte antigen genes (HLA) and 16S rRNA genes in
XX  CC particular
XX
XX  Sequence 25 BP; 4 A; 1 C; 3 G; 17 T; 0 U; 0 Other;
XX
XX  Query Match      0.2%; Score 16.6; DB 1; Length 25;
XX  Best Local Similarity 82.6%; Pred. No. 1.4e+03;
XX  Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX  4469 TTTTGTGTTGCTTGAG 4491
XX  Db      1 TTTTGTGTTGCTTGAG 23
XX
XX  RESULT 1524
XX  AAC96294
XX  ID AAC96294 standard; DNA; 25 BP.
XX
XX  AAC96294;
XX
XX  26-FEB-2001 (first entry)
XX
XX  HLA DPB1 gene PCR primer #26.
XX
XX  DNA sequence analysis; sequencing; protein sequence; protein structure;
XX  KW gene typing; organ donation; bacteria identification; 16S rRNA; HLA;
XX  KW human leukocyte antigen; PCR primer; ss.
XX
XX  Homo sapiens.
XX
XX  WO200065088-A2.
XX
XX  02-NOV-2000.
XX
XX  20-APR-2000; 2000WO-EP003636.
XX
XX  26-APR-1999; 99EP-00303215.
XX
XX  (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
XX  PA
XX  PI ULfendahl P, Wong K;
XX
XX  DR MPI; 2000-679677/66.
XX
XX  Identifying extendible primers for use in identification, or
XX  PT classification of a nucleic acid of an organism, allele or gene such as
XX  PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
XX  PT specific length.
XX
XX  Claim 14; Page 49; 66pp; English.
XX
XX  The present invention provides a method for identifying a set of
XX  CC extendible primers which can be used in the identification, typing and
XX  CC classification of genes. This can then be used to predict protein
XX  CC sequence and structure, in organ donation to match the organ with the
XX  CC receiver, and to identify bacteria in a sample. The method can be used to

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```

CC  type the human leukocyte antigen genes (HLA) and 16S rRNA genes in
XX  CC particular
XX
XX  Sequence 25 BP; 6 A; 1 C; 2 G; 16 T; 0 U; 0 Other;
XX
XX  Query Match      0.2%; Score 16.6; DB 1; Length 25;
XX  Best Local Similarity 82.6%; Pred. No. 1.4e+03;
XX  Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX  5473 TTTTGTGTTGCTTGAG 5495
XX  Db      3 TTTTGTGTTGCTTGAG 25
XX
XX  RESULT 1525
XX  AAC96216
XX  ID AAC96216 standard; DNA; 25 BP.
XX
XX  AAC96216;
XX
XX  26-FEB-2001 (first entry)
XX
XX  16S rRNA gene PCR primer #183.
XX
XX  DNA sequence analysis; sequencing; protein sequence; protein structure;
XX  KW gene typing; organ donation; bacteria identification; 16S rRNA; HLA;
XX  KW human leukocyte antigen; PCR primer; ss.
XX
XX  Homo sapiens.
XX
XX  WO200065088-A2.
XX
XX  02-NOV-2000.
XX
XX  20-APR-2000; 2000WO-EP003636.
XX
XX  26-APR-1999; 99EP-00303215.
XX
XX  (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
XX  PA
XX  PI ULfendahl P, Wong K;
XX
XX  DR MPI; 2000-679677/66.
XX
XX  Identifying extendible primers for use in identification, or
XX  PT classification of a nucleic acid of an organism, allele or gene such as
XX  PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
XX  PT specific length.
XX
XX  Claim 14; Page 47; 66pp; English.
XX
XX  The present invention provides a method for identifying a set of
XX  CC extendible primers which can be used in the identification, typing and
XX  CC classification of genes. This can then be used to predict protein
XX  CC sequence and structure, in organ donation to match the organ with the
XX  CC receiver, and to identify bacteria in a sample. The method can be used to
XX  CC type the human leukocyte antigen genes (HLA) and 16S rRNA genes in
XX  CC particular
XX
XX  Sequence 25 BP; 4 A; 2 C; 4 G; 15 T; 0 U; 0 Other;
XX
XX  Query Match      0.2%; Score 16.6; DB 1; Length 25;
XX  Best Local Similarity 82.6%; Pred. No. 1.4e+03;
XX  Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX  4469 TTTTGTGTTGCTTGAG 4491
XX  Db      1 TTTTGTGTTGCTTGAG 23
XX
XX  RESULT 1526
XX  AAC95681
XX  ID AAC95681 standard; DNA; 25 BP.

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XX AAC95681;
AC 26-FEB-2001 (first entry)
XX
DE HLA DPB1 gene PCR primer #16.
XX
XX DNA sequence analysis; sequencing; protein sequence; protein structure;
XX gene typing; organ donation; bacteria identification; 16S rRNA; HLA;
XX human leukocyte antigen; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX MO200065088-A2.
XX
XX 02-NOV-2000.
XX
XX 20-APR-2000; 2000WO-EP003636.
XX
XX 26-APR-1999; 99EP-00303215.
XX
XX (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
XX Ulfendahl P, Wong K;
XX
XX WPI; 2000-679677/66.
XX
XX Identifying extendible primers for use in identification, or
XX classification of a nucleic acid of an organism, allele or gene such as
XX class 1/2 HLA comprises identifying all possible nucleotide sequences of
XX specific length.
XX
XX Claim 14; Page 38; 66pp; English.
XX
XX The present invention provides a method for identifying a set of
XX extendible primers which can be used in the identification, typing and
XX classification of genes. This can then be used to predict protein
XX sequence and structure, in organ donation to match the organ with the
XX receiver, and to identify bacteria in a sample. The method can be used to
XX type the human leukocyte antigen genes (HLA) and 16S rRNA genes in
XX particular
XX
XX Sequence 25 BP; 1 A; 4 C; 6 G; 14 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 16.6; DB 1; Length 25;
XX Best Local Similarity 82.6%; Pred. No. 1.4e+03;
XX Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 4471 TTTTGTCTGTGAGAC 4493
XX Db 1 TTTTGTCTGTGAGAC 23
XX
XX RESULT 1527
XX AAA66482/c
XX ID AAA66482 standard; DNA; 25 BP.
XX
XX AAA66482;
XX
XX 09-OCT-2000 (first entry)
XX
XX Dog genomic marker oligonucleotide sequence SEQ ID NO:344.
XX
XX Dog; genome; genomic marker; radiation hybrid map; identification;
XX chromosome location; gene marker; polymorphic microsatellite marker;
XX phenotype; behaviour; pedigree; ss.
XX
XX Canis familiaris.
XX
XX WO200029615-A2.
XX
XX 25-MAY-2000.
XX

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PF 15-NOV-1999; 99WO-1B001907.
XX
XX 13-NOV-1998; 98US-0108193P.
XX
XX (CNRS ) CNRS CENT NAT RECH SCI.
XX
XX Galibert F, Andre C;
XX
XX WPI; 2000-387821/33.
XX
XX New radiation hybrid map of the dog, Canine familiaris, genome, useful
XX for e.g. identifying genes implicated in phenotypic and behavioral traits
XX or in genetic diseases and for studying dog pedigrees.
XX
XX Claim 1; Page 67; 87pp; English.
XX
XX The present invention describes a radiation hybrid map of the dog (Canine
XX familiaris) genome comprising the genome location of a marker selected
XX from AAA66139 to AAA66942. The radiation hybrid map is useful for
XX identifying and localising dog genes, since it covers approximately 80 %
XX of the dog genome and provides a dense map integrating different types
XX (i.e. Type I and Type II) of markers. The map and the dog genome markers
XX (or complementary sequences) are especially useful to identify genes
XX responsible for phenotypic and behavioural traits in dogs, to identify
XX morbid genes, to analyse diseases and identify implicated genes in such
XX diseases and their alleles, and to study dog pedigrees. They may also be
XX useful for isolating corresponding human gene sequences e.g. genes
XX involved in genetic diseases
XX
XX Sequence 25 BP; 17 A; 3 C; 4 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 16.6; DB 1; Length 25;
XX Best Local Similarity 82.6%; Pred. No. 1.4e+03;
XX Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 4466 TTTTGTCTGTGAGAC 4488
XX Db 25 TTTTGTCTGTGAGAC 3
XX
XX RESULT 1528
XX AAA75725
XX ID AAA75725 standard; DNA; 25 BP.
XX
XX AAA75725;
XX
XX 22-JAN-2001 (first entry)
XX
XX PCR primer for murine interferon-alpha polypeptide (Zcyto13).
XX
XX Mouse; interferon-alpha; Zcyto13; chromosome 4; framework marker D4Mit94;
XX viral infection; tumour cell; gene therapy; PCR primer; ss.
XX
XX Mus sp.
XX
XX WO200055324-A1.
XX
XX 21-SEP-2000.
XX
XX 17-MAR-2000; 2000WO-US006993.
XX
XX 18-MAR-1999; 99US-00271839.
XX
XX 23-SEP-1999; 99US-00405545.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Presnell SR, Feldhaus AL, Gao Z;
XX
XX WPI; 2000-647073/62.
XX
XX Novel murine interferon-alpha, Zcyto13, useful for treating autoimmune
XX diseases, certain cancers and enhancement of immune response against
XX infectious agents and also in diagnosis of the disorders.
XX

```

```
XX Example 1; Page 88; 110pp; English.
XX
CC PCR primers AAA75724-25 were used to amplify DNA encoding a murine
CC interferon-alpha polypeptide, designated Zcyto13. The Zcyto13 gene is
CC mapped to mouse chromosome 4 (framework marker D4Mit194, located at 4.6
CC centimorgans). The Zcyto13 polypeptide is useful for inhibiting viral
CC infection of cells and inhibiting proliferation of tumor cells. The
CC nucleic acid molecules encoding the Zcyto13 polypeptides are useful as
CC probes for in vivo diagnosis and as primers. Anti-Zcyto13 antibodies are
CC used to screen biological samples in vitro for the presence of Zcyto13
CC and for detecting Zcyto13 in tissue sections prepared from a biopsy
CC specimen. The nucleic acid molecules encoding the Zcyto13 protein are
CC also useful in gene therapy
XX
SQ Sequence 25 BP; 7 A; 5 C; 7 G; 6 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1921 GGTGGATTACACATCTCTACT 1943
DB 2 GGTAGCATTAGCAGCATCTCTGT 24
XX
RESULT 1529
AADI3801
ID AADI3801 standard; DNA; 25 BP.
XX
AC AADI3801;
XX
DT 06-NOV-2001 (first entry)
XX
DE gp120 encoding sequence amplifying PCR primer, AV312.
XX
KW Recombination assay; HIV; Human immunodeficiency virus; integrase;
KW phenotypic resistance; genotypic resistance; molecular target study;
KW chemotherapy; envelope gene; gp120; PCR primer; ss.
XX
OS Unidentified.
XX
PN WO200157245-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-BE000017.
XX
PR 04-FEB-2000; 2000GB-00002533.
XX
PR 15-JAN-2001; 2001GB-00001011.
XX
PA (LEUV-) LEUVEN RES & DEV.
XX
PI Witvrouw M, Fikkert V, Pannecoque C, Cherepanov P, Van Laethem K;
PI De Clercq E, Vandamme A, Debyser Z;
XX
DR WPI; 2001-496927/54.
XX
PT Determining susceptibility of HIV isolate to anti-HIV compounds, by
PT excising sequence encoding viral glycoprotein, processing, co-
PT transfecting and culturing cell with obtained isolates, harvesting
PT chimeric stock.
XX
PS Claim 25; Page 40; 59pp; English.
XX
CC The invention relates to recombination assay for the HIV (Human
CC immunodeficiency virus) envelope genes, gp120, gp41 and gp160. The
CC invention further relates to env-deleted proviral clones, the
CC optimisation of the PCR amplification of the corresponding env-genes and
CC the subsequent sequencing of these genes. These techniques have been
CC applied on several HIV-1(NL4.3) strains selected in vitro in the presence
CC of increasing concentrations of inhibitors of HIV entry and evaluated for
CC the phenotypic resistance of these recombined viruses. This phenotypic
```

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CC resistance has been correlated with genotypic resistance. The invention
CC also involves a recombination assay for the integrase gene. Determining
CC susceptibility of HIV is useful to study molecular target and resistance
CC profile of action of compounds with anti-HIV activity and to adapt
CC chemotherapy administered to an HIV patient. A genetic information data
CC set on anti-HIV resistance is useful to influence anti-HIV therapy. The
CC present sequence is a PCR primer used to amplify gp120 encoding sequence
CC from HIV infected cells
XX
SQ Sequence 25 BP; 10 A; 5 C; 7 G; 1 T; 0 U; 2 Other;
XX
Query Match 0.2%; Score 16.6; DB 1; Length 25;
Best Local Similarity 76.0%; Pred. No. 1.4e+03;
Matches 19; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 3279 AGAGAGAAATGAAACGACCCG 3303
DB 1 AGAGAGATGACGACCAAGCCCCAG 25
XX
RESULT 1530
AAF58644/C
ID AAF58644 standard; DNA; 25 BP.
XX
AC AAF58644;
XX
DT 27-APR-2001 (first entry)
XX
DE Human HX2004-6 hybridisation probe oligo #13.
XX
KW Human; HX0024-6; cytosolic; adenocarcinoma; in situ hybridisation;
KW probe; ss.
XX
OS Homo sapiens.
XX
PN WO200107614-A1.
XX
PD 01-FEB-2001.
XX
PF 25-JUL-2000; 2000WO-US020233.
XX
PR 26-JUL-1999; 99US-0145612P.
XX
PR 13-AUG-1999; 99US-0148936P.
XX
PA (CHIR ) CHIRON CORP.
XX
PI Kennedy GC;
XX
DR WPI; 2001-182794/18.
XX
PT New human HX2004-6 polypeptides and polynucleotides differentially
PT expressed in adenocarcinomas, useful for measuring the level of HX2004-6
PT polypeptide, or for diagnosing diseases associated with HX2004-6
PT overexpression.
XX
PS Example 5; Page 38; 78pp; English.
XX
CC The present sequence is a probe used for in situ hybridisation analysis
CC of HX2004-6 expression in cancer tissue. The human HX2004-6 polypeptides
CC and polynucleotides are useful in identifying human HX2004-6 polypeptide-
CC binding compounds. These compounds that specifically bind human HX2004-6
CC are useful in diagnostic assays to detect the presence of, and/or measure
CC the level of, HX2004-6 polypeptide. In addition, the human HX2004-6
CC polypeptides, polynucleotides and antibodies are useful in diagnosing,
CC preventing or treating diseases associated with human HX2004-6
CC overexpression, such as pancreatic, duct epithelial cell, breast or colon
CC adenocarcinomas. The human HX2004-6 polynucleotides and antibodies
CC specific for HX2004-6 polypeptides are also useful in screening assays to
CC identify substances that modulate HX2004-6 expression in a cell, for
CC producing HX2004-6 polypeptide, or for detecting HX2004-6 mRNA in a
CC biological sample
XX
SQ Sequence 25 BP; 2 A; 6 C; 5 G; 12 T; 0 U; 0 Other;
```

Query Match 0.2%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1324 CCAGACGACGAGGATGATCAG 1346
|||
DB 24 CCAGACGACGATGATGATACAG 2

RESULT 1531
AAF98579/c
ID AAF98579 standard; DNA; 25 BP.
XX AAF98579;
AC AAF98579;
XX
XX 02-JUL-2001 (first entry)
XX
XX Human kinase marker 19 forward primer.
DE
XX Human; ovarian cancer; identification; detection; characterisation;
XX tumour; kinase; marker; cytostatic; antisense gene therapy; probe;
KW primer; ss.
XX Homo sapiens.
OS
XX WO200118542-A2.
XX
XX 15-MAR-2001.
XX
XX 01-SEP-2000; 2000WO-US024199.
XX
XX 03-SEP-1999; 99US-0152547P.
XX 16-MAR-2000; 2000US-0190347P.
XX 21-MAR-2000; 2000US-0191321P.
XX 31-MAY-2000; 2000US-0208382P.
XX 20-JUL-2000; 2000US-00220467.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Lee J, Thompsho P, Little J;
PI WPI; 2001-211428/21.
XX
XX Detection, assessment, prevention and therapy of ovarian cancer,
PT comprises detecting changes in the expression of a variety of markers.
XX
XX Disclosure; Page 102; 1198pp; English.

CC The present invention describes a method for assessing whether a patient
CC is afflicted with ovarian cancer by comparing: (1) the expression of a
CC marker (1) (see AAF98594 to AAF98730), in a patient sample; and (2) the
CC normal level of expression of (1) in a control non-ovarian cancer sample,
CC where a significant difference between the level of expression in (a) and
CC (b) is an indication that the patient is afflicted with ovarian cancer.
CC (1) have cytostatic activities and can be used in antisense gene therapy.
CC The method, compositions and kits from the present invention can be used
CC for: (1) assessing and treating ovarian cancer; (2) making isolated
CC hybridoma, which produces an antibody useful for ovarian cancer
CC assessment; and (3) inhibiting ovarian cancer in a patient. AAF98573 to
CC AAF98593 represent human kinase marker primers and probes which are used
CC in the exemplification of the present invention

XX
XX Sequence 25 BP; 9 A; 4 C; 6 G; 6 T; 0 U; 0 Other;
SQ

Query Match 0.2%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4678 ATCTATCTGATCTGATGATGAA 4700
|||
DB 25 ATCTCCCTGATATCGTATGATGAA 3

RESULT 1532
ABN04416/c
ID ABN04416 standard; DNA; 25 BP.
XX
XX AC ABN04416;
XX
XX 29-MAY-2002 (first entry)
XX
XX Human GDMLP-1 25-mer scanning SEQ ID NO:4 sequence SEQ ID NO:4408.
DE
XX Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
XX muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
XX Homo sapiens.
OS
XX WO200192524-A2.
XX
XX 06-DEC-2001.
XX
XX 25-MAY-2001; 2001WO-US016981.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX 30-JAN-2001; 2001WO-US000661.
XX 30-JAN-2001; 2001WO-US000662.
XX 30-JAN-2001; 2001WO-US000663.
XX 30-JAN-2001; 2001WO-US000664.
XX 30-JAN-2001; 2001WO-US000665.
XX 30-JAN-2001; 2001WO-US000666.
XX 30-JAN-2001; 2001WO-US000667.
XX 30-JAN-2001; 2001WO-US000668.
XX 30-JAN-2001; 2001WO-US000669.
XX 30-JAN-2001; 2001WO-US000670.
XX 05-FEB-2001; 2001US-0266860P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
PI WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
XX description ionization, comprises human myosin-like protein hGDMLP-1.
XX
XX Disclosure; SEQ ID NO 4408; 214pp; English.

CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMLP-
CC 1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser description ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMLP-1, in particular heart
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence

XX	Sequence	25 BP, 6 A, 5 C, 13 G, 1 T, 0 U, 0 Other,	
XX	Query Match	0.2%; Score 16.6; DB 1; Length 25;	
XX	Best Local Similarity	82.6%; Pred. No. 1.4e+03;	
XX	Matches 19; Conservative	0; Mismatches 4; Indels 0; Gaps 0	
OY	5766	GCTTGCCTGCGCCGCGCTGCTGCC 5788	
DB	24	GCTTGCCTGCGCCAGCCTCCCTCC 2	
RESULT 1533			
ID	ABN03242/c		
XX	ABN03242 standard; DNA; 25 BP.		
XX	ABN03242;		
AC			
XX	29-MAY-2002 (first entry)		
DT			
XX	Human GDMLP-1 25-mer scanning SEQ ID NO:4 sequence SEQ ID NO:3234.		
DE			
XX			
KW	Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;		
KW	muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;		
KW	skeletal muscle disorder; amplicon; screening; 88.		
XX			
OS	Homo sapiens.		
PN			
XX	WO200192524-A2.		
PD			
XX	06-DEC-2001.		
PF			
XX	25-MAY-2001; 2001WO-US016981.		
XX			
PR	26-MAY-2000; 2000US-0207456P.		
PR	21-SEP-2000; 2000US-0234687P.		
ER	27-SEP-2000; 2000US-0236359P.		
PR	04-OCT-2000; 2000GB-00024263.		
PR	30-JAN-2001; 2001WO-US000661.		
PR	30-JAN-2001; 2001WO-US000662.		
PR	30-JAN-2001; 2001WO-US000663.		
PR	30-JAN-2001; 2001WO-US000664.		
PR	30-JAN-2001; 2001WO-US000665.		
PR	30-JAN-2001; 2001WO-US000666.		
PR	30-JAN-2001; 2001WO-US000667.		
PR	30-JAN-2001; 2001WO-US000668.		
PR	30-JAN-2001; 2001WO-US000669.		
PR	30-JAN-2001; 2001WO-US000670.		
PR	05-FEB-2001; 2001US-0268680P.		
XX			
PA	(AEOM-) AEOMICA INC.		
XX			
PI	Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;		
XX			
DR	WPI; 2002-179446/23.		
PT			
PT	New polypeptide, for raising antibodies that recognise hGDMLP-1 proteins,		
PT	or as specific biomolecule capture probes for surface-enhanced laser		
PT	desorption ionization, comprises human myosin-like protein hGDMLP-1.		
PS			
XX	Disclosure; SEQ ID NO 3234; 214pp; English.		
XX			
CC	The present invention describes a human genome-derived myosin-like		
CC	protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1		
CC	can be used in gene therapy and vaccine production. The hGDMLP-1		
CC	nucleic acid can be used as probes to detect, characterise and quantify		
CC	hGDMLP-1 nucleic acids in samples, as amplification substrates, to		
CC	provide initial substrates for the recombinant engineering of hGDMLP-1		
CC	protein variants having desired phenotypic improvements, and for		
CC	expressing the proteins. The hGDMLP-1 proteins or polypeptides may be		
CC	used as immunogens to raise antibodies that specifically recognise hGDMLP-1		
CC	-1 proteins, as standards in assays used to determine the concentration		
CC	and/or amount specifically of hGDMLP proteins, as specific biomolecule		
CC			

CC	captureprobes for surface-enhanced laser desorption/ionisation, as
CC	therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC	production, and in vaccines or for replacement therapy. The
CC	polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC	disorder associated with the expression of hGDMLP-1, in particular heart
CC	and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC	The present sequence represents an oligomer used in the screening of the
CC	hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC	The sequence data for this patent did not form part of the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequence
SQ	Sequence 25 BP; 7 A; 5 C; 11 G; 2 T; 0 U; 0 Other;
OY	Query Match 0.2%; Score 16.6; DB 1; Length 25; Best Local Similarity 82.6%; Pred.No. 1.4e+03; Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
DB	4298 GCATCTTTTTCCTTCCTCGAC 4320 24 GCCTCTTTTTCAGTCCCGCGAC 2
RESULT 1534	
ID	ABN05210 standard; DNA; 25 BP.
AC	ABN05210;
XX	
DT	29-MAY-2002 (first entry)
XX	
DE	Human GDMLP-1 25-mer scanning SEQ ID NO:4 sequence SEQ ID NO:5202.
KW	Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KV	muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KM	skeletal muscle disorder; amplicon; screening; ss.
XX	
OS	Homo sapiens.
XX	
PV	WO200192524-A2.
PD	
XX	06-DEC-2001.
PF	25-MAY-2001; 2001WO-US016981.
XX	
PR	26-MAY-2000; 2000US-0207456P.
PR	21-SEP-2000; 2000US-0234687P.
PR	27-SEP-2000; 2000US-0236359P.
PR	04-OCT-2000; 2000GB-00024283.
PR	30-JAN-2001; 2001WO-US000661.
PR	30-JAN-2001; 2001WO-US000662.
PR	30-JAN-2001; 2001WO-US000663.
PR	30-JAN-2001; 2001WO-US000664.
PR	30-JAN-2001; 2001WO-US000665.
PR	30-JAN-2001; 2001WO-US000666.
PR	30-JAN-2001; 2001WO-US000667.
PR	30-JAN-2001; 2001WO-US000668.
PR	30-JAN-2001; 2001WO-US000669.
PR	30-JAN-2001; 2001WO-US000670.
PR	05-FEB-2001; 2001US-0268860P.
XX	
PA	(AEOM-) AEOMICA INC.
XX	
PI	Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
DR	WPI; 2002-179446/23.
XX	
PT	New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT	or as specific biomolecule capture probes for surface-enhanced laser
PT	desorption/ionization, comprises human myosin-like protein hGDMLP-1.
XX	
PS	Disclosure, SEQ ID NO 5202; 214pp; English.
XX	

CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMLP-1, in particular heart
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 25 BP; 1 A; 11 C; 6 G; 7 T; 0 U; 0 Other;
Query Match 0.2%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 4319 ACTGTCCTCGACCTTGAGCTC 4341
DB 2 ACTGTCCTCGAGCCTTGAGCTC 24
RESULT 1535
ABN03243/C
ID ABN03243 standard; DNA; 25 BP.
AC ABN03243;
XX
XX 29-MAY-2002 (first entry)
DE Human GDMLP-1 25-mer scanning SEQ ID NO:4 sequence SEQ ID NO:3235.
XX
XX Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
XX muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
XX skeletal muscle disorder; amplicon; screening; ss.
OS Homo sapiens.
XX
XX WO200192524-A2.
PN
XX
XX 06-DEC-2001.
PD
XX
XX 25-MAY-2001; 2001WO-US016981.
PF
XX
XX 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-026666P.
XX
XX (AEOM-) AEOMICA INC.

XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
XX WPI; 2002-179446/23.
DR
XX
XX New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption/ionization, comprises human myosin-like protein hGDMLP-1.
XX
XX Disclosure; SEQ ID NO 3235; 214pp; English.
PS
XX
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMLP-1, in particular heart
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 25 BP; 8 A; 5 C; 10 G; 2 T; 0 U; 0 Other;
Query Match 0.2%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 4298 GCATCTTTTCCCTCCCTGAGC 4320
DB 23 GCCTCTTTTTCAGTCCCGGAC 1
RESULT 1536
ABN12703
ID ABN12703 standard; DNA; 25 BP.
AC ABN12703;
XX
XX 29-MAY-2002 (first entry)
DE Human GDMLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:12695.
XX
XX Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
XX muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
XX skeletal muscle disorder; amplicon; screening; ss.
OS Homo sapiens.
XX
XX WO200192524-A2.
PN
XX
XX 06-DEC-2001.
PD
XX
XX 25-MAY-2001; 2001WO-US016981.
PF
XX
XX 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.

PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX (AECOM-) AECOMICA INC.
XX PA
XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX DR
XX PT New polypeptide, for raising antibodies that recognize hGDMRP-1 proteins,
XX PT or as specific biomolecule capture probes for surface-enhanced laser
XX PT desorption ionization, comprises human myosin-like protein hGDMRP-1.
XX PS
XX PS Disclosure; SEQ ID NO 12695; 214pp; English.
XX CC
XX CC The present invention describes a human genome-derived myosin-like
XX CC protein 1 (hGDMRP-1). The protein and polynucleotide sequences of hGDMRP-
XX CC 1 can be used in gene therapy and vaccine production. The hGDMRP-1
XX CC nucleic acids can be used as probes to detect, characterize and quantify
XX CC hGDMRP-1 nucleic acids in samples, as amplification substrates, to
XX CC provide initial substrates for the recombinant engineering of hGDMRP-1
XX CC protein variants having desired phenotypic improvements, and for
XX CC expressing the proteins. The hGDMRP-1 proteins or polypeptides may be
XX CC used as immunogens to raise antibodies that specifically recognise hGDMRP
XX CC -1 proteins, as standards in assays used to determine the concentration
XX CC and/or amount specifically of hGDMRP proteins, as specific biomolecule
XX CC capture probes for surface-enhanced laser desorption ionisation, as
XX CC therapeutic supplement in patients having specific deficiency in hGDMRP-1
XX CC production, and in vaccines or for replacement therapy. The
XX CC polynucleotide sequences encoding hGDMRP-1 may be used for diagnosing a
XX CC disorder associated with the expression of hGDMRP-1, in particular heart
XX CC and skeletal muscle disorders. hGDMRP-1 is localised to chromosome 22.
XX CC The present sequence represents an oligomer used in the screening of the
XX CC hGDMRP-1 sequence in the exemplification of the present invention. N.B.
XX CC The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequence
XX SQ
XX Sequence 25 BP; 8 A; 8 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 0.2%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 7407 CAACATCAGCAGCAGCAGCAGCA 7429
DB 2 CAGCTTCAGCAGCAGCAGCAGCA 24
RESULT 1537
ABN04417/c
ID ABN04417 standard; DNA; 25 BP.
XX
XX AC ABN04417;
XX
XX DT 29-MAY-2002 (first entry)
XX
XX DE Human GDMRP-1 25-mer scanning SEQ ID NO:4 sequence SEQ ID NO:4409.
XX
XX KM Human; genome-derived myosin-like protein 1; hGDMRP-1; heart;
XX KM muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
XX KM skeletal muscle disorder; amplicon; screening; ss.
XX OS Homo sapiens.
XX PN WO200192524-A2.

XX
XX PD 06-DEC-2001.
XX
XX PF 25-MAY-2001; 2001WO-US016981.
XX
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PR 30-JAN-2001; 2001WO-US000661.
XX PR 30-JAN-2001; 2001WO-US000662.
XX PR 30-JAN-2001; 2001WO-US000663.
XX PR 30-JAN-2001; 2001WO-US000664.
XX PR 30-JAN-2001; 2001WO-US000665.
XX PR 30-JAN-2001; 2001WO-US000666.
XX PR 30-JAN-2001; 2001WO-US000667.
XX PR 30-JAN-2001; 2001WO-US000668.
XX PR 30-JAN-2001; 2001WO-US000669.
XX PR 30-JAN-2001; 2001WO-US000670.
XX PR 05-FEB-2001; 2001US-0266860P.
XX
XX PA (AECOM-) AECOMICA INC.
XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX DR
XX PT New polypeptide, for raising antibodies that recognize hGDMRP-1 proteins,
XX PT or as specific biomolecule capture probes for surface-enhanced laser
XX PT desorption ionization, comprises human myosin-like protein hGDMRP-1.
XX PS
XX PS Disclosure; SEQ ID NO 4409; 214pp; English.
XX CC
XX CC The present invention describes a human genome-derived myosin-like
XX CC protein 1 (hGDMRP-1). The protein and polynucleotide sequences of hGDMRP-
XX CC 1 can be used in gene therapy and vaccine production. The hGDMRP-1
XX CC nucleic acids can be used as probes to detect, characterize and quantify
XX CC hGDMRP-1 nucleic acids in samples, as amplification substrates, to
XX CC provide initial substrates for the recombinant engineering of hGDMRP-1
XX CC protein variants having desired phenotypic improvements, and for
XX CC expressing the proteins. The hGDMRP-1 proteins or polypeptides may be
XX CC used as immunogens to raise antibodies that specifically recognise hGDMRP
XX CC -1 proteins, as standards in assays used to determine the concentration
XX CC and/or amount specifically of hGDMRP proteins, as specific biomolecule
XX CC capture probes for surface-enhanced laser desorption ionisation, as
XX CC therapeutic supplement in patients having specific deficiency in hGDMRP-1
XX CC production, and in vaccines or for replacement therapy. The
XX CC polynucleotide sequences encoding hGDMRP-1 may be used for diagnosing a
XX CC disorder associated with the expression of hGDMRP-1, in particular heart
XX CC and skeletal muscle disorders. hGDMRP-1 is localised to chromosome 22.
XX CC The present sequence represents an oligomer used in the screening of the
XX CC hGDMRP-1 sequence in the exemplification of the present invention. N.B.
XX CC The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequence
XX SQ
XX Sequence 25 BP; 6 A; 5 C; 13 G; 1 T; 0 U; 0 Other;
Query Match 0.2%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 5766 GCTTCTGCGCAGCCTGCTGCGC 5788
DB 23 GCTTCTGCGCAGCCTGCTGCGC 1
RESULT 1538
ABN12702
ID ABN12702 standard; DNA; 25 BP.
XX
XX AC ABN12702;
XX
XX

DT 29-MAY-2002 (first entry)
XX Human GDMLP-1 25-mer scanning SEQ ID NO:5 sequence SEQ ID NO:12694.
DE
XX Human; genome-derived myosin-like protein 1; GDMLP-1; heart;
KM muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
XX skeletal muscle disorder; amplicon; screening; ss.
OS
XX Homo sapiens.
XX WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX
XX (AEOM-) AEOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX MPI; 2002-179446/23.
XX
PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
PS Disclosure; SEQ ID NO 12694; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
XX protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
XX 1 can be used in gene therapy and vaccine production. The hGDMLP-1
XX nucleic acids can be used as probes to detect, characterize and quantify
XX hGDMLP-1 nucleic acids in samples, as amplification substrates, to
XX provide initial substrates for the recombinant engineering of hGDMLP-1
XX protein variants having desired phenotypic improvements, and for
XX expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
XX used as immunogens to raise antibodies that specifically recognise hGDMLP
XX -1 proteins, as standards in assays used to determine the concentration
XX and/or amount specifically of hGDMLP proteins, as specific biomolecule
XX capture probes for surface-enhanced laser desorption ionisation, as
XX therapeutic supplement in patients having specific deficiency in hGDMLP-1
XX production, and in vaccines or for replacement therapy. The
XX polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
XX disorder associated with the expression of hGDMLP-1, in particular heart
XX and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
XX The present sequence represents an oligomer used in the screening of the
XX hGDMLP-1 sequence in the exemplification of the present invention. N.B.
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 25 BP; 7 A; 8 C; 7 G; 3 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Query 7407 CAACATCAGACGACGACGACGA 7429
DB 3 CAGCTTCAGACGACGACGACGACGA 25
RESULT 1539
ABN03241/C
ID ABN03241 standard; DNA; 25 BP.
XX
XX ABN03241;
XX
DT 29-MAY-2002 (first entry)
XX
XX Human GDMLP-1 25-mer scanning SEQ ID NO:4 sequence SEQ ID NO:3233.
DE
XX Human; genome-derived myosin-like protein 1; GDMLP-1; heart;
XX muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
XX skeletal muscle disorder; amplicon; screening; ss.
OS
XX Homo sapiens.
XX
XX WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX
XX (AEOM-) AEOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX MPI; 2002-179446/23.
XX
PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
PS Disclosure; SEQ ID NO 3233; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
XX protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
XX 1 can be used in gene therapy and vaccine production. The hGDMLP-1
XX nucleic acids can be used as probes to detect, characterize and quantify
XX hGDMLP-1 nucleic acids in samples, as amplification substrates, to
XX provide initial substrates for the recombinant engineering of hGDMLP-1
XX protein variants having desired phenotypic improvements, and for
XX expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
XX used as immunogens to raise antibodies that specifically recognise hGDMLP
XX -1 proteins, as standards in assays used to determine the concentration
XX and/or amount specifically of hGDMLP proteins, as specific biomolecule
XX capture probes for surface-enhanced laser desorption ionisation, as
XX therapeutic supplement in patients having specific deficiency in hGDMLP-1
XX production, and in vaccines or for replacement therapy. The
XX polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
XX disorder associated with the expression of hGDMLP-1, in particular heart
XX and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
XX The present sequence represents an oligomer used in the screening of the

CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 25 BP; 7 A; 4 C; 11 G; 3 T; 0 U; 0 Other;
Query Match 0.2%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4298 GCATCTTTTCTCTCCCTGGAC 4320
DB 25 GCCTCTTTTCAGTCCCGGAC 3
RESULT 1540
ABN04415/c
ID ABN04415 standard; DNA; 25 BP.
XX
AC ABN04415;
XX
DT 29-MAY-2002 (first entry)
XX
DE Human GDMLP-1 25-mer scanning SEQ ID NO:4 sequence SEQ ID NO:4407.
XX
KW Human; genome-derived myosin-like protein 1; GDMLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
PN WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
DR WPI; 2002-179446/23.
XX
PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX
PS Disclosure; SEQ ID NO 4407; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC nucleic acids can be used as probes to detect, characterize and quantify
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMLP-1
CC protein variants having desired phenotypic improvements, and for

CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC as immunogens to raise antibodies that specifically recognise hGDMLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMLP-1, in particular heart
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 25 BP; 6 A; 4 C; 13 G; 2 T; 0 U; 0 Other;
Query Match 0.2%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 5766 GCTTCTGCGCGGCTGCTGCC 5788
DB 25 GCTTCTGCGCGGCTGCTGCC 3
RESULT 1541
ABN05209
ID ABN05209 standard; DNA; 25 BP.
XX
AC ABN05209;
XX
DT 29-MAY-2002 (first entry)
XX
DE Human GDMLP-1 25-mer scanning SEQ ID NO:4 sequence SEQ ID NO:5201.
XX
KW Human; genome-derived myosin-like protein 1; GDMLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
OS Homo sapiens.
XX
PN WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
DR WPI; 2002-179446/23.
XX
PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser

PT desorption ionization, comprises human myosin-like protein hGDMPL-1.
 XX
 XX Disclosure; SEQ ID NO 5201; 214pp; English.
 XX
 CC The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPL-1). The protein and polynucleotide sequences of hGDMPL-
 CC 1 can be used in gene therapy and vaccine production. The hGDMPL-1
 CC nucleic acids can be used as probes to detect, characterize and quantify
 CC hGDMPL-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMPL-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMPL-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPL-
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPL proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption/ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPL-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPL-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPL-1, in particular heart
 CC and skeletal muscle disorders. hGDMPL-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPL-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX
 SQ Sequence 25 BP; 1 A; 11 C; 6 G; 7 T; 0 U; 0 Other;
 Query Match 0.2%; Score 16.6; DB 1; Length 25;
 Best Local Similarity 82.6%; Pred. No. 1.4e+03;
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 4319 ACTGTCCTCTGACCCCTTGCGTC 4341
 Db 3 ACTGTCCTCGGCGCCTTGCGCTC 25
 RESULT 1542
 ABN05211
 ID ABN05211 standard; DNA; 25 BP.
 XX
 AC ABN05211;
 XX
 DT 29-MAY-2002 (first entry)
 XX
 DE Human GDMPL-1 25-mer scanning SEQ ID NO:4 sequence SEQ ID NO:5203.
 XX
 KM Human; genome-derived myosin-like protein 1; GDMPL-1; hGDMPL-1; heart;
 KM muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KM skeletal muscle disorder; amplicon; screening; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200192524-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 25-MAY-2001; 2001WO-US016981.
 XX
 PR 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-023659P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.

PR 30-JAN-2001; 2001WO-US000670.
 PR 05-FEB-2001; 2001US-0266860P.
 XX
 XX (ABOM-) ABOMICA INC.
 PA
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 PI WPI; 2002-179446/23.
 DR
 XX
 PT New polypeptide, for raising antibodies that recognize hGDMPL-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption ionization, comprises human myosin-like protein hGDMPL-1.
 XX
 PS Disclosure; SEQ ID NO 5203; 214pp; English.
 XX
 CC The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPL-1). The protein and polynucleotide sequences of hGDMPL-
 CC 1 can be used in gene therapy and vaccine production. The hGDMPL-1
 CC nucleic acids can be used as probes to detect, characterize and quantify
 CC hGDMPL-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMPL-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMPL-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPL-
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPL proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption/ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPL-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPL-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPL-1, in particular heart
 CC and skeletal muscle disorders. hGDMPL-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPL-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX
 SQ Sequence 25 BP; 1 A; 10 C; 7 G; 7 T; 0 U; 0 Other;
 Query Match 0.2%; Score 16.6; DB 1; Length 25;
 Best Local Similarity 82.6%; Pred. No. 1.4e+03;
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 4319 ACTGTCCTCTGACCCCTTGCGTC 4341
 Db 1 ACTGTCCTCGGCGCCTTGCGCTC 23
 RESULT 1543
 AAD22835
 ID AAD22835 standard; DNA; 25 BP.
 XX
 AC AAD22835;
 XX
 DT 26-FEB-2002 (first entry)
 XX
 DE Mouse alpha-interferon Zcyto13 DNA constructing ZC21591 RACE PCR primer.
 XX
 KM Mouse; alpha-interferon; Zcyto13; immune response; tumour; gene therapy;
 KM viral infection; hepatotropic; neuroprotective; hairy cell leukaemia;
 KM ophthalmological; cytostatic; antisense therapy; multiple sclerosis;
 KM atherosclerosis; retinopathy; renal cell carcinoma; malignant melanoma;
 KM hepatitis; multiple myeloma; cervical carcinoma; autoimmune disease;
 KM RACE; rapid amplification of cDNA end; PCR primer; ss.
 XX
 OS Mus sp.
 XX
 PN US6312924-B1.
 XX
 PD 06-NOV-2001.
 XX
 PF 17-MAR-2000; 2000US-00528760.

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XX 18-MAR-1999; 99US-0125045P.
PR 23-SEP-1999; 99US-0155739P.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Presnell SR, Feldhaus AL, Gao Z;
XX WPI; 2002-024905/03.
XX
XX New nucleic acid molecule encoding murine interferon alpha polypeptide,
XX designated Zcyto13, useful as probes and primers, and to augment
XX immunological response to tumor or viral infection.
XX
XX Example 1; Col 66; 44bp; English.
XX
XX The present sequence is a RACE (rapid amplification of cDNA end) PCR
XX primer used for amplifying mouse interferon alpha DNA designated Zcyto13.
XX Zcyto13 DNA is useful in gene therapy, as a probe for detecting the
XX presence of Zcyto13 RNA in a biological sample, to determine whether a
XX subject's chromosomes contain a mutation in the Zcyto13 gene. Zcyto13 DNA
XX is also useful for augmenting immunological response to tumour or viral
XX infection in a subject, and to inhibit Zcyto13 gene expression, such as
XX antisense molecule, a ribozyme or an external guide sequence molecule.
XX Zcyto13 DNA is useful for producing Zcyto13 protein recombinantly which
XX is useful for treating autoimmune diseases, renal cell carcinoma,
XX malignant melanoma, chronic hepatitis B, hepatitis C and hepatitis D,
XX multiple myeloma, cervical carcinoma, multiple sclerosis, hairy cell
XX leukaemia, atherosclerosis and retinopathy
XX
XX Sequence 25 BP; 7 A; 5 C; 7 G; 6 T; 0 U; 0 Other;
XX
SQ
XX
XX Query Match 0.2%; Score 16.6; DB 1; Length 25;
XX Best Local Similarity 82.6%; Pred. No. 1.4e+03;
XX Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 1921 GGTGCATTACACATCCTAGT 1943
XX |||||
XX 2 GGTAGCATTCAGCATCTCTGCT 24
XX
XX
XX RESULT 1544
XX ABV82434
XX ID ABV82434 standard; DNA; 25 BP.
XX
XX AC ABV82434;
XX
XX DT 03-JAN-2003 (first entry)
XX
XX DE Human HTPPL scanning oligonucleotide SEQ ID 3680.
XX
XX KW Human; gene therapy; tumour suppressor; HTPPL; chromosome 10p12.1;
XX human testis expressed Patched like protein; testis; adrenal; liver;
XX male germ cell development; bone marrow; brain; kidney; lung; placenta;
XX prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
XX OS Homo sapiens.
XX
XX PN EPI229046-A2.
XX
XX PD 07-AUG-2002.
XX
XX PF 28-JAN-2002; 2002EP-00001167.
XX
XX PR 30-JAN-2001; 2001WO-US000663.
XX PR 30-JAN-2001; 2001WO-US000664.
XX PR 30-JAN-2001; 2001WO-US000665.
XX PR 30-JAN-2001; 2001WO-US000667.
XX PR 30-JAN-2001; 2001WO-US000668.
XX PR 30-JAN-2001; 2001WO-US000669.
XX PR 23-MAY-2001; 2001US-00864761.
XX PR 09-OCT-2001; 2001US-0327898P.
XX

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PA (AEOM-) AEOMICA INC.
XX
XX Zhan J;
XX
XX WPI; 2002-676582/73.
XX
XX Novel isolated human testis expressed Patched like protein (HTPL), useful
XX for identifying agonist and antagonist and specific binding partners, and
XX for treating subjects having defects in HTPL.
XX
XX Example 2; Page 546; 718bp; English.
XX
XX The present invention relates to human testis expressed Patched like
XX protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
XX has two isoforms, with a few single base pair differences between the
XX two. One of the single base pair changes introduces a premature stop
XX codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
XX shares an overall structure organisation with the Patched protein. The
XX shared structural features strongly imply that HTPL plays a role similar
XX to that of Patched, and is a potential tumour suppressor. HTPL is
XX important in regulating male germ cell development, and the HTPL gene was
XX mapped to human chromosome 10p12.1. HTPL and its coding sequence are
XX useful for diagnosing a disorder caused by mutation in HTPL, and in
XX therapy and manufacture of a medicament for treatment or prevention of
XX such disorder associated with decreased expression or activity of human
XX HTPL. Such disorders include disorders of testis, or adrenal, adult and
XX foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
XX skeletal muscle or colon function. HTPL proteins and nucleic acids are
XX clinically useful diagnostic markers and potential therapeutic agents for
XX male infertility and cancer. The present oligonucleotide was used in an
XX example from the invention
XX
XX Sequence 25 BP; 6 A; 4 C; 3 G; 12 T; 0 U; 0 Other;
XX
SQ
XX
XX Query Match 0.2%; Score 16.6; DB 1; Length 25;
XX Best Local Similarity 82.6%; Pred. No. 1.4e+03;
XX Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 4040 TGTATTTTATACATCACTTG 4062
XX |||||
XX 2 TGTATTTTATACATCAGTGG 24
XX
XX
XX RESULT 1545
XX ABV82433
XX ID ABV82433 standard; DNA; 25 BP.
XX
XX AC ABV82433;
XX
XX DT 03-JAN-2003 (first entry)
XX
XX DE Human HTPPL scanning oligonucleotide SEQ ID 3679.
XX
XX KW Human; gene therapy; tumour suppressor; HTPPL; chromosome 10p12.1;
XX human testis expressed Patched like protein; testis; adrenal; liver;
XX male germ cell development; bone marrow; brain; kidney; lung; placenta;
XX prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
XX OS Homo sapiens.
XX
XX PN EPI229046-A2.
XX
XX PD 07-AUG-2002.
XX
XX PF 28-JAN-2002; 2002EP-00001167.
XX
XX PR 30-JAN-2001; 2001WO-US000663.
XX PR 30-JAN-2001; 2001WO-US000664.
XX PR 30-JAN-2001; 2001WO-US000665.
XX PR 30-JAN-2001; 2001WO-US000667.
XX PR 30-JAN-2001; 2001WO-US000668.
XX PR 30-JAN-2001; 2001WO-US000669.
XX PR 23-MAY-2001; 2001US-00864761.
XX

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PR 09-OCT-2001; 2001US-0327898P.
XX (AEOM-) AEOMICA INC.
XX Zhan J;
XX WPI; 2002-676582/73.
DR Novel isolated human testis expressed Patched like protein (HTPL), useful
PT for identifying agonist and antagonist and specific binding partners, and
PT for treating subjects having defects in HTPL.
XX
XX Example 2; Page 546; 718pp; English.
XX
CC The present invention relates to human testis expressed Patched like
CC protein (HTPL, see ABV78759 to ABV78762 and AB898519 to AB898520). HTPL
CC has two isoforms, with a few single base pair differences between the
CC two. One of the single base pair changes introduces a premature stop
CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC shares an overall structure organisation with the Patched protein. The
CC shared structural features strongly imply that HTPL plays a role similar
CC to that of Patched, and is a potential tumour suppressor. HTPL is
CC important in regulating male germ cell development, and the HTPL gene was
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC useful for diagnosing a disorder caused by mutation in HTPL, and in
CC therapy and manufacture of a medicament for treatment or prevention of
CC such disorder associated with decreased expression or activity of human
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC clinically useful diagnostic markers and potential therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention
SQ Sequence 25 BP; 6 A; 4 C; 3 G; 12 T; 0 U; 0 Other;
XX
QY Query Match 0.2%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Db 4040 TGTATTTTATACCATCACTTG 4062
1 TCGTATTTTATACCATCACTG 25
RESULT 1546
ABV82435
ID ABV82435 standard; DNA; 25 BP.
XX
XX ABV82435;
AC
XX 03-JAN-2003 (first entry)
DT
XX Human HTPL scanning oligonucleotide SEQ ID 3681.
DE
XX Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW human testis expressed Patched like protein; testis; adrenal; liver;
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
XX Homo sapiens.
OS
XX EPI229046-A2.
PN
XX 07-AUG-2002.
PD
XX
XX 28-JAN-2002; 2002EP-00001167.
PF
XX 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.

PR 30-JAN-2001; 2001WO-US000669.
PR 23-MAY-2001; 2001US-00864761.
PR 09-OCT-2001; 2001US-0327898P.
XX
XX (AEOM-) AEOMICA INC.
XX Zhan J;
XX WPI; 2002-676582/73.
DR Novel isolated human testis expressed Patched like protein (HTPL), useful
PT for identifying agonist and antagonist and specific binding partners, and
PT for treating subjects having defects in HTPL.
XX
XX Example 2; Page 546; 718pp; English.
XX
CC The present invention relates to human testis expressed Patched like
CC protein (HTPL, see ABV78759 to ABV78762 and AB898519 to AB898520). HTPL
CC has two isoforms, with a few single base pair differences between the
CC two. One of the single base pair changes introduces a premature stop
CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC shares an overall structure organisation with the Patched protein. The
CC shared structural features strongly imply that HTPL plays a role similar
CC to that of Patched, and is a potential tumour suppressor. HTPL is
CC important in regulating male germ cell development, and the HTPL gene was
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC useful for diagnosing a disorder caused by mutation in HTPL, and in
CC therapy and manufacture of a medicament for treatment or prevention of
CC such disorder associated with decreased expression or activity of human
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC clinically useful diagnostic markers and potential therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention
SQ Sequence 25 BP; 6 A; 4 C; 3 G; 12 T; 0 U; 0 Other;
XX
QY Query Match 0.2%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Db 4040 TGTATTTTATACCATCACTTG 4062
1 TCGTATTTTATACCATCACTG 23
RESULT 1547
ABV92626/c
ID ABV92626 standard; DNA; 25 BP.
XX
XX ABV92626;
AC
XX 23-DEC-2002 (first entry)
DT
XX Human POSHL1 scanning oligonucleotide SEQ ID NO 3339.
DE
XX Human; POSHL 1; SH3 domain; POSHL-like signalling protein 1; oncogene;
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW gene therapy; transgenic; ss.
XX
XX Homo sapiens.
OS
XX EPI239051-A2.
PN
XX 11-SEP-2002.
PD
XX
XX 28-JAN-2002; 2002EP-00001165.
PF
XX 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.

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PR 30-JAN-2001; 2001WO-US0000667.
PR 30-JAN-2001; 2001WO-US0000668.
PR 30-JAN-2001; 2001WO-US0000669.
PR 30-JAN-2001; 2001WO-US0000670.
PR 23-MAY-2001; 2001US-00864761.
PR 10-OCT-2001; 2001US-0328205P.
PA (AEOM-) AEOmica INC.
XX
XX Shannon M;
XX
XX WPI; 2002-684061/74.
XX
XX
XX Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide, POSHL
XX PT -1, useful for treating disorders associated with decreased expression or
XX PT activity of human POSHL1.
XX
XX Example 2; SEQ ID NO 3339; 60pp + Sequence Listing; English.
XX
XX The invention relates to an isolated SH3 domain (POSH)-like signalling
XX CC protein 1 (POSHL1) polypeptide (I), comprising a sequence of 730 amino
XX CC acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
XX CC (S1) having 95% deviations, especially conservative substitutions or a
XX CC fragment of the sequences comprising at least 8 contiguous amino acids.
XX CC Human POSHL1 is a proto-oncogene/oncogene product that functions as an
XX CC adaptor protein that interacts with Rho family small GTPases as well as
XX CC downstream components of the signal transduction pathway. (I) is useful
XX CC for identifying a specific binding partner. (I) and nucleic acids (II)
XX CC encoding (I) are useful for diagnosing, monitoring disease and treating
XX CC caused by altered expression of human POSHL1 including diagnosing and
XX CC treating cancer, they useful in the development of vaccines and (II) is
XX CC useful in gene therapy. (II) is useful for constructing microarrays which
XX CC are useful for measuring and for surveying gene expression and creating
XX CC transgenic non-human animals capable of producing the proteins. The
XX CC present sequence is that of a scanning oligonucleotide useful in examples
XX CC of the invention. Note: The present sequence did not form part of the
XX CC printed specification, but is based on sequence information supplied to
XX CC Derwent by the European Patent Office
XX
XX SQ Sequence 25 BP; 9 A; 8 C; 6 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 16.6; DB 1; Length 25;
XX Best Local Similarity 82.6%; Pred. No. 1.4e+03;
XX Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 6857 TGCCTTCTCCTGGGAGGAGAGA 6879
XX Db 23 TGCCTTCTCCTGGGAGGAGAGA 1
XX
XX RESULT 1548
XX ABV92624/c
XX ID ABV92624 standard; DNA; 25 BP.
XX
XX AC ABV92624;
XX
XX DT 23-DEC-2002 (first entry)
XX
XX DE Human POSHL1 scanning oligonucleotide SEQ ID NO 3337.
XX
XX KW Human; POSHL1; SH3 domain; POSH-like signalling protein 1; oncogene;
XX KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
XX KW gene therapy; transgenic; ss.
XX
XX OS Homo sapiens.
XX
XX PN EP1239051-A2.
XX
XX PD 11-SEP-2002.
XX
XX PF 28-JAN-2002; 2002EP-00001165.
XX
XX PR 30-JAN-2001; 2001WO-US0000663.

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PR 30-JAN-2001; 2001WO-US0000664.
PR 30-JAN-2001; 2001WO-US0000665.
PR 30-JAN-2001; 2001WO-US0000666.
PR 30-JAN-2001; 2001WO-US0000667.
PR 30-JAN-2001; 2001WO-US0000668.
PR 30-JAN-2001; 2001WO-US0000669.
PR 30-JAN-2001; 2001WO-US0000670.
PR 23-MAY-2001; 2001US-00864761.
PR 10-OCT-2001; 2001US-0328205P.
PA (AEOM-) AEOmica INC.
XX
XX Shannon M;
XX
XX WPI; 2002-684061/74.
XX
XX
XX Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide, POSHL
XX PT -1, useful for treating disorders associated with decreased expression or
XX PT activity of human POSHL1.
XX
XX Example 2; SEQ ID NO 3337; 60pp + Sequence Listing; English.
XX
XX The invention relates to an isolated SH3 domain (POSH)-like signalling
XX CC protein 1 (POSHL1) polypeptide (I), comprising a sequence of 730 amino
XX CC acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
XX CC (S1) having 95% deviations, especially conservative substitutions or a
XX CC fragment of the sequences comprising at least 8 contiguous amino acids.
XX CC Human POSHL1 is a proto-oncogene/oncogene product that functions as an
XX CC adaptor protein that interacts with Rho family small GTPases as well as
XX CC downstream components of the signal transduction pathway. (I) is useful
XX CC for identifying a specific binding partner. (I) and nucleic acids (II)
XX CC encoding (I) are useful for diagnosing, monitoring disease and treating
XX CC caused by altered expression of human POSHL1 including diagnosing and
XX CC treating cancer, they useful in the development of vaccines and (II) is
XX CC useful in gene therapy. (II) is useful for constructing microarrays which
XX CC are useful for measuring and for surveying gene expression and creating
XX CC transgenic non-human animals capable of producing the proteins. The
XX CC present sequence is that of a scanning oligonucleotide useful in examples
XX CC of the invention. Note: The present sequence did not form part of the
XX CC printed specification, but is based on sequence information supplied to
XX CC Derwent by the European Patent Office
XX
XX SQ Sequence 25 BP; 9 A; 8 C; 6 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 0.2%; Score 16.6; DB 1; Length 25;
XX Best Local Similarity 82.6%; Pred. No. 1.4e+03;
XX Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 6857 TGCCTTCTCCTGGGAGGAGAGA 6879
XX Db 25 TGCCTTCTCCTGGGAGGAGAGA 3
XX
XX RESULT 1549
XX ABV92625/c
XX ID ABV92625 standard; DNA; 25 BP.
XX
XX AC ABV92625;
XX
XX DT 23-DEC-2002 (first entry)
XX
XX DE Human POSHL1 scanning oligonucleotide SEQ ID NO 3338.
XX
XX KW Human; POSHL1; SH3 domain; POSH-like signalling protein 1; oncogene;
XX KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
XX KW gene therapy; transgenic; ss.
XX
XX OS Homo sapiens.
XX
XX PN EP1239051-A2.
XX
XX PD 11-SEP-2002.
XX
XX PF 28-JAN-2002; 2002EP-00001165.
XX
XX PR 30-JAN-2001; 2001WO-US0000663.

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PF 28-JAN-2002; 2002EP-00001165.
XX
XX 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 23-MAY-2001; 2001US-00864761.
PR 10-OCT-2001; 2001US-0328205P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M;
XX
XX WPI; 2002-684061/74.
XX
XX Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSH1-1, useful for treating disorders associated with decreased expression or activity of human POSH1.
XX
XX Example 2; SEQ ID NO 3338; 60pp + Sequence Listing; English.
XX
XX The invention relates to an isolated SH3 domain (POSH)-like signalling protein 1 (POSH1) polypeptide (I), comprising a sequence of 730 amino acids (S1, ABB83999), a sequence having 65% sequence identity to (S1), (S1) having 95% deviations, especially conservative substitutions or a fragment of the sequences comprising at least 8 contiguous amino acids.
XX
XX Human POSH1.1 is a proto-oncogene/oncogene product that functions as an adaptor protein that interacts with Rho family small GTPases as well as downstream components of the signal transduction pathway. (I) is useful for identifying a specific binding partner. (I) and nucleic acids (II) encoding (I) are useful for diagnosing, monitoring disease and treating CC caused by altered expression of human POSH1 including diagnosing and CC treating cancer. they useful in the development of vaccines and (II) is CC useful in gene therapy. (III) is useful for constructing microarrays which CC are useful for measuring and for surveying gene expression and creating CC transgenic non-human animals capable of producing the proteins. The CC present sequence is that of a scanning oligonucleotide useful in examples of the invention. Note: The present sequence did not form part of the CC printed specification, but is based on sequence information supplied to CC Derwent by the European Patent Office
XX
XX Sequence 25 BP; 9 A; 8 C; 6 G; 2 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 6857 TGCCTTCTCCCTGGCGAGGAGA 6879
Db 24 TGCTTCTCATGCGCTGGGTGA 2
RESULT 1550
ACI92457/c
ID ACI92457 standard; DNA; 25 BP.
XX
XX ACI92457;
XX
XX 14-OCT-2003 (first entry)
XX
XX Human microarray DNA oligonucleotide SEQ ID NO 92448.
XX
XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
KM genetic variation; diallelic marker; polymorphism; human;
XX cross-species comparison.
XX
XX Homo sapiens.
XX
XX US2003104410-A1.
XX
XX PN

XX
XX 05-JUN-2003.
XX
XX 15-MAR-2002; 2002US-00098263.
XX
XX 16-MAR-2001; 2001US-0276759P.
XX
XX (AFFY-) AFFIMETRIX INC.
XX
XX Miltmann MP;
XX
XX WPI; 2003-567953/53.
XX
XX New array of nucleic acid probes, useful for in situ hybridization, in PT Southern, Northern or dot-blot hybridization to identify or detect the PT sequence or specific mutations of any gene.
XX
XX Claim 1; SEQ ID NO 92448; 9pp; English.
XX
XX The invention discloses a microarray comprising a plurality of nucleic CC acid probes including one of 2,018,500 fully defined sequences, or its CC acid probes including one of 2,018,500 fully defined sequences, or its CC perfect match, perfect mismatch, antisense match or antisense mismatch. CC Also disclosed is a method of gene expression analysis. The array is used CC in monitoring gene expression levels by hybridisation to a DNA library, CC in analysis of genetic variation or in hybridisation of tag-labelled CC compounds. The nucleic acid probes are specifically designed for analysis CC of at least one target sequence. The method of analysis comprises CC hybridising at least one or more nucleic acids to at least two or more CC nucleic acid probes and detecting the hybridisation. The nucleic acid CC probes are attached to a solid support. The analysis comprises monitoring CC gene expression levels, identifying diallelic markers or polymorphisms, CC or family members of a gene and a cross-species comparison. Each of the CC nucleic acids further comprises a tag sequence. The array of nucleic acid CC probes is useful in in situ hybridisation, in Southern, Northern or dot- CC blot hybridisation to identify or detect the sequence or specific CC mutations of any gene, in mapping the 5' termini of mRNA molecules by CC primer extensions or in screening cDNA or genomic libraries or subclones CC for additional subclones containing segments of DNA that have been CC isolated and previously sequenced. The sequence presented is one of the CC nucleic acid probes incorporated in the microarray. Note: The sequence CC data for this patent can also be obtained in electronic format directly CC from USPTO at seqdata.uspto.gov/sequence.html
XX
XX Sequence 25 BP; 4 A; 5 C; 7 G; 9 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3742 TAAAGATCACAACCTCAAGATG 3764
Db 23 TCAAGTCAACAGCTCAAGATG 1
RESULT 1551
ACI12071/c
ID ACI12071 standard; DNA; 25 BP.
XX
XX ACI12071;
XX
XX 13-OCT-2003 (first entry)
XX
XX Human microarray DNA oligonucleotide SEQ ID NO 12062.
XX
XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
KM genetic variation; diallelic marker; polymorphism; human;
XX cross-species comparison.
XX
XX Homo sapiens.
XX
XX US2003104410-A1.
XX
XX 05-JUN-2003.
XX
XX PD

XX 15-MAR-2002; 2002US-00098263.
PF 16-MAR-2001; 2001US-0276759P.
XX (AFPRY-) AFFYMETRIX INC.
XX Miltmann MP;
XX WPI; 2003-567953/53.
DR New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
PS Claim 1; SEQ ID NO 12062; 9pp; English.
XX
XX The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridization to a DNA library,
CC in analysis of genetic variation or in hybridization of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridizing at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridization. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridization, in Southern, Northern or dot-
CC blot hybridization to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 25 BP; 7 A; 5 C; 6 G; 7 T; 0 U; 0 Other;
Query Match 0.2%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 496 AAGAGACATTACACTGTCTAC 518
DB 24 AAGAGTACCTTGACACACTGTCTC 2
RESULT 1552
AC143199
ID AC143199 standard; DNA; 25 BP.
XX
XX AC143199;
AC
XX
DT 13-OCT-2003 (first entry)
XX
XX Human microarray DNA oligonucleotide SEQ ID NO 43190.
DE
XX
XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.
XX
OS Homo sapiens.
XX
XX US2003104410-A1.
PN
XX
XX 05-JUN-2003.
PD
XX
XX 15-MAR-2002; 2002US-00098263.
PF

XX 16-MAR-2001; 2001US-0276759P.
XX (AFPRY-) AFFYMETRIX INC.
XX Miltmann MP;
XX WPI; 2003-567953/53.
DR New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
PS Claim 1; SEQ ID NO 43190; 9pp; English.
XX
XX The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridization to a DNA library,
CC in analysis of genetic variation or in hybridization of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridizing at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridization. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in in situ hybridization, in Southern, Northern or dot-
CC blot hybridization to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 25 BP; 6 A; 5 C; 5 G; 9 T; 0 U; 0 Other;
Query Match 0.2%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4399 CTTGCTTACAAAATGAATT 4421
DB 2 CTTGCTTACAGACGAAATT 24
RESULT 1553
AC183518
ID AC183518 standard; DNA; 25 BP.
XX
XX AC183518;
AC
XX
DT 14-OCT-2003 (first entry)
XX
XX Human microarray DNA oligonucleotide SEQ ID NO 83509.
DE
XX
XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.
XX
OS Homo sapiens.
XX
XX US2003104410-A1.
PN
XX
XX 05-JUN-2003.
PD
XX
XX 15-MAR-2002; 2002US-00098263.
PF
XX
XX 16-MAR-2001; 2001US-0276759P.
PR

XX (AFFY-) AFFYMETRIX INC.
 XX PI Miltmann MP;
 XX DR MPI; 2003-567953/53.
 XX PT New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.
 XX
 PS Claim 1; SEQ ID NO 83509; 9pp; English.
 XX
 CC The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying diallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html
 CC
 SQ Sequence 25 BP; 6 A; 5 C; 6 G; 8 T; 0 U; 0 Other;
 Query Match 0.2%; Score 16.6; DB 1; Length 25;
 Best Local Similarity 82.6%; Pred. No. 1.4e+03;
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 4922 TCAGACTGTTGAGTACTCTC 4944
 DB 3 TCAGAACTGTTGAGTACGCTC 25
 RESULT 1554
 ACCK03814/C
 ID ACCK03814 standard; DNA; 25 BP.
 XX
 AC ACCK03814;
 XX
 DT 14-OCT-2003 (first entry)
 XX
 DE Human microarray DNA oligonucleotide SEQ ID NO 103795.
 XX
 KM EST; ss; probe; expressed sequence tag; microarray; gene expression;
 KM genetic variation; diallelic marker; polymorphism; human;
 KM cross-species comparison.
 XX
 OS Homo sapiens.
 OS
 PN US2003104410-A1.
 XX
 PD 05-JUN-2003.
 XX
 PF 15-MAR-2002; 2002US-00098263.
 XX
 PR 16-MAR-2001; 2001US-0276759P.
 XX
 PA (AFFY-) AFFYMETRIX INC.
 XX

XX
 XX PI Miltmann MP;
 XX DR MPI; 2003-567953/53.
 XX PT New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.
 XX
 PS Claim 1; SEQ ID NO 103795; 9pp; English.
 XX
 CC The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying diallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html
 CC
 SQ Sequence 25 BP; 8 A; 5 C; 7 G; 5 T; 0 U; 0 Other;
 Query Match 0.2%; Score 16.6; DB 1; Length 25;
 Best Local Similarity 82.6%; Pred. No. 1.4e+03;
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 6563 GACAGTTTGACCTGAGATCAT 6585
 DB 24 GACAGTCTCTGACCTGAGATCTT 2
 RESULT 1555
 ACI38951
 ID ACI38951 standard; DNA; 25 BP.
 XX
 AC ACI38951;
 XX
 DT 13-OCT-2003 (first entry)
 XX
 DE Human microarray DNA oligonucleotide SEQ ID NO 38942.
 XX
 KM EST; ss; probe; expressed sequence tag; microarray; gene expression;
 KM genetic variation; diallelic marker; polymorphism; human;
 KM cross-species comparison.
 XX
 OS Homo sapiens.
 OS
 PN US2003104410-A1.
 XX
 PD 05-JUN-2003.
 XX
 PF 15-MAR-2002; 2002US-00098263.
 XX
 PR 16-MAR-2001; 2001US-0276759P.
 XX
 PA (AFFY-) AFFYMETRIX INC.
 XX
 PI Miltmann MP;
 XX

XX
DR WPI; 2003-567953/53.
XX
PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
PS Claim 1; SEQ ID NO 38942; 9pp; English.
XX
CC The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridization to a DNA library,
CC in analysis of genetic variation or in hybridization of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridizing at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridization. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying allelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in situ hybridization, in Southern, Northern or dot-
CC blot hybridization to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 25 BP; 4 A; 8 C; 9 G; 4 T; 0 U; 0 Other;
Query Match 0.2%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2321 TTGTGTGCGAAGACGCATCAC 2343
DB 3 TCGTGTGCGACGACGCGCATCCG 25
RESULT 1556
AC141780
ID AC141780 standard; DNA; 25 BP.
XX
AC AC141780;
XX
DT 13-OCT-2003 (first entry)
XX
DE Human microarray DNA oligonucleotide SEQ ID NO 41771.
XX
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; allelic marker; polymorphism; human;
KW cross-species comparison.
XX
OS Homo sapiens.
XX
PN US2003104410-A1.
XX
PD 05-JUN-2003.
XX
PF 15-MAR-2002; 2002US-00098263.
XX
PR 16-MAR-2001; 2001US-0276759P.
XX
PA (AFY-) AFFYMETRIX INC.
XX
PI Miltmann MP;
XX
DR WPI; 2003-567953/53.

XX
PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
PS Claim 1; SEQ ID NO 41771; 9pp; English.
XX
CC The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridization to a DNA library,
CC in analysis of genetic variation or in hybridization of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
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CC hybridizing at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridization. The nucleic acid
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CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in situ hybridization, in Southern, Northern or dot-
CC blot hybridization to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 25 BP; 8 A; 8 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 0.2%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 214 ATGGAAGCGGACCTCGGAGC 236
DB 2 ATCGAAGCGGACCTCGGAGC 24
RESULT 1557
AC180464/C
ID AC180464 standard; DNA; 25 BP.
XX
AC AC180464;
XX
DT 14-OCT-2003 (first entry)
XX
DE Human microarray DNA oligonucleotide SEQ ID NO 80455.
XX
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; allelic marker; polymorphism; human;
KW cross-species comparison.
XX
OS Homo sapiens.
XX
PN US2003104410-A1.
XX
PD 05-JUN-2003.
XX
PF 15-MAR-2002; 2002US-00098263.
XX
PR 16-MAR-2001; 2001US-0276759P.
XX
PA (AFY-) AFFYMETRIX INC.
XX
PI Miltmann MP;
XX
DR WPI; 2003-567953/53.
PT New array of nucleic acid probes, useful for in situ hybridization, in

CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying allelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
CC
XX
SQ Sequence 25 BP; 7 A; 7 C; 8 G; 3 T; 0 U; 0 Other;
Query Match 0.2%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1331 GACAGAGAGATCACTGCGCTG 1353
Db 3 GACAGAGATGAGCGCTGCGCTG 25
RESULT 1562
ACI70488
ID ACI70488 standard; DNA; 25 BP.
XX
AC ACI70488;
XX
DT 14-OCT-2003 (first entry)
XX
DE Human microarray DNA oligonucleotide SEQ ID NO 70479.
XX
KM EST; ss; probe; expressed sequence tag; microarray; gene expression;
XX genetic variation; allelic marker; polymorphism; human;
XX cross-species comparison.
XX
OS Homo sapiens.
XX
PN US2003104410-A1.
XX
PD 05-JUN-2003.
XX
PF 15-MAR-2002; 2002US-00098263.
XX
PR 16-MAR-2001; 2001US-0276759P.
XX
PA (AFY-) AFFYMETRIX INC.
XX
PI Miltmann MP;
XX
DR WPI; 2003-567953/53.
XX
PT New array of nucleic acid probes, useful for in situ hybridization, in
XX Southern, Northern or dot-blot hybridization to identify or detect the
XX sequence or specific mutations of any gene.
XX
PS Claim 1; SEQ ID NO 70479; 9pp; English.
XX
CC The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,

CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying allelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
CC
XX
SQ Sequence 25 BP; 3 A; 7 C; 4 G; 11 T; 0 U; 0 Other;
Query Match 0.2%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 5659 ATCCTTCTTAGTGGCTCTTGT 5681
Db 2 ACCCTTCTTAGTGGCTCTTGT 24
RESULT 1563
ACI50716
ID ACI50716 standard; DNA; 25 BP.
XX
AC ACI50716;
XX
DT 13-OCT-2003 (first entry)
XX
DE Human microarray DNA oligonucleotide SEQ ID NO 50707.
XX
KM EST; ss; probe; expressed sequence tag; microarray; gene expression;
XX genetic variation; allelic marker; polymorphism; human;
XX cross-species comparison.
XX
OS Homo sapiens.
XX
PN US2003104410-A1.
XX
PD 05-JUN-2003.
XX
PF 15-MAR-2002; 2002US-00098263.
XX
PR 16-MAR-2001; 2001US-0276759P.
XX
PA (AFY-) AFFYMETRIX INC.
XX
PI Miltmann MP;
XX
DR WPI; 2003-567953/53.
XX
PT New array of nucleic acid probes, useful for in situ hybridization, in
XX Southern, Northern or dot-blot hybridization to identify or detect the
XX sequence or specific mutations of any gene.
XX
PS Claim 1; SEQ ID NO 50707; 9pp; English.
XX
CC The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis

CC of at least one target sequence. The method of analysis comprises
CC hybridizing at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying allelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
CC
SQ Sequence 25 BP; 4 A; 6 C; 5 G; 10 T; 0 U; 0 Other;
Query Match 0.2%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 7114 TGAATTACTTCTCTGTGCACAC 7136
DB 2 TGAACCTACTTCTCTGTGCGC 24
RESULT 1564
ACK27118/c
ID ACK27118 standard; DNA; 25 BP.
XX
AC ACK27118;
XX
DT 14-OCT-2003 (first entry)
XX
DE Human microarray DNA oligonucleotide SEQ ID NO 127099.
XX
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; diallelic marker; polymorphism; human;
KW cross-species comparison.
XX
OS Homo sapiens.
XX
PN US2003104410-A1.
XX
PD 05-JUN-2003.
XX
PF 15-MAR-2002; 2002US-00098263.
XX
PR 16-MAR-2001; 2001US-0276759P.
XX
PA (AFYX-) AFFYMETRIX INC.
XX
PI Miltmann M;
XX
DR MPI; 2003-567953/53.
XX
PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
PS Claim 1; SEQ ID NO 127099; 9pp; English.
XX
CC The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridization to a DNA library,
CC in analysis of genetic variation or in hybridization of tag-labeled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridizing at least one or more nucleic acids to at least two or more

CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying allelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
CC
SQ Sequence 25 BP; 8 A; 8 C; 5 G; 4 T; 0 U; 0 Other;
Query Match 0.2%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4627 GGGAGTTGCAACTTCAGTGTGCA 4649
DB 24 GGGAGTTGCAACTTCAGTGTGCA 2
RESULT 1565
ACH64361
ID ACH64361 standard; DNA; 25 BP.
XX
AC ACH64361;
XX
DT 17-OCT-2003 (first entry)
XX
DE DNA target sequence #13497 useful in array for genetic analyses.
XX
KW Gene expression analysis; array; hybridisation; genetic variation;
KW tag-labelled compound; gene family; in situ hybridisation;
KW library screening; Southern hybridisation; northern hybridisation;
KW dot-blot hybridisation; gene sequence; mutation detection;
KW target sequence; probe; PCR; primer; ss.
XX
OS Unidentified.
XX
PN US2003082596-A1.
XX
PD 01-MAY-2003.
XX
PF 08-AUG-2002; 2002US-00215112.
XX
PR 08-AUG-2001; 2001US-0311040P.
XX
PA (MITT/) MITTMANN M.
XX
PI Miltmann M;
XX
DR MPI; 2003-576608/54.
XX
PT New probe array useful e.g. for monitoring gene expression levels, for
PT analyzing genetic variations, or for hybridizing tag-labeled compounds,
PT comprises multiple nucleic acid probes.
XX
PS Claim 1; SEQ ID NO 13497; 9pp; English.
XX
CC The present invention relates to nucleic acid sequences that are
CC complementary to particular genes, and can be used as probes for a
CC variety of analyses such as gene expression analysis. Each probe
CC comprises 9 or more consecutive nucleotides from at least one of 14936
CC nucleotide sequences defined in the patent, or their perfect sense match,
CC sense mismatch, antisense match or antisense mismatch oligonucleotides.
CC The probes may be used in an array comprising at least 10 distinct
CC nucleic acid probes. The array is useful in monitoring gene expression
CC levels by hybridisation to a DNA library, in analysing genetic

CC variations, and in hybridising tag-labelled compounds. The probes are
CC useful for identifying family members of a gene. The probes are also
CC useful in situ hybridisations, in screening cDNA or genomic libraries
CC (or derived subclones) for additional clones containing segments of DNA
CC that have been previously isolated and sequenced, in Southern, northern,
CC or dot-blot hybridisation of genomic DNA to identify or detect the
CC sequence of any gene or detect specific mutations in any gene, and in
CC mapping the 5' termini of mRNA molecules by primer extensions. The
CC nucleic acid sequences of the invention are also useful as PCR primers.
CC The invention provides a large collection of nucleic acid sequences
CC complementary to particular genes with a wide range of analytical uses.
CC ACH50865-ACH65260 represent the target sequences of the invention. Note:
CC The sequence data for this patent was obtained in electronic format
CC directly from the USPTO web site at seqdata.uspto.gov/patidbentry.html
XX

Seq Sequence 25 BP; 10 A; 4 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2282 TCAACTGAAAAGACTACCAG 2304
Db 2 TGAACCTAGAAAAGCTCTACTAG 24

RESULT 1566
ADB99277
ID ADB99277 standard; DNA; 25 BP.
XX
AC ADB99277;
XX
DT 04-DEC-2003 (first entry)
XX
DE Mouse interferon alpha Zcytol3 PCR primer ZC21591.
XX
XX Mouse; ss; PCR; interferon alpha; Zcytol3; immunosuppressive;
KM neuroprotective; antithrombotic; cytostatic; virucide; hepatotropic;
KM antiinflammatory; viral infection; tumour cell proliferation;
KM autoimmune disease; renal cell carcinoma; chronic hepatitis B;
KM hepatitis C; multiple myeloma; multiple sclerosis; atherosclerosis;
KM arteriosclerosis; primer.
XX
XX Mus sp.
OS
XX US2002168378-A1.
PN
XX
PD 14-NOV-2002.
XX
PP 12-SEP-2001; 2001US-00951843.
XX
PR 18-MAR-1999; 99US-0125045P.
XX
PR 23-SEP-1999; 99US-0155739P.
PR 17-MAR-2000; 2000US-00528760.
XX
PA (ZYMO) ZYMOGENETICS INC.
PI
XX Presnell SR, Feldhaus AL, Gao Z;
PI
XX
DR WPI; 2003-755026/71.
XX
XX Novel isolated murine interferon-alpha polypeptide useful for treating
PT autoimmune diseases, renal cell carcinoma, chronic hepatitis B, hepatitis
PT C, multiple myeloma, multiple sclerosis, atherosclerosis.
XX
XX Example 1; SEQ ID NO 10; 48pp; English.

CC The invention relates to an isolated polypeptide comprising the mature
CC form of mouse interferon alpha/Zcytol3 or an amino acid sequence that is
CC 70% identical to the mature or full length Zcytol3. The isolated
CC polypeptide either binds with an antibody, or exhibits anti-viral or anti
CC -proliferative activity. Also included are the encoding polynucleotide
CC (either encoding the full length or mature protein), a (expression)

CC vector comprising the polynucleotide, a recombinant host cell (producing
CC Zcytol3) comprising the expression vector, an anti-Zcytol3 antibody (or
CC antibody fragment), an anti-idiotypic antibody (or fragment) which
CC specifically binds with the anti-Zcytol3 antibody (where the anti-
CC idiotypic antibody or anti-idiotypic antibody fragment possesses anti-viral
CC activity or anti-proliferative activity) and mouse interferon alpha
CC motifs appearing as ADB99283 and ADB99284. Zcytol3 nucleic acid is useful
CC for inhibiting a viral infection of cells or proliferation of tumour
CC cells. Zcytol3 nucleic acid and the antibody are useful for detecting the
CC presence of Zcytol3 gene expression in a biological sample. Zcytol3 is
CC useful for treating autoimmune diseases, renal cell carcinoma, chronic
CC hepatitis B, hepatitis C, multiple myeloma, multiple sclerosis,
CC arteriosclerosis and atherosclerosis. The present sequence is a PCR
CC primer used in the isolation of the cDNA encoding Zcytol3.
XX

Seq Sequence 25 BP; 7 A; 5 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.6; DB 1; Length 25;
Best Local Similarity 82.6%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1921 GGTCGATTACACATCTCTAGT 1943
Db 2 GGTCGATTACGACATCTCTGCT 24

RESULT 1567
ADE82412
ID ADE82412 standard; DNA; 25 BP.
XX
XX ADE82412;
XX
DT 29-JAN-2004 (first entry)
XX
XX Murine interferon-alpha polypeptide, Zcytol3, PCR primer #4.
DE
XX
XX ss; PCR; mouse; interferon-alpha; Zcytol3; cancer; viral infection;
KM autoimmune disease; primer.
XX
XX Mus sp.
OS
XX US2003147851-A1.
PN
XX
PD 07-AUG-2003.
XX
PP 05-FEB-2003; 2003US-00358619.
XX
PR 18-MAR-1999; 99US-0125045P.
XX
PR 23-SEP-1999; 99US-0155739P.
PR 17-MAR-2000; 2000US-00528760.
PR 12-SEP-2001; 2001US-00951843.
XX
PA (PRES/) PRESNELL S R.
PA (FELD/) FELSHAUS A L.
PA (GAOZ/) GAO Z.
PI
XX Presnell SR, Feldhaus AL, Gao Z;
PI
XX
DR WPI; 2003-897514/82.
XX
XX New murine interferon-alpha polypeptide, Zcytol3, useful for preparing a
PT composition for treating cancer, viral infections or autoimmune diseases.
PT composition for treating cancer, viral infections or autoimmune diseases.
XX
XX Example 1; SEQ ID NO 10; 48pp; English.

CC The invention relates to a new isolated murine interferon-alpha
CC polypeptide, Zcytol3. The polypeptide is useful for preparing a
CC composition for treating cancer, viral infections or autoimmune diseases.
CC The present sequence represents a murine interferon-alpha polypeptide,
CC Zcytol3, PCR primer.
XX
XX Sequence 25 BP; 7 A; 5 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.6; DB 1; Length 25;
 Best Local Similarity 82.6%; Pred. No. 1.4e+03;
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1921 GGTGGCATTACACATCTCTAGT 1943
 |||||
 DB 2 GGATGACATTAGCAGCATCTCGT 24

RESULT 1568
 ADA14837/C
 ID ADA14837 standard; DNA; 30 BP.
 AC ADA14837;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Hairpin oligonucleotide, #2, used in an example of the invention.
 XX
 KW Hairpin sensor; hairpin loop; complementary probe; inverse repeat arm;
 KW quenchable fluorescing agent; microarray; semiconductor; nanocrystal;
 KW rhodamine B-labelled dye; detection; gold support; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER= thiol group"
 FT misc_binding 6..25
 FT /*tag= b
 FT /bound_moiety= "Target sequence #2"
 FT /note= "forms a double-stranded region with the target
 FT sequence shown in examples 3, 4 and 5"
 FT modified_base 30
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "OTHER= amino group"
 XX
 PN US2003013109-A1.
 XX
 XX 16-JAN-2003.
 PD
 XX 21-JUN-2002; 2002US-00176055.
 PF
 XX 21-JUN-2001; 2001US-0299460P.
 PR
 XX (BALU/) BALLINGER C T.
 PA (LOCA/) LOCASCIO M.
 PA (LAND/) LANDRY D P.
 XX
 PI Ballinger CT, Locascio M, Landry DP;
 XI
 DR WPI; 2003-596312/56.
 XX
 PT Hairpin sensor useful for detecting a target nucleotide sequence in a
 PT sample, comprises a hairpin loop assembly including a complementary probe
 PT and a quenchable fluorescing agent.
 XX
 PS Example 3; Page 11; 16pp; English.
 XX
 CC The invention discloses a hairpin sensor comprising a hairpin loop
 CC assembly including a complementary probe positioned between a first
 CC inverse repeat arm and a second inverse repeat arm, and a quenchable
 CC fluorescing agent joined, directly or indirectly, to the end of the
 CC second inverse repeat arm of the hairpin loop assembly opposite the
 CC complementary probe. Also claimed is a microarray comprising the hairpin
 CC sensor, where the end of the first inverse repeat arm opposite the
 CC complementary probe is bound, directly or indirectly, to a support, a kit
 CC for detecting a target nucleotide sequence in a sample comprising the
 CC hairpin sensor, and a support, and a hairpin sensor system, in which the
 CC particle is conductive or semi-conductive, including at least one of the

CC above hairpin sensor assemblies. The hairpin sensor further comprises a
 CC functional group joined to the end of the first inverse repeat arm
 CC opposite the complementary probe, or first spacer opposite the first
 CC inverse repeat arm, the functional group selected from amino, carboxyl,
 CC thiol and hydroxyl. Further, the sensor comprises a ligand positioned
 CC between the second inverse repeat arm and the quenchable fluorescing
 CC agent, where the ligand is selected from mercapto, hydroxyl, amino, the
 CC nitrile and carboxyl, carboxylic acid, organic acid and amino acid. The
 CC second spacer is positioned between the second inverse repeat arm and the
 CC quenchable fluorescing agent which comprises a semiconductor nanocrystal
 CC or rhodamine B-labelled dye. Within the microarray the support is capable
 CC of accepting a charge. At least one hairpin sensor comprises two or more
 CC hairpin sensors. The two or more hairpin sensors include complementary
 CC probes that are the same or different and respective quenchable
 CC fluorescing agents that are the same or different. The two or more
 CC hairpin sensors are arranged in a spatially-defined pattern. The sensor
 CC and system are useful for detecting a target nucleotide sequence in a
 CC sample. Further, the method involves identifying the target nucleotide
 CC sequence by the location of the complementary probe to which the target
 CC nucleotide sequence binds. The two or more hairpin sensors include
 CC complementary probes or quenchable fluorescing agents, that are
 CC different. The sequence presented is the hairpin oligonucleotide, #2,
 CC used in an example of the invention.
 XX
 SQ Sequence 30 BP; 1 A; 4 C; 4 G; 21 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.6; DB 1; Length 30;
 Best Local Similarity 82.6%; Pred. No. 1.7e+03;
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4017 GAGAAAAAGAGAGAAAAA 4039
 |||||
 DB 28 GAGAAAAAGAGAGAAAAA 6

RESULT 1569
 ABN83375
 ID ABN83375 standard; DNA; 32 BP.
 XX
 AC ABN83375;
 XX
 DT 15-AUG-2002 (first entry)
 XX
 DE Mononucleotide repeat locus BAT26 probe #2.
 XX
 KW Mononucleotide repeat locus; human; BAT26; probe; microsatellite; tumour;
 KW ss.
 XX
 OS Homo sapiens.
 XX
 OS
 XX
 FH Key Location/Qualifiers
 FT modified_base 1
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "Labelled with LightCycler fluorescent dye LC-Red-
 FT 640"
 XX
 PN EP1207210-A1.
 XX
 PD 22-MAY-2002.
 XX
 XX 13-NOV-2001; 2001EP-00126930.
 PF
 XX 15-NOV-2000; 2000EP-00124897.
 PR
 XX (HOFF) ROCHE DIAGNOSTICS GMBH.
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX
 PI Dietmaier W;
 XX
 DR WPI; 2002-437469/47.
 XX
 PT Analyzing repeat sequences in DNA using a probe which hybridizes to

PT adjacent repetitive and non-repetitive regions and determining hybrid
PT melting point is useful to detect microsatellite instability such as in
PT hereditary cancer.
XX
XX
PS Claim 16; Page 7; 19pp; English.
XX
CC The present invention relates to a method for analysing a target nucleic
CC acid consisting of repetitive and non-repetitive sequences. The method
CC comprises hybridising a polynucleotide probe comprising a segment
CC complementary to a non-repetitive region and a segment complementary to
CC an adjacent repetitive region, where the second segment consists of a
CC defined number of repeats, and determining the melting point temperature
CC of the hybrid. The method is used to analyse microsatellites, especially
CC microsatellite instability, particularly as a means for detecting
CC hereditary tumours. Alternatively, the method is used to identify an
CC individual in a population. The present sequence is a probe for
CC Mononucleotide repeat locus BAT26, and was used to illustrate the
CC invention
XX
SQ Sequence 32 BP; 27 A; 1 C; 2 G; 2 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 16.6; DB 1; Length 32;
Best Local Similarity 71.0%; Pred. No. 1.8e+03;
Matches 22; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 4004 TTAGCTTAATGAGAAAAAGAGAAAA 4034
DB 1 TCAGTAAAAAATAAAAAAAAAAAAAA 31
RESULT 1570
AAQ25501/c
ID AAQ25501 standard; DNA; 18 BP.
XX
XX AAQ25501;
XX AC 25-MAR-2003 (revised)
XX DT 07-DEC-1992 (first entry)
XX DE Purine rich HUMNFR target duplex sequence.
XX
XX Target; human tumour necrosis factor receptor mRNA; AIDS; triplex; HIV;
XX hepatitis; malignancy; inflammation; ds.
XX
XX Synthetic.
XX
XX WO9209705-A1.
XX
XX 11-JUN-1992.
XX PD 25-NOV-1991; 91WO-US008811.
XX PF 23-NOV-1990; 90US-00617907.
XX PR 18-JAN-1991; 91US-00643382.
XX PR 08-APR-1991; 91US-00683420.
XX PR 17-APR-1991; 91US-00686544.
XX PR 17-APR-1991; 91US-00686546.
XX PR 17-APR-1991; 91US-00686547.
XX PR 27-SEP-1991; 91US-00766733.
XX
XX (GILE-) GILEAD SCI INC.
XX
XX Froehner B, Krawczyk S, Matteucci MD, Milligan J;
XX
XX WPI; 1992-217083/26.
XX
XX New oligomers contg. modified bases - which form a triplex with G-C
XX doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
XX herpes malignancy and inflammation.
XX
XX Claim 11; Page 64; 77pp; English.
XX
XX The sequence depicts a HUMNFR (tumour necrosis factor receptor) mRNA

CC sequence beginning at nucleotide 2354. The sequence is a viral duplex
CC 'sequence contg. a putine-rich region concentrated on one chain of the
CC duplex. The sequence may be prep'd. by standard DNA synthesis. The HUMNFR
CC duplex sequence is used as a target for novel oligomers which are capable
CC of forming a triplex at physiological pH by coupling into the major
CC groove of the DNA duplex. Three such oligomers TNFR 941-32 are capable of
CC forming a triplex with this sequence. The oligomers are used in the
CC treatment of inflammation. Similar oligomers may be used to target viral
CC DNA duplexes specific for HIV, herpes and other viruses. The triple
CC helices form under mild conditions thus assays may be carried out without
CC subjecting the test specimen to harsh conditions. The oligomer is able to
CC inhibit gene expression, as verified by in vitro systems. See also
CC AAQ25452-25500 and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 18 BP; 16 A; 0 C; 2 G; 0 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 9.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4463 CTTTTTTTTTTTTTTTTT 4480
DB 18 CTTTTTTTTTTCTTTT 1
RESULT 1571
AA63292/c
ID AA63292 standard; RNA; 18 BP.
XX
XX AA63292;
XX AC 16-JUL-1999 (first entry)
XX DT
XX DE Delta-9 desaturase hairpin ribozyme substrate SEQ ID NO:1167.
XX
XX Maize; corn; Zea mays; delta-9 desaturase; GBS; target; substrate;
XX granule bound starch synthase; hammerhead ribozyme; hairpin ribozyme;
XX modulation; gene expression; transgenic plant; cleavage; canola plant;
XX caffeine synthesis; coffee plant; nicotine production; tobacco;
XX fruit ripening; flower pigmentation; lignin production; ss.
XX
XX Zea mays.
XX
XX WO9710328-A2.
XX PN 20-MAR-1997.
XX PD 12-JUL-1996; 96WO-US011689.
XX PF 13-JUL-1995; 95US-0001135P.
XX PR
XX (RIBO-) RIBOZYME PHARM INC.
XX (IDWC) DOWELANCO.
XX
XX Zwick MG, Edington BE, Mcswigen JA, Merlo PAO, Guo L, Skokut TA;
XX Young SA, Folkerts O, Merlo DJ;
XX WPI; 1997-202224/18.
XX
XX ribozyme which modulates plant gene expression - preferably modulates
XX expression of DELTA-9 desaturase or granule bound starch synthase in
XX maize or canola.
XX
XX Claim 40; Page 93; 155pp; English.
XX
XX The present invention describes an enzymatic nucleic acid molecule (I)
XX with RNA cleaving activity, which modulates the expression of a plant
XX gene. Also described is a gene comprising a cDNA sequence encoding maize
XX Delta-9 desaturase. (I) can be used to modulate expression of a gene,
XX preferably Delta-9 desaturase or a granule bound starch synthase (GBSS)
XX gene, in a plant (preferably a maize or canola plant). (I) can be used to
XX modulate caffeine synthesis in a coffee plant, nicotine production in a

CC tobacco plant, fruit ripening processes in an apple, tomato, pear, plum
 CC or peach plant, flower pigmentation in a rose, petunia, chrysanthemum or
 CC marigold plant or lignin production in a tobacco, aspen, poplar or pine
 CC plant

SQ Sequence 18 BP, 1 A; 11 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.4; DB 1; Length 18;
 Best Local Similarity 94.4%; Pred. No. 9.7e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 65 GCTGCGGCGGCGGCGG 82
 |||||
 DB 18 GCTGCGGCGGCGGCGG 1

RESULT 1572

AAK18373
 ID AAK18373 standard; DNA; 18 BP.

XX AAK18373;

XX 11-MAY-1999 (first entry)

DE RT-PCR primer of the invention SEQ ID 14.

XX RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.

OS Synthetic.

XX JP11032765-A.

XX 09-FEB-1999.

PF 18-UTL-1997; 97GP-00208312.

PR 18-JUL-1997; 97GP-00208312.

PA (TAKI) TAKARA SHUZO CO LTD.

DR WPI; 1999-183822/16.

PT Peptides having at least two new nucleotides - useful as primers in RT-PCR.

PS Disclosure; Page 11; 19pp; Japanese.

CC This sequence represents a primer of the invention. The invention relates
 CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
 CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
 CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
 CC natural number indicating the repetition of alpha; beta, delta = V or N;
 CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
 CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
 CC repetition of gamma, in which thymine expressed by gamma is composed of
 CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
 CC useful as primers for RT-PCR and determination of base sequences. The new
 CC sequences allow for reproductive and highly efficient analysis of gene
 CC sequences

SQ Sequence 18 BP, 1 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.4; DB 1; Length 18;
 Best Local Similarity 94.4%; Pred. No. 9.7e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4481
 |||||
 DB 1 TTTT TTTT TTTT TTTT TTTT 18

RESULT 1573

AAA63144/c

ID AAA63144 standard; DNA; 18 BP.

XX AAA63144;

XX 07-DEC-2000 (first entry)

DE Antisense oligonucleotide for use in RNase H mapping assay SEQ ID NO: 48.

XX Immunoregulator; antisense oligonucleotide; cancer; tumour cell vaccine;
 KW rheumatoid arthritis; autoimmune disease; diabetes mellitus; thyroiditis;
 KW ss.

XX Mus sp.

XX WO200034467-A1.

XX 15-JUN-2000.

PF 24-NOV-1999; 99WO-US028096.

PR 04-DEC-1998; 98US-00205995.

PA (ANTI-) ANTIGEN EXPRESS INC.

PI Xu M, Qiu G, Humphreys R;

DR WPI; 2000-423417/36.

PT Cancer cell vaccine for treating malignancies, autoimmune disorders and
 PT isolating autodeterminant peptides comprises a regulator of invariant
 PT chain protein expression or immunoregulatory function.

PS Claim 21; Page 47; 94pp; English.

CC The present sequence is an antisense oligonucleotide which was used in an
 CC RNase mapping experiment. This enables the identification of sites within
 CC the 3' RNA strand which hybridise to antisense DNA. These sites can then
 CC be used as targets for antisense strands which may, using gene therapy,
 CC be used as tumour cell vaccines (for example to treat carcinomas,
 CC melanoma, leukaemia, lymphomas, stomach, breast, colon or rectum, lung,
 CC prostate, bladder, pancreas, brain and ovarian cancers), or they can be
 CC used to treat autoimmune diseases including rheumatoid arthritis,
 CC diabetes mellitus and thyroiditis

SQ Sequence 18 BP; 0 A; 5 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.4; DB 1; Length 18;
 Best Local Similarity 94.4%; Pred. No. 9.7e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7413 CAGCAGCAGCAGCAGCAG 7430
 |||||
 DB 18 CAGCAGCAGCAGCAGCAG 1

RESULT 1574

ID AAK13935
 ID AAK13935 standard; DNA; 18 BP.

XX AAK13935;

DT 21-MAY-2002 (first entry)

DE 5'-PCR primer used to produce single pattern characteristic by HaeII.

XX Identification of transcribed gene; mRNA profile; gene expression;
 KW cellular process; fingerprinting; susceptibility to external factor;
 KW development; disease; PCR; primer; ss.

OS Synthetic.

XX WO2000208461-A2.

PD		31-JAN-2002.
PF	XX	23-JUL-2001; 2001WO-IB001539.
PR	XX	21-JUL-2000; 2000GB-00018016.
PR	XX	21-JUL-2000; 2000US-0219925P.
PA	XX	(GLOB-) GLOBAL GENOMICS AB.
P1	XX	Linnarsson S, Ernfors P, Bauren G;
DR	XX	WPI; 2002-217065/27.
PT	XX	Providing mRNA profile, by generating two independent patterns
PT	XX	characteristic of sample mRNA population, analyzing patterns, comparing
PT	XX	gene expression by cell types under varied conditions, and identifying
PS	XX	genes.
PS	XX	Disclosure; Fig 1; 67pp; English.
CC	XX	The present invention relates to a method for providing a profile of mRNA
CC	XX	molecules present in a sample. The method comprises generating two
CC	XX	independent patterns characteristic of the population of mRNA molecules
CC	XX	expressed in the sample and analysing the patterns using a combinatorial
CC	XX	algorithm, comparing gene expression by different or same cell types
CC	XX	under different conditions, and identifying genes having a role in
CC	XX	various cellular processes. The method is useful for the analysis and
CC	XX	identification of transcribed genes, and fingerprinting. The method can
CC	XX	be used to identify genes which play a role in determining various
CC	XX	cellular processes, including susceptibility to external factors,
CC	XX	development, and disease. The present sequence for a PCR primer is used
CC	XX	in the production of a single pattern characteristic of a sample,
CC	XX	employing a Type II restriction enzyme (I.e. HaeII) in the methods of the
SQ	XX	present invention
		Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;
OY		Query Match 0.2%; Score 16.4; DB 1; Length 18;
		Best Local Similarity 94.4%; Pred. No. 9, 7e+02;
Dd		Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0
		4467 TTTTTTTTTTTTTTTTGG 4484
		1 TTTTTTTTTTTTTTCG 18
RESULT 1575		
ID	ABK99284/C	
ID	ABK99284 standard; RNA; 18 BP.	
XX	AC	
XX	ABK99284;	
DT	21-OCT-2002 (first entry)	
DE	Hepatitis C virus (HCV) NS5B replicase RNA synthesis template #14.	
XX	XX	
KM	Hepatitis C virus; HCV; NS5B replicase; ss; RNA polymerase.	
OS	Synthetic.	
XX	FN	US2002064771-A1.
XX	PD	30-MAY-2002.
PF	06-APR-2001; 2001US-00828034.	
XX	XX	
PR	07-APR-2000; 2000US-0195852P.	
XX	XX	
PA	(ZHON/) ZHONG W.	
PA	(HONG/) HONG Z.	
PA	(FERR/) FERRARI E.	
XX	XX	
P1	Zhong W, Hong Z, Ferrari E;	

XX	WPI; 2002-582330/62.
XX	
XX	Novel replicase complex comprising hepatitis C virus NS5B replicase, a 3
XX	nucleotide-long template to which a 2 nucleotide-long primer is annealed,
XX	and template and primer which do not form a stable duplex in the absence
XX	of HCV NS5B.
XX	
XX	Example; Page 6, 17pp; English.
XX	
XX	The invention relates to a replicase complex comprising a hepatitis C
XX	virus (HCV) NS5B replicase protein, a linear nucleic acid template and a
XX	complementary nucleic acid primer which is annealed to the 3' terminus of
XX	the template, where the template is at least three nucleotides and the
XX	primer is two or three nucleotides, and the template and primer do not
XX	form a stable duplex in solution in the absence of the HCV NS5B protein.
XX	The complex is useful for detecting HCV replicase activity and permits
XX	establishment of sensitive RNA-dependent RNA polymerase assays to screen
XX	and evaluate antiviral inhibitors and to improve the specificity and
XX	efficacy of the inhibitors. The complex is also useful in the development
XX	of a reliable system for determining kinetic and thermodynamic constants
XX	of HCV NS5B-catalysed nucleotide incorporation and investigation of
XX	mechanistic inhibitors for mis-incorporation or chain termination.
XX	Specifically, the short RNA template and primer pairs are useful in
XX	screening assays which are used for determining kinetic, thermodynamic
XX	and mechanistic properties of NS5B replication and ultimately in the
XX	development of inhibitors of NS5B. Newly identified inhibitors of
XX	replicase activity may be used for developing anti-HCV pharmaceuticals.
XX	Sequences ABR9271-ABR9296 represent HCV NS5B replicase RNA synthesis
XX	templates
XX	
SQ	Sequence 18 BP; 13 A; 3 C; 1 G; 0 T; 1 U; 0 Other;
	Query Match 0.2%; Score 16.4; DB 1; Length 18;
	Best Local Similarity 94.4%; Pred. No. 9.7e+02;
	Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0
QY	4460 GGACTTTT TTTT TTTT TTTT 4477
DB	18 GGACTGTT TTTT TTTT TTTT 1
RESULT 1576	
ABA93493	
ID	ABA93493 standard; DNA; 18 BP.
XX	
AC	ABA93493;
XX	
DT	25-APR-2002 (first entry)
XX	
DE	GAGA-B receptor 1a (gb1a) antisense oligonucleotide.
XX	
KM	Identification; gamma-amino-butyric acid; GABA, GABA-B receptor;
KW	gamma-amino-butyric acid B receptor; epilepsy; pain syndrome;
KW	antisense oligonucleotide; ss.
XX	
OS	Home sapiens.
XX	
OS	Synthetic.
XX	
FN	WO200198779-A2.
XX	
PD	27-DEC-2001.
XX	
PF	19-JUN-2001; 2001WO-CA000909.
XX	
FR	19-JUN-2000; 2000US-0212426P.
PR	24-APR-2001; 2001US-0285969P.
XX	
PA	(MERI) MERCK FROST CANADA & CO.
XX	
PI	Ng G;
XX	
DR	WPI; 2002-062650/08.

```
XX Identifying agonists of GABA(B) receptors, useful for treating epilepsy
PT and certain pain syndromes, comprises determining that the substance is
PT not an agonist of GABA(B) receptors with gb-1b or gb-1c subunits.
XX
XX Example 7; Page 79; 142pp; English.
XX
XX The present invention describes a method for identifying gb-1a subtype-
CC specific agonists of the gamma-amino-butyric acid B (GABA-B) receptor,
CC comprising determining the substance is an agonist of GABA-B receptors
CC with a gb-1a subunit, and is not an agonist of GABA-B receptors
CC comprising gb-1b or gb-1c subunits. The method can be used for
CC identifying agonists of GABA-B receptors which are heteromers of gb-1a
CC and gb2 subunits. The substances are useful for treating conditions such
CC as epilepsy, and pain syndromes. The method identifies substances that
CC are not agonists of GABA-A receptors, which exhibit more selectivity for
CC effector pathways and distinct mechanisms of action compared to other
CC compounds such as baclofen. The present sequence represents a GABA-B
CC receptor 1a (gb1a) antisense oligonucleotide, which is used in an example
CC from the present invention
XX
XX Sequence 18 BP; 6 A; 7 C; 5 G; 0 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 9.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7410 CAGCAGCAGCAGCAGCAG 7427
DB 1 CAGCAGCAGCAGCAGCAG 18
RESULT 1577
AB281780
ID AB281780 standard; DNA; 18 BP.
XX
XX AB281780;
AC
XX
XX 11-JUN-2003 (first entry)
DT
XX
XX Huntington's disease gene mutated exon 1 region.
DE
XX
XX Huntington's disease; noctropic; anticonvulsant; huntingtin; human;
KW
XX gene therapy; mutant; ds.
XX
XX Homo sapiens.
OS
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH mutation replace(5,A)
FT /*tag= a
FT
XX
XX WO2003013437-A2.
FN
XX
XX 20-FEB-2003.
PD
XX
XX 07-AUG-2002; 2002MO-US025352.
PF
XX
XX 07-AUG-2001; 2001US-0310757P.
PR
XX 08-AUG-2001; 2001US-0310770P.
PR
XX 08-AUG-2001; 2001US-0310889P.
PR
XX 04-DEC-2001; 2001US-0337219P.
XX
XX (UNDE ) UNIV DELAWARE.
PA
XX Kmiec EB, Parekh-Olmedo H;
PI
XX
XX WPI; 2003-256478/25.
DR
XX
XX New single stranded oligonucleotides comprising a DNA domain having at
PT least one mismatch with respect to the genetic sequence of the
PT Huntington's disease gene to be altered, useful for treating or
PT preventing Huntington's disease.
```

```
XX
XX Example 7; Fig 20; 133pp; English.
XX
XX The present sequence is that of a portion of a mutated glutamine (CAG)
CC triplet repeat region of exon 1 of the human Huntington's disease (HD)
CC gene (see also AB281760). The triplet repeat region is mutated following
CC treatment with single-stranded phosphorothioate-containing HD gene-
CC targeted oligonucleotide HD3S/52 (see AB281756). The second glutamine
CC (CAG) repeat triplet is converted to CTG, creating a restriction fragment
CC length polymorphism site that enables cleavage by PvuII. HD3S/25 is an
CC example of oligonucleotides of the invention for targeted alteration of
CC the HD gene. Such oligonucleotides can be used for the treatment or
CC prevention of HD
XX
XX Sequence 18 BP; 5 A; 6 C; 6 G; 1 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 9.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7413 CAGCAGCAGCAGCAGCAG 7430
DB 1 CAGCTGCAGCAGCAGCAG 18
RESULT 1578
AB281779
ID AB281779 standard; DNA; 18 BP.
XX
XX AB281779;
AC
XX
XX 11-JUN-2003 (first entry)
DT
XX
XX Huntington's disease gene mutated exon 1 region.
DE
XX
XX Huntington's disease; noctropic; anticonvulsant; huntingtin; human;
KW
XX gene therapy; mutant; ds.
XX
XX Homo sapiens.
OS
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH mutation replace(5,A)
FT /*tag= a
FT
XX
XX WO2003013437-A2.
FN
XX
XX 20-FEB-2003.
PD
XX
XX 07-AUG-2002; 2002MO-US025352.
PF
XX
XX 07-AUG-2001; 2001US-0310757P.
PR
XX 08-AUG-2001; 2001US-0310770P.
PR
XX 08-AUG-2001; 2001US-0310889P.
PR
XX 04-DEC-2001; 2001US-0337219P.
XX
XX (UNDE ) UNIV DELAWARE.
PA
XX Kmiec EB, Parekh-Olmedo H;
PI
XX
XX WPI; 2003-256478/25.
DR
XX
XX New single stranded oligonucleotides comprising a DNA domain having at
PT least one mismatch with respect to the genetic sequence of the
PT Huntington's disease gene to be altered, useful for treating or
PT preventing Huntington's disease.
XX
XX Example 7; Fig 20; 133pp; English.
XX
XX The present sequence is that of a portion of a mutated glutamine (CAG)
CC triplet repeat region of exon 1 of the human Huntington's disease (HD)
CC gene (see also AB281760). The triplet repeat region is mutated following
CC treatment with single-stranded phosphorothioate-containing HD gene-
```



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ACF36364
ID   ACF36364 standard; DNA; 18 BP.
XX
XX
AC   ACF36364;
XX
XX
DT   04-DEC-2003 (first entry)
XX
DE   Nucleotide sequence of a double stranded product DNA.
XX
XX
KM   Nucleic acid manipulation; mRNA profiling; polymerase chain reaction;
XX   electrophoresis; type II restriction enzyme; HaeII; ds.
XX
OS   Synthetic.
XX
XX
PN   WO2003064691-A2.
XX
PD   07-AUG-2003.
XX
PF   28-JAN-2003; 2003WO-IB000843.
XX
PR   29-JAN-2002; 2002US-0352215P.
XX
PA   (GLOB-) GLOBAL GENOMICS AB.
XX
PI   Linnarsson S, Ernfora P, Bauren G, Metsis A, Pihlak A;
XX   Montelius A;
XX
DR   WPI; 2003-618365/58.
XX
XX
PT   Producing a population of double-stranded product DNA molecules, useful
XX   for mRNA profiling, comprises amplification by nested polymerase chain
XX   reaction.
XX
PS   Example; Fig 1; 105pp; English.
XX
CC   The invention relates to producing a population of double-stranded
CC   product DNA molecules comprising amplification by a nested PCR method.
CC   The method is useful in profiling mRNA transcribed in a system under
CC   investigation. The oligonucleotides are used as size standards in
CC   electrophoresis, and as internal controls allowing for calculation of
CC   relative amounts of material present. The present sequence represents a
CC   double stranded product DNA, which aids in outlining an approach to
CC   production of a single pattern characteristic of a sample, employing a
CC   type II restriction enzyme (HaeII)
XX
SQ   Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;
XX
Query Match      0.2%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 9.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY      4467 TTTT TTTT TTTT TTTT TTTT G 4484
Db      1 TTTT TTTT TTTT TTTT TTTT CG 18

RESULT 1582
ADCG9951
ID   ADCG9951 standard; DNA; 18 BP.
XX
XX
AC   ADCG9951;
XX
XX
DT   18-DEC-2003 (first entry)
XX
DE   Primer oligo used for analysing CpG islands in genomic DNA (SeqID 440).
XX
XX   PCR; primer; ss; lung cell proliferative disorder; CpG dinucleotide;
XX   adenocarcinoma; squamous cell carcinoma; cytostatic; probe; PNA-oligomer;
XX   cytosine methylation state.
XX
OS   Unidentified.
XX
XX   WO2003052135-A2.
XX

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XX
XX
PD   26-JUN-2003.
XX
XX
PF   10-DEC-2002; 2002WO-EP014026.
XX
XX
PR   14-DEC-2001; 2001DE-01061625.
XX
XX
PA   (EPIC-) EPIGENOMICS AG.
XX
XX
PI   Burger M, Field JK, Genc B, Lilioglou T, Lipscher E, Maier S;
XX   Nimrich I;
XX
DR   WPI; 2003-533029/50.
XX
XX
PT   Detecting and differentiating cytosine methylation state of genomic DNA,
XX   useful for diagnosing, treating prognosticating and/or monitoring lung
XX   cell proliferative disorders e.g. adenocarcinoma and squamous cell
XX   carcinoma.
XX
PS   Claim 15; SEQ ID NO 440; 58pp; English.
XX
XX
CC   This invention relates to a novel method for detecting and
XX   differentiating between lung cell proliferative disorders associated with
XX   at least one gene and/or their regulatory regions. Specifically, it
XX   refers to a method comprising contacting a target nucleic acid in a
XX   biological sample with at least one reagent, wherein the reagent is able
XX   to distinguish between methylated and non-methylated CpG dinucleotides
XX   present in the target DNA. As such, it is possible to further
XX   differentiate and diagnose medical conditions including adenocarcinoma
XX   and squamous cell carcinoma, and their respective adjacent lung tissue.
XX   The present invention describes cytosine methylation and PNA-oligomers
XX   that are useful as probes for determining the cytosine methylation state
XX   or single nucleotide polymorphisms (SNPs) of the target sequence. This
XX   oligonucleotide sequence is a primer oligomer used for the analysis of
XX   CpG positions within genomic DNA, used in an exemplification of the
XX   invention.
XX
SQ   Sequence 18 BP; 2 A; 1 C; 7 G; 8 T; 0 U; 0 Other;
XX
Query Match      0.2%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 9.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY      6672 TTGGGCGACGTTATTTT 6689
Db      1 TTGGGCGACGTTATTTT 18

RESULT 1583
AAA83188/C
ID   AAA83188 standard; DNA; 19 BP.
XX
XX
AC   AAA83188;
XX
XX
DT   04-DEC-2000 (first entry)
XX
DE   cdk7 ribozyme binding site #109.
XX
XX   Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX   Mammalia.
XX
OS   Mammalia.
XX
XX
PN   WO200032765-A2.
XX
XX
PD   08-JUN-2000.
XX
XX
PF   06-DEC-1999; 99WO-US028772.
XX
XX
PR   04-DEC-1998; 98US-0110954P.
XX
XX
PA   (IMMU-) IMMUSOL INC.
XX
XX   Tritz R, Welch PJ, Barber JR, Robbins JW;
XX

```

XX
DR WPI; 2000-412314/35.
XX
PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT PCNA and Cyclin B1.
XX
PS Disclosure; Page 57; 109pp; English.
XX
CC The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AA82415 to AA86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells. The
CC ribozyme is resistant to endonuclease activity and hence is efficient in
CC restenosis treatment
XX
SQ Sequence 19 BP; 2 A; 7 C; 7 G; 3 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2642 GGGCAGATACCACTCG 2659
DB 18 GGGCCGATACCACTCG 1
XX
RESULT 1584
AAZ75763
ID AAZ75763 standard; DNA; 19 BP.
XX
AC AAZ75763;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker downstream amplification primer SEQ ID NO:10119.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
XX Homo sapiens.
OS
XX
XX WO954500-A2.
XX
XX 28-OCT-1999.
XX
XX 21-APR-1999; 99WO-IB000822.
XX
XX 21-APR-1999; 98US-0082614P.
XX
XX 23-NOV-1998; 98US-0109732P.
XX
XX (GEST) GENSET.
XX
XX Cohen D, Blumenfeld M, Chumakov I;
PI
XX WPI; 2000-013267/01.
XX
XX Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
PS Claim 8; Page 2388; 2745pp; English.
XX
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies

CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID Nos 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence listing from the
CC present invention
XX
SQ Sequence 19 BP; 10 A; 1 C; 6 G; 2 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6181 AAGAGTGTAGAGAGAGA 6198
DB 1 AAAAGTGTAGAGAGAGA 18
XX
RESULT 1585
AAH58350/C
ID AAH58350 standard; DNA; 19 BP.
XX
AC AAH58350;
XX
DT 10-SEP-2001 (first entry)
XX
DE Cell-cycle dependent kinase cdk7 ribozyme binding site SEQ ID NO:774.
XX
KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW recognition site; target; ribozyme binding site; eye disease; vulnery;
KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
KW antiproliferative; dermatological; antiseborrheic; antidiabetic; vitruide;
KW antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW sickle cell retinopathy; ss.
XX
XX Homo sapiens.
OS
XX
XX Synthetic.
XX
XX WO200130362-A2.
XX
XX 03-MAY-2001.
XX
XX 26-OCT-2000; 2000WO-US029500.
XX
XX 26-OCT-1999; 99US-0161532P.
XX
XX (IMMU-) IMMUSOL INC.
XX
XX Robbins JM, Triltz R;
PI
XX WPI; 2001-300427/31.
XX
XX Treating proliferative skin or eye diseases and scarring, using ribozymes
PT that cleave RNA encoding cytokines involved in inflammation, matrix
PT metalloproteinases, growth factors and cell-cycle dependent kinases.
XX
XX Example 1; Page 128; 408pp; English.
XX
CC The present invention describes a method for treating a proliferative
CC skin or eye disease and scarring. The method involves administering a
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC dependent kinase, growth factor or a reductase, or administering a
CC nucleic acid molecule (II) comprising a promoter operably linked to a
CC nucleic acid segment encoding (I). (I) can have antiproliferative,
CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,

CC ophthalmological, vulnery, keratolytic and virucide activities, and
 CC cleaves RNA encoding cytokine involved in inflammation. (1) can be used
 CC in gene therapy. (1) and (II) are useful for treating proliferative skin
 CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
 CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
 CC also be used for treating proliferative eye diseases such as diabetic
 CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
 CC prematurity and retinal detachment, and for treating and preventing
 CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
 CC scar. AH57577 to AH62099 represent sequences used in the
 CC exemplification of the present invention

SQ Sequence 19 BP; 2 A; 7 C; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.4; DB 1; Length 19;
 Best Local Similarity 94.4%; Pred. No. 1e+03; Mismatches 1; Indels 0; Gaps 0;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2642 GGGCAGATACCACTGG 2659
 DB 18 GGGCCGATACCACTGG 1

RESULT 1586
 ADE29544
 ID ADE29544 standard; RNA; 19 BP.
 AC ADE29544;
 DT 29-JAN-2004 (first entry)
 DE Mitogen activated protein kinase siNA oligonucleotide SEQ ID NO:166.
 XX short interfering nucleic acid; siNA; downregulation; inhibition;
 KM mitogen-activated protein kinase; MAP kinase; MAPK; RNA interference;
 KM cytosolic; anorectic; antidiabetic; antinflammatory; antiseptic;
 KM immunosuppressive; antibacterial; antirheumatic; antiarthritic;
 KM antipsoriatic; gastrointestinal; obesity; diabetes; tumour;
 KM inflammatory disease; asthma; septic shock; rheumatoid arthritis;
 KM psoriasis; inflammatory bowel disease; drug screening;
 KM genetic engineering; pharmacogenomic; gene mapping; ss.
 XX
 XX Synthetic.
 OS
 XX
 XX WO2003072590-A1.
 PN
 XX
 PD 04-SEP-2003.
 XX
 XX
 PF 28-JAN-2003; 2003WO-US002510.
 XX
 XX 20-FEB-2002; 2002US-0358580P.
 PR 11-MAR-2002; 2002US-0363124P.
 PR 06-JUN-2002; 2002US-0386782P.
 PR 29-AUG-2002; 2002US-0406784P.
 PR 05-SEP-2002; 2002US-0408378P.
 PR 09-SEP-2002; 2002US-0409293P.
 PR 15-JAN-2003; 2003US-0440129P.
 XX
 XX (SIRN-) SIRNA THERAPEUTICS INC.
 PA
 XX Mcswigen J, Beigelman L, Usman N, Haeblerl P, Chowrira B;
 PI WPI; 2003-689980/65.
 DR
 XX New short interfering nucleic acid, useful e.g. for treatment and
 PT diagnosis of cancer, downregulates expression of mitogen-activated
 PT protein kinase genes.
 XX
 XX Example 3; SEQ ID NO 166; 164pp; English.
 PS
 XX The present invention describes a short interfering nucleic acid (siNA)
 CC that downregulates expression of a mitogen-activated protein kinase
 CC (MAPK) genes by RNA interference. Also described: (1) a method for

CC modulating expression of MAPK genes in cells, tissue explants or
 CC organisms by introduction of siNA; (2) kits for in vitro or in vivo
 CC delivery of siNA; (3) conjugates and/or complexes of siNA; and (4)
 CC vectors that express siNA and cells containing these vectors. MAPK siNA
 CC have cytosolic, anorectic, antidiabetic, antinflammatory,
 CC antiseptic, immunosuppressive, antibacterial, antirheumatic,
 CC antiarthritic, antipsoriatic and gastrointestinal activities. The MAPK
 CC siNA can be used to modulate the expression of MAPK genes, in cells,
 CC tissue explants or organisms, e.g. for treating obesity; diabetes types I
 CC and II; a wide range of tumours, and inflammatory diseases (asthma,
 CC septic shock, rheumatoid arthritis, psoriasis and inflammatory bowel
 CC disease). They can also be used for drug screening; diagnosis; target
 CC identification and validation; genetic engineering; pharmacogenomics;
 CC studying gene function and gene mapping (e.g. of single-nucleotide
 CC polymorphisms). The present sequence represents a MAPK siNA which is used
 CC in the exemplification of the present invention.

SQ Sequence 19 BP; 1 A; 8 C; 5 G; 0 T; 5 U; 0 Other;

Query Match 0.2%; Score 16.4; DB 1; Length 19;
 Best Local Similarity 72.2%; Pred. No. 1e+03; Mismatches 4; Indels 0; Gaps 0;
 Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 5781 TGCCCTGCTGCTGCTG 5798
 DB 2 UGCCUGCCUGCCUGCCAG 19

RESULT 1587
 ADE29381/G
 ID ADE29381 standard; RNA; 19 BP.
 AC ADE29381;
 DT 29-JAN-2004 (first entry)
 DE Mitogen activated protein kinase siNA oligonucleotide SEQ ID NO:3.
 XX short interfering nucleic acid; siNA; downregulation; inhibition;
 KM mitogen-activated protein kinase; MAP kinase; MAPK; RNA interference;
 KM cytosolic; anorectic; antidiabetic; antinflammatory; antiseptic;
 KM immunosuppressive; antibacterial; antirheumatic; antiarthritic;
 KM antipsoriatic; gastrointestinal; obesity; diabetes; tumour;
 KM inflammatory disease; asthma; septic shock; rheumatoid arthritis;
 KM psoriasis; inflammatory bowel disease; drug screening;
 KM genetic engineering; pharmacogenomic; gene mapping; ss.
 XX
 XX Synthetic.
 OS
 XX
 XX WO2003072590-A1.
 PN
 XX
 PD 04-SEP-2003.
 XX
 XX
 PF 28-JAN-2003; 2003WO-US002510.
 XX
 XX 20-FEB-2002; 2002US-0358580P.
 PR 11-MAR-2002; 2002US-0363124P.
 PR 06-JUN-2002; 2002US-0386782P.
 PR 29-AUG-2002; 2002US-0406784P.
 PR 05-SEP-2002; 2002US-0408378P.
 PR 09-SEP-2002; 2002US-0409293P.
 PR 15-JAN-2003; 2003US-0440129P.
 XX
 XX (SIRN-) SIRNA THERAPEUTICS INC.
 PA
 XX Mcswigen J, Beigelman L, Usman N, Haeblerl P, Chowrira B;
 PI WPI; 2003-689980/65.
 DR
 XX New short interfering nucleic acid, useful e.g. for treatment and
 PT diagnosis of cancer, downregulates expression of mitogen-activated
 PT protein kinase genes.
 XX

PS Example 3; SEQ ID NO 3; 164pp; English.

XX The present invention describes a short interfering nucleic acid (siNA)

CC that downregulates expression of a mitogen-activated protein kinase

CC (MAPK) genes by RNA interference. Also described: (1) a method for

CC modulating expression of MAPK genes in cells, tissue explants or

CC organisms by introduction of siNA; (2) kits for in vitro or in vivo

CC delivery of siNA; (3) conjugates and/or complexes of siNA; and (4)

CC vectors that express siNA and cells containing these vectors. MAPK siNAs

CC have cytostatic, anorectic, antidiabetic, antibacterial, antiinflammatory,

CC antisthmatic, immunosuppressive, and gastrointestinal activities. The MAPK

CC siNAs can be used to modulate the expression of MAPK genes, in cells,

CC tissue explants or organisms, e.g. for treating obesity; diabetes types I

CC and II; a wide range of tumours, and inflammatory diseases (asthma,

CC septic shock, rheumatoid arthritis, psoriasis and inflammatory bowel

CC disease). They can also be used for drug screening; diagnosis; target

CC identification and validation; genetic engineering; pharmacogenomics;

CC studying gene function and gene mapping (e.g. of single-nucleotide

CC polymorphisms). The present sequence represents a MAPK siNA which is used

CC in the exemplification of the present invention.

CC

XX Sequence 19 BP; 5 A; 5 C; 8 G; 0 T; 1 U; 0 Other;

SQ

Query Match 0.2%; Score 16.4; DB 1; Length 19;

Best Local Similarity 94.4%; Pred. No. 1e+03; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5781 TGCGTGGCTGCTGCTGCTG 5798

Db 18 TGCCTGCTGCTGCTGCTGCG 1

RESULT 1588

AAA66287

ID AAA66287 standard; DNA; 20 BP.

XX

AC AAA66287;

XX

DT 09-OCT-2000 (first entry)

XX

DE Dog genomic marker oligonucleotide sequence SEQ ID NO:149.

XX

KW Dog; genome; genomic marker; radiation hybrid map; identification;

KW Chromosome location; gene marker; polymorphic microsatellite marker;

KW phenotype; behaviour; pedigree; ss.

XX

PI Canis familiaris.

OS

XX

PN WO200029615-A2.

XX

PD 25-MAY-2000.

XX

PF 15-NOV-1999; 99WO-IB001907.

XX

PR 13-NOV-1998; 98US-0108193P.

XX

PA (CNRS) CNRS CENT NAT RECH SCI.

XX

PI Galibert F, Andre C;

XX

DR WPI; 2000-387821/33.

XX

PT New radiation hybrid map of the dog, Canine familiaris, genome, useful

PT for e.g. identifying genes implicated in phenotypic and behavioral traits

PT or in genetic diseases and for studying dog pedigrees.

XX

PS Claim 1; Page 59; 87pp; English.

XX

CC The present invention describes a radiation hybrid map of the dog (Canine

CC familiaris) genome comprising the genome location of a marker selected

CC from AAA66139 to AAA66942. The radiation hybrid map is useful for

CC identifying and localising dog genes, since it covers approximately 80 %

CC of the dog genome and provides a dense map integrating different types

CC (i.e. Type I and Type II) of markers. The map and the dog genome markers

CC (or complementary sequences) are especially useful to identify genes

CC responsible for phenotypic and behavioural traits in dogs, to identify

CC morbid genes, to analyse diseases and identify implicated genes in such

CC diseases and their alleles, and to study dog pedigrees. They may also be

CC useful for isolating corresponding human gene sequences e.g. genes

CC involved in genetic diseases

XX

SQ

Query Match 0.2%; Score 16.4; DB 1; Length 20;

Best Local Similarity 94.4%; Pred. No. 1.1e+03; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7413 CAGCAGCAGCAGCAGCAGCAG 7430

Db 1 CAGCAGCAGCAGCAGCAGCAG 18

RESULT 1589

AAD15629/C

ID AAD15629 standard; DNA; 20 BP.

XX

AC AAD15629;

XX

DT 15-NOV-2001 (first entry)

XX

DE Human Bcl-2 protein target DNA #3.

XX

KW Human; Bcl-2 protein; genetic disease; antisense target; therapeutic; ss.

XX

OS Homo sapiens.

OS

XX

PN WO200161030-A2.

XX

PD 23-AUG-2001.

XX

PF 14-FEB-2001; 2001WO-US004732.

XX

PR 14-FEB-2000; 2000US-00504653.

XX

PA (BOLL/) BOLLON A P.

PA (GRAY/) GRAY D M.

PA (JUSE/) JU-SEOG L.

XX

PI Bollon AP, Gray DM, Ju-Seog L;

XX

DR WPI; 2001-529916/58.

XX

PT Selecting optimal subsequence antisense targets for inhibition of mRNA

PT expression of target mRNA for the therapeutic treatment of genetic

PT disease.

XX

PS Example 9; Page 28; 87pp; English.

XX

CC The invention relates to a method for selecting optimal subsequence

CC antisense targets. The method involves preparing an antisense

CC oligonucleotide capable of inhibiting mRNA expression of target mRNA

CC sequences, as well as antisense oligonucleotides capable of binding DNA.

CC The antisense and antigene libraries are useful for preparing therapeutic

CC agents for the treatment of genetic disease. The present DNA sequence is

CC human Bcl-2 protein target DNA related to the invention. Note: The

CC present sequence is shown as DNA in the specification; however, in vivo,

CC this target sequence would be mRNA

XX

SQ

Sequence 20 BP; 0 A; 9 C; 10 G; 1 T; 0 U; 0 Other;

QY

Query Match 0.2%; Score 16.4; DB 1; Length 20;

Best Local Similarity 94.4%; Pred. No. 1.1e+03; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 38 GCAGGCTCCGCGGCGGCG 55

```
Db      19 GCAGGCCCGCGCGCG 2
|||||
RESULT 1590
AADI5631/c
ID      AADI5631 standard; DNA; 20 BP.
XX
XX
AC      AADI5631;
XX
XX      15-NOV-2001 (first entry)
DT
XX      Human Bcl-2 protein target DNA #5.
DE
XX      Human; Bcl-2 protein; genetic disease; antisense target; therapeutic; ss.
KM
XX      Homo sapiens.
OS
XX      WO200161030-A2.
PN
XX      23-AUG-2001.
PD
XX      14-FEB-2001; 2001WO-US004732.
PF
XX      14-FEB-2000; 2000US-00504653.
PR
XX      (BOLL/) BOLLON A P.
PA      (GRAY/) GRAY D M.
PA      (JU-SEOG) JU-SEOG L.
XX
XX      BOLLON AP, Gray DM, Ju-Seog L;
PI
XX      MPI; 2001-529916/58.
DR
XX
XX      Selecting optimal subsequence antisense targets for inhibition of mRNA
PT      expression of target mRNA for the therapeutic treatment of genetic
PT      disease.
XX
XX      Example 9; Page 28; 87pp; English.
PS
XX
XX      The invention relates to a method for selecting optimal subsequence
CC      antisense targets. The method involves preparing an antisense
CC      oligonucleotide capable of inhibiting mRNA expression of target mRNA
CC      sequences, as well as antisense oligonucleotides capable of binding DNA.
CC      The antisense and antigene libraries are useful for preparing therapeutic
CC      agents for the treatment of genetic disease. The present DNA sequence is
CC      human Bcl-2 protein target DNA related to the invention. Note: The
CC      present sequence is shown as DNA in the specification; however, in vivo,
CC      this target sequence would be mRNA
XX
XX      Sequence 20 BP; 0 A; 10 C; 9 G; 1 T; 0 U; 0 Other;
SQ
Query Match      0.2%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY      38 GCAGGCTCGCGCGCG 55
Db      18 GCAGGCCCGCGCGCG 1
|||||
RESULT 1591
AAF99943/c
ID      AAF99943 standard; DNA; 20 BP.
XX
XX      AAF99943;
AC
XX      12-JUL-2001 (first entry)
DT
XX
XX      Synthetic oligonucleotide #9.
DE
XX      Oligonucleotide purification; liquid chromatography;
KM      hydrophobic protective group; deprotection; ds.
XX
```

```
XX
XX      Synthetic.
OS
XX      JP2000342265-A.
PN
XX      12-DEC-2000.
PD
XX      02-JUN-1999; 99JP-00154974.
PF
XX      02-JUN-1999; 99JP-00154974.
PR
XX      (TOAG ) TOA GOSSEI CHEM IND LTD.
PA
XX      MPI; 2001-268251/28.
DR
XX
XX      A process for purification of oligonucleotides using liquid
PT      chromatography.
PT
XX      Example 1; Page 4; 13pp; Japanese.
XX
XX      The present sequence is an oligonucleotide provided in a specification
CC      relating to the simplified purification of oligonucleotides by liquid
CC      chromatography. The process comprises: (a) pouring oligonucleotides
CC      protected with a hydrophobic group and oligonucleotide with no protective
CC      group into a liquid chromatography column packed with an acid and alkali
CC      resistant packing agent, such as polystyrene resin; (b) pouring a mixed
CC      developing solvent composed of a buffer made from a volatile salt and a
CC      water soluble organic solvent at a suitable concentration gradient into
CC      the column; (c) pouring an acid, particularly 6-16 v/v% acetic acid, into
CC      the column to deprotect the oligonucleotides protected with the
CC      hydrophobic group; (d) pouring a mixed developing solvent composed of a
CC      buffer made from a volatile salt, particularly 0.05-0.5 N aqueous
CC      ammonium hydrogencarbonate solution adjusted at pH 8-10, and a water
CC      soluble organic solvent at a suitable concentration gradient to elute the
CC      deprotected oligonucleotides; and (e) removal of the solvent and the salt
CC      from the eluted oligonucleotides
XX
XX      Sequence 20 BP; 17 A; 1 C; 1 G; 1 T; 0 U; 0 Other;
SQ
Query Match      0.2%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY      4464 TTTTCTTTCTTTT 4481
Db      19 TTTTCTTTCTTTT 2
|||||
RESULT 1592
ABL57070/c
ID      ABL57070 standard; DNA; 20 BP.
XX
XX      ABL57070;
AC
XX      22-JUL-2002 (first entry)
DT
XX
XX      Molecular beacon target sequence.
DE
XX      Molecular beacon; fluorophore; nanoparticle; nucleic acid detection; ss.
KM
XX      Synthetic.
OS
XX      Key
FH      misc_binding      Location/Qualifiers
FT      1..20
FT      /*tag= a
FT      /bound_molecly= "Molecular beacon"
FT      /note= "forms double-stranded region with bases 1-20 of
FT      sequence in ABL57069"
XX
XX      WO200218951-A2.
XX
XX      07-MAR-2002.
XX
```

```
PF 29-AUG-2001; 2001WO-US041941.
XX
XX 29-AUG-2000; 2000US-0228728P.
PR 30-MAR-2001; 2001US-0280350P.
XX
XX (UYRQ ) UNIV ROCKEFELLER.
XX
XX Dubertret B, Calame M, Libchaber A;
XX
XX WPI; 2002-404569/43.
XX
XX Sensitive detecting proximity changes in a system that utilizes an
PT interacting fluorophore and quencher, for high sensitivity applications,
PT involves utilizing a metal surface as quencher.
XX
XX Example 2; Page 26; 62pp; English.
XX
XX The present sequence is that of a perfectly matched target sequence for a
CC molecular beacon comprising an oligonucleotide probe (see ABL57069)
CC covalently attached at the 3' end to fluorescent dye and at the 5' end to
CC a nanoparticle. In the native state, the probe forms a hairpin
CC conformation with hybridised termin. The proximity of the fluorophore
CC and quencher (gold nanoparticle) in the molecular beacon results in
CC little or no detectable fluorescence. Upon hybridisation of the central
CC complementary stretch of the probe to a target sequence, such as the
CC present sequence, the hairpin undergoes a conformational change resulting
CC in an increase in fluorescence, the extent of which is proportional to
CC the amount of target sequence present. Single mismatches can be detected.
CC The invention relates generally to the use of metal surface quenchers
CC such as particles or films for high sensitivity applications in, for
CC example, detection and diagnostic systems
XX
XX SEQ Sequence 20 BP; 15 A; 3 C; 1 G; 1 T; 0 U; 0 Other;

Query Match      0.2%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4461 GACTTTTCTTTTCTTTT 4478
   |||||
DB 18 GAGTTTTTTTTTTTTT 1

RESULT 1593
ABZ93124/C
ID ABZ93124 standard; DNA; 20 BP.
XX
XX AC ABZ93124;
XX
XX 17-OCT-2003 (first entry)
XX
XX Human oligonucleotide sequence.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; de.
XX
XX Homo sapiens.
XX
XX MO200285308-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013135.
XX
XX 24-APR-2001; 2001US-0286137P.
XX
XX (EPIC-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
```

```
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX Disclosure; SEQ ID NO 8366; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
XX SEQ Sequence 20 BP; 4 A; 5 C; 7 G; 4 T; 0 U; 0 Other;

Query Match      0.2%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3822 TGACAGGCCCTGCGCTT 3839
   |||||
DB 18 TGACAGGCCCTGCGACTT 1

RESULT 1594
AAD57844/C
ID AAD57844 standard; DNA; 20 BP.
XX
XX AC AAD57844;
XX
XX 20-NOV-2003 (first entry)
XX
XX Target oligonucleotide #1 used in nonlinear optical technique.
XX
XX Nonlinear optical technique; screening; ss.
XX
XX Unidentified.
XX
XX MO2003064991-A2.
XX
XX 07-AUG-2003.
XX
XX 17-JUL-2002; 2002WO-US022681.
XX
XX 17-JUL-2001; 2001US-0306040P.
XX
XX 23-OCT-2001; 2001US-0347821P.
XX
XX 06-FEB-2002; 2002US-0354668P.
XX
XX (SALA/) SALAFSKY J S.
XX
XX Salafsky JS;
XX
XX WPI; 2003-646172/61.
```

PT Screening candidate binding partner(s) for binding to test molecule by
PT applying external force field to sample in homogeneous phase, and
PT illuminating sample with light beam(s) at fundamental frequencies, and
PT measuring physical properties.
PS Disclosure; Fig 20B; 146pp; English.
XX
XX The present invention relates to a method for detecting interactions
CC between biological components using a nonlinear optical technique. The
CC invention is used for screening candidate binding partner(s) for binding
CC to test molecule. It can also be used to detect changes in orientation or
CC conformation of the probe and/or target. The present sequence is a target
CC oligonucleotide used in nonlinear optical technique
XX
SQ Sequence 20 BP, 15 A, 3 C, 1 G, 1 T, 0 U, 0 Other;

Query Match 0.2%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4461 GACTTTT TTTT TTTT TTTT 4478
DB 18 GAGTTT TTTT TTTT TTTT 1

RESULT 1595
AAT72522/c
ID AAT72522 standard; DNA; 21 BP.
XX
XX AAT72522;
AC
XX
XX 17-OCT-1997 (first entry)
DT
XX
XX 5-Cys-encoding oligonucleotide.
DE
XX
XX Streptavidin; mutagenesis; stabilisation; Stv-43; ss.
KM
XX
XX Synthetic.
OS
XX
XX WO9711183-A1.
PN
XX
XX 27-MAR-1997.
PD
XX
XX 10-SEP-1996; 96WO-US005169.
PF
XX
XX 11-APR-1995; 95US-00420010.
PR
XX
XX (UYBO-) UNIV BOSTON.
PA
XX
XX Sano T, Cantor CR, Vajda S, Reznik GO, Smith CL, Pandori MW;
PI
XX
XX WPI; 1997-202890/18.
DR
XX
XX New streptavidin mutants - have increased stability or altered affinity
PT for biotin.
PT
XX
XX Example 14; Page 33; 91pp; English.
PS
XX
XX Two 21-mer oligonucleotides (AAT72522 and AAT72523) were annealed and the
CC resulting double-stranded DNA was ligated into the EcoRI and BamHI sites
CC of the predigested DNA of a plasmid encoding residues 16 to 133 of
CC streptavidin with lys at position 127. The gene was cloned into a
CC bacterial expression vector and the mutated streptavidin expressed and
CC purified. The mutant streptavidin forms heterotetramers in solution and,
CC with Phe at position 120, has a reduced biotin-binding affinity of less
CC than about 10 power 8/M. It can be conjugated to other proteins and
CC macromolecules, and also to solid supports through the sulphhydryl group
CC on the cysteine residues
XX
SQ Sequence 21 BP, 4 A, 5 C, 5 G, 7 T, 0 U, 0 Other;

Query Match 0.2%; Score 16.4; DB 1; Length 21;
Best Local Similarity 94.4%; Pred. No. 1.2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7412 TCAGCAGCAGCAGCAGCA 7429
DB 21 TTAGCAGCAGCAGCAGCA 4

RESULT 1596
AAZ26142/c
ID AAZ26142 standard; DNA; 21 BP.
XX
XX AAZ26142;
AC
XX
XX 30-NOV-1999 (first entry)
DT
XX
XX Human polymorphic region 331.
DE
XX
XX Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KM cell viability; loss of heterozygosity; precancerous condition; ASI;
KM allele specific inhibitor; somatic cell; diagnosis; prevention;
KM atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KM dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KM graft versus host disease; malignant cell removal; bone marrow; ss.
XX
XX Homo sapiens.
OS
XX
XX WO9841648-A2.
PN
XX
XX 24-SEP-1998.
PD
XX
XX 19-MAR-1998; 98WO-US005419.
PF
XX
XX 20-MAR-1997; 97US-0041057P.
PR
XX
XX (VARI-) VARIAGENICS INC.
PA
XX
XX Houseman D, Ledley FD, Stanton VP;
PI
XX
XX WPI; 1998-521232/44.
DR
XX
XX Identifying target genes for allele-specific drugs - used for diagnosis,
PT prevention and treatment of, e.g. cancers, atherosclerotic plaque,
PT dysplastic lesions, endometriosis or graft versus host disease.
PT
XX
XX Disclosure; Fig 7; 605pp; English.
PS
XX
XX This invention describes a novel method for identifying an inhibitor
CC potentially useful for treatment of cancer, where the inhibitor is active
CC on a gene vital for cell growth or viability, and where the gene is
CC subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC used for preventing the development of cancer in a patient having a
CC precancerous condition, by administering to the patient a first allele
CC specific inhibitor (ASI) targeted to an allele of a first essential gene
CC present in cells of the precancerous condition, where the normal somatic
CC cells of the patient are heterozygous for the first gene, the inhibitor
CC is active on at least one but less than all allelic forms of the gene
CC present in a population and targets only one allelic form present in the
CC normal somatic cells, and the first gene. The products and methods can be
CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.
CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
CC lesions, benign tumours, endometriosis, polycystic kidney disease, and
CC graft versus host disease. The method can also be used to remove
CC malignant cells from bone marrow transplants. AAZ25812-236825 represent
CC human polymorphic sites described in the method of the invention
XX
SQ Sequence 21 BP, 17 A, 3 C, 0 G, 1 T, 0 U, 0 Other;

Query Match 0.2%; Score 16.4; DB 1; Length 21;
Best Local Similarity 94.4%; Pred. No. 1.2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT 4481
DB 11 TTTT TTTT TTTT TTTT 11

Db 18 TTTTTTTTTTTTATT 1

RESULT 1597

AA226141/c

ID AA226141 standard; DNA; 21 BP.

XX AA226141;

XX 30-NOV-1999 (first entry)

XX Human polymorphic region 330.

XX Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;

XX cell viability; loss of heterozygosity; precancerous condition; ASI;

XX allele specific inhibitor; somatic cell; diagnosis; prevention;

XX atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;

XX dysplastic lesion; benign tumour; polycystic kidney disease; transplant;

XX graft versus host disease; malignant cell removal; bone marrow; ss.

XX Homo sapiens.

XX WO9841648-A2.

XX 24-SEP-1998.

XX 19-MAR-1998; 98WO-US005419.

XX 20-MAR-1997; 97US-0041057P.

XX (VARI-) VARAGENICS INC.

XX Housman D, Ledley FD, Stanton VP;

XX WPI; 1998-521232/44.

XX Identifying target genes for allele-specific drugs - used for diagnosis,

XX prevention and treatment of, e.g. cancers, atherosclerotic plaque,

XX dysplastic lesions, endometriosis or graft versus host disease.

XX Disclosure; Fig 7; 605pp; English.

XX This invention describes a novel method for identifying an inhibitor

XX potentially useful for treatment of cancer, where the inhibitor is active

XX on a gene vital for cell growth or viability, and where the gene is

XX subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is

XX used for preventing the development of cancer in a patient having a

XX precancerous condition, by administering to the patient a first allele

XX specific inhibitor (ASI) targeted to an allele of a first essential gene

XX present in cells of the precancerous condition, where the normal somatic

XX cells of the patient are heterozygous for the first gene, the inhibitor

XX is active on at least one but less than all allelic forms of the gene

XX present in a population and targets only one allelic form present in the

XX normal somatic cells, and the first gene. The products and methods can be

XX used in the diagnosis, prevention and treatment of LOH disorders, e.g.

XX cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic

XX lesions, benign tumours, endometriosis, polycystic kidney disease, and

XX graft versus host disease. The method can also be used to remove

XX malignant cells from bone marrow transplants. AA226141-226825 represent

XX human polymorphic sites described in the method of the invention

XX Sequence 21 BP; 17 A; 3 C; 0 G; 1 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 16.4; DB 1; Length 21;

XX Best Local Similarity 94.4%; Pred. No. 1.2e+03;

XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4464 TTTTTTTTTTTTTTTT 4481

Db 18 TTTTTTTTTTTTATT 1

RESULT 1598

ABLS7071/c ID ABL57071 standard; DNA; 21 BP.

XX ABL57071;

XX 22-JUL-2002 (first entry)

XX Molecular beacon target sequence.

XX Molecular beacon; fluorophore; nanoparticle; nucleic acid detection; ss.

XX Synthetic.

XX Key Location/Qualifiers

XX misc_binding 1..21

XX /tag=a

XX /bound_moiety="Molecular beacon"

XX /note="forms double-stranded region with bases 1-21 of

XX sequence in ABL57069"

XX WO200218951-A2.

XX 07-MAR-2002.

XX 29-AUG-2001; 2001WO-US041941.

XX 29-AUG-2000; 2000US-0228728P.

XX 30-MAR-2001; 2001US-0280350P.

XX (UVRQ) UNIV ROCKEFELLER.

XX Dubertret B, Calame M, Libchaber A;

XX WPI; 2002-404569/43.

XX Sensitive detecting proximity changes in a system that utilizes an

XX interacting fluorophore and quencher, for high sensitivity applications,

XX involves utilizing a metal surface as quencher.

XX Example 3; Page 62; 62pp; English.

XX The present sequence is that of a perfectly matched target sequence for a

XX molecular beacon comprising an oligonucleotide probe (see ABL57069)

XX covalently attached at the 3' end to fluorescent dye and at the 5' end to

XX a nanoparticle. In the native state, the probe forms a hairpin

XX conformation with hybridised termini. The proximity of the fluorophore

XX and quencher (gold nanoparticle) in the molecular beacon results in

XX little or no detectable fluorescence. Upon hybridisation of the central

XX complementary stretch of the probe to a target sequence, such as the

XX present sequence, the hairpin undergoes a conformational change resulting

XX in an increase in fluorescence, the extent of which is proportional to

XX the amount of target sequence present. Single mismatches can be detected.

XX The invention relates generally to the use of metal surface quenchers

XX such as particles or films for high sensitivity applications in, for

XX example, detection and diagnostic systems

XX Sequence 21 BP; 15 A; 3 C; 2 G; 1 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 16.4; DB 1; Length 21;

XX Best Local Similarity 94.4%; Pred. No. 1.2e+03;

XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4461 GACTTTTTTTTTTTTTT 4478

Db 19 GAGTTTTTTTTTTTTTTT 2

RESULT 1599

ABBS59610 ID ABBS59610 standard; DNA; 22 BP.

XX ABBS59610;

DT 05-NOV-2002 (first entry)
 XX Real-time reverse PCR primer, used to determine NOV1 expression, #6.
 DE
 XX Human; PCR; ss; SEC; NOV; immunosuppressive; hepatotropic;
 KW antiinflammatory; angiogenic-associated disorder; diagnostic;
 KW gene therapy; developmental disorder; immune disease;
 KW signal transduction pathway disorder; metabolic disorder;
 KW feeding disorder; obesity; wasting disorder; neurodegenerative disorder;
 KW Alzheimer's disease; Parkinson's disease; behavioural disorder; allergy;
 KW asthma; atherosclerosis; cardiomyopathy; angina pectoris;
 KW autoimmune disease; retinal disease; cirrhosis; diabetes;
 KW infectious disease; human immunodeficiency virus; HIV; cancer;
 KW hypertension; hypotension; multiple sclerosis; urinary retention;
 KW osteoporosis; Crohn's disease; ulcer; neurological disorder; anxiety;
 KW haemophilia; cirrhosis; immunogen; vaccine; primer.
 XX
 OS Homo sapiens.
 XX
 PN WO200255705-A2.
 XX
 PD 18-JUL-2002.
 XX
 PF 11-JAN-2002; 2002WO-US000609.
 XX
 PR 11-JAN-2001; 2001US-0261013P.
 PR 11-JAN-2001; 2001US-0261014P.
 PR 11-JAN-2001; 2001US-0261018P.
 PR 11-JAN-2001; 2001US-0261026P.
 PR 11-AUG-2001; 2001US-0261029P.
 PR 17-SEP-2001; 2001US-0313170P.
 PR 10-SEP-2001; 2001US-0318410P.
 XX
 XX (CURA-) CURAGEN CORP.
 XX
 PA Mezes PS, Rastelli L, Herrmann JL, MacDougall JR, Zhong H;
 PI Casman SJ, Boldog F, Shinkets RA, Gorman L, Craeta OR, Mysore KK;
 PI Folkerts O, Martin GB, Eisen A, Spaderna SK, Verne CM, Bergh C;
 PI Spytek KA, Dippio VA, Zeehnen BD, Peyman JA, Ellerman K, Stone DJ;
 PI Grose WM, Albrook JP, Lepley DM, Rieger DK, Burgess CE;
 PI Edinger S;
 XX
 DR WPI; 2002-590675/63.
 XX
 PT Human SECX/NOVX polypeptide useful for diagnosing, preventing or treating
 PT disorders associated with aberrant expression or activity of SECX/NOVX
 PT nucleic acids and proteins e.g., diabetes.
 PT
 XX
 PS Example 2; Page 378; 443pp; English.
 XX
 CC The invention discloses the isolated human polypeptides, and
 CC polynucleotides encoding them, that have been designated SECX and NOVX.
 CC The polypeptides can be used for treating, or delaying, the onset of an
 CC angiogenic-associated disorder or treating a pathological state in a
 CC subject, preferably a mammal. They can also be used in determining the
 CC presence of, or predisposition to, a disease associated with altered
 CC levels of the polypeptides and polynucleotides of any one of the 12
 CC sequences (SEC1-12), for raising antibodies, for identifying an agent
 CC that binds to, or that modulates the expression or activity of the
 CC polypeptide, for treating or preventing a NOVX-associated disorder (NOV1-
 CC 8) and as a pharmaceutical composition comprising the polypeptide,
 CC polynucleotide or the antibody. The polypeptides and polynucleotides are
 CC useful in diagnostic applications where their amounts are assessed, or
 CC for the manufacture of a medicament (e.g. gene therapy) for treating or
 CC preventing disorders or syndromes such as developmental disorders, immune
 CC diseases, signal transduction pathway disorders, metabolic disorders,
 CC feeding disorders (including obesity), wasting disorders,
 CC neurodegenerative disorders (including Alzheimer's disease and
 CC Parkinson's disease), behavioural disorders, allergies, asthma,
 CC atherosclerosis, cardiomyopathy, angina pectoris, autoimmune diseases,
 CC retinal disease, cirrhosis, diabetes, infectious disease (bacterial,
 CC fungal, protozoal and viral e.g. human immunodeficiency virus, HIV),
 CC cancer (e.g. prostate cancer), hypertension, hypotension, multiple

CC sclerosis, urinary retention, osteoporosis, Crohn's disease, ulcers,
 CC neurological disorders (e.g. anxiety), haemophilia or cirrhosis. They may
 CC also be used as immunogens to produce antibodies specific for the
 CC invention, and as vaccines. Further, they are useful for screening
 CC potential agonist and antagonist compounds. The sequences presented in
 CC AB559542-AB559699 are the PCR primers and probes which were used to
 CC amplify and detect expression of human SEC1-12 and NOV1-8 cDNA
 XX
 SQ Sequence 22 BP; 6 A; 9 C; 2 G; 5 T; 0 U; 0 Other;
 Query Match 0.2%; Score 16.4; DB 1; Length 22;
 Best Local Similarity 94.4%; Pred. No. 1.3e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 6395 CCTATGCCACCTGCTA 6412
 DB 1 CCTAATGCCACCTCTTA 18
 RESULT 1600
 ADE27662
 ID ADE27662 standard; RNA; 22 BP.
 AC
 AC ADE27662;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:606.
 XX
 XX short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
 KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
 KW antiarteriosclerotic; cytostatic; virocid; obesity; diabetes;
 KW atherosclerosis; cancer; viral infection; drug screening;
 KW genetic engineering; pharmacogenomic; gene mapping; ss.
 KW
 XX
 OS Synthetic.
 XX
 PN WO2003070885-A2.
 XX
 PD 28-AUG-2003.
 XX
 PF 13-FEB-2003; 2003WO-US004317.
 XX
 PR 20-FEB-2002; 2002US-0358580P.
 PR 11-MAR-2002; 2002US-0363124P.
 PR 06-JUN-2002; 2002US-0386782P.
 PR 29-AUG-2002; 2002US-0406784P.
 PR 05-SEP-2002; 2002US-0408378P.
 PR 09-SEP-2002; 2002US-0409293P.
 PR 20-SEP-2002; 2002US-0412304P.
 PR 15-JAN-2003; 2003US-0440129P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Mcswiggen J, Belgelman L, Thompson J;
 PI
 XX
 DR WPI; 2003-721687/68.
 XX
 PT New short interfering nucleic acid, useful e.g. for treatment and
 PT diagnosis of obesity or diabetes, downregulates expression of the
 PT stearoyl-CoA desaturase gene.
 PT
 XX
 PS Example 3; SEQ ID NO 606; 139pp; English.
 XX
 CC The present invention describes a short interfering nucleic acid (siNA)
 CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
 CC by RNA interference. Also described: (1) modulating expression of SCD
 CC genes in cells, tissue explants or organisms by introduction of siNA;
 CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
 CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
 CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
 CC virocid activities. The siNAs can be used to modulate expression of SCD
 CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;

CC diabetes (types I and II); atherosclerosis; cancer and viral infections.
CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 22 BP; 4 A; 8 C; 2 G; 2 T; 5 U; 1 Other;
Query Match 0.2%; Score 16.4; DB 1; Length 22;
Best Local Similarity 65.0%; Pred. No. 1.3e+03;
Matches 13; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY 7232 TCCCTCTCAAGTCCAGCANG 7251
DB 2 UCCAUCCUAGUCCAGCATS 21
RESULT 1601
ADE27654
ID ADE27654 standard; RNA; 22 BP.
XX
AC ADE27654;
XX
DT 29-JUN-2004 (first entry)
XX
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:598.
XX
KM short interfering nucleic acid; siNA; downregulation; inhibition; SCD;
KM stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;
KM antiarteriosclerotic; cytostatic; virucide; obesity; diabetes;
KM atherosclerosis; cancer; viral infection; drug screening;
KM genetic engineering; pharmacogenomic; gene mapping; ss.
XX
OS Synthetic.
XX
PN MO2003070885-A2.
XX
PD 28-AUG-2003.
XX
PF 13-FEB-2003; 2003MO-US004317.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 20-SEP-2002; 2002US-0412304P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L, Thompson J;
XX
DR WPI; 2003-721687/68.
XX
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of obesity or diabetes, downregulates expression of the
PT stearoyl-CoA desaturase gene.
XX
XX
PS Example 3; SEQ ID NO 598; 139pp; English.
XX
CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene
CC by RNA interference. Also described: (1) modulating expression of SCD
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and
CC virucide activities. The siNAs can be used to modulate expression of SCD
CC gene, in cells, tissue explants or organisms, e.g. for treating obesity;
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.

CC They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents an SCD siNA, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 22 BP; 4 A; 8 C; 2 G; 2 T; 5 U; 1 Other;
Query Match 0.2%; Score 16.4; DB 1; Length 22;
Best Local Similarity 65.0%; Pred. No. 1.3e+03;
Matches 13; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY 7232 TCCCTCTCAAGTCCAGCANG 7251
DB 2 UCCAUCCUAGUCCAGCATS 21
RESULT 1602
AA330209
ID AA330209 standard; DNA; 23 BP.
XX
AC AA330209;
XX
DT 18-JUN-1999 (first entry)
XX
DE F9 gene PCR primer #19.
XX
KM p53 gene; F9 gene; PCR primer; amplification; linking; linkage; ss.
XX
OS Synthetic.
XX
PN MO9916904-A1.
XX
PD 08-APR-1999.
XX
PF 25-SEP-1998; 98MO-US019968.
XX
PR 29-SEP-1997; 97US-0060319P.
XX
PA (CITY) CITY OF HOPE.
XX
PI Liu Q;
XX
DR WPI; 1999-255105/21.
XX
PT Linking by PCR DNA segments which occur in non-adjacent portions.
XX
PS Example; Page 17; 49pp; English.
XX
CC The present invention describes linking by PCR DNA segments which occur
CC in non-adjacent portions of target DNA by using a primer complementary to
CC the antisense strand of the first DNA segment to be linked and a second
CC primer complementary to the sense strand of the last DNA segment to be
CC linked. The method is used to produce and amplify DNA containing at least
CC three linked DNA segments occurring in non-adjacent portions of target
CC DNA. This is useful for producing copies of genes lacking large introns
CC or where a DNA product contains a mutation. The techniques can also be
CC used to produce DNA from one or more different species. The technique can also be
CC used to produce DNA without large introns. The method involves multiple
CC PCR amplifications of gene sequences and linkage of the exons in a single
CC reaction. AA330191 to AA330214 represent PCR primers used in the
CC exemplification of the present invention
XX
SQ Sequence 23 BP; 8 A; 2 C; 10 G; 3 T; 0 U; 0 Other;
Query Match 0.2%; Score 16.4; DB 1; Length 23;
Best Local Similarity 94.4%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2867 CAAGGAGGAGGAGGTGG 2884
DB 2 CAAGGAGGAGGAGGTGG 19

```

RESULT 1603
AAFe0172/C
ID AAF60172 standard; DNA; 24 BP.
XX
XX AC
XX AAF60172;
XX
XX DT 27-APR-2001 (first entry)
XX
XX DE Human ATM gene exon 31 forward primer.
XX
XX KW Human; ATM; ataxia telangiectasia; mutation detection;
XX single-stranded conformation polymorphism; SSCP; electrophoresis;
XX PCR primer; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200107660-A1.
XX
XX PD 01-FEB-2001.
XX
XX PF 21-JUL-2000; 2000MO-US020011.
XX
XX PR 23-JUL-1999; 99US-00360416.
XX
XX PA (REGC ) UNIV CALIFORNIA.
XX
XX PI Gatti RA;
XX
XX DR WPI; 2001-168574/17.
XX
XX PT Detecting a mutation or polymorphism in human ataxia telangiectasia gene
XX or polyelexonic eukaryotic gene, involves using mega-single stranded
XX conformation polymorphism analysis.
XX
XX PS Claim 7; Page 53; 118pp; English.
XX
XX
XX The present sequence is one of a number of primers used in a method for
XX detecting a mutation or a polymorphism in the human ATM gene, which is
XX associated with the disease ataxia telangiectasia, or a polyelexonic
XX eukaryotic gene of at least 4 kb. The method uses an improved version of
XX single-stranded conformation polymorphism (SSCP) electrophoresis that
XX allows electrophoresis of two or three amplified segments in a single
XX lane. The method is useful for screening large, complex polyelexonic
XX eukaryotic genes such as the ATM gene for mutations and polymorphisms.
XX The new mutations and polymorphisms in the ATM gene are useful for
XX performing more accurate screening of human DNA samples for mutations,
XX for distinguishing mutations from polymorphisms, and for improving the
XX efficiency of automated screening methods. The mega-SSCP method provides
XX a screening method of genes for multiple polymorphisms and mutations at
XX once. The method is particularly suitable for large, polyelexonic,
XX eukaryotic genes, having mutations and polymorphisms at many points and
XX not merely in the disclosure and claims of the the specification is one
XX number lower than the number given in the sequence listing
XX
XX
XX Sequence 24 BP; 11 A; 6 C; 0 G; 7 T; 0 U; 0 Other;
XX
XX
XX Query Match 0.2%; Score 16.4; DB 1; Length 24;
XX Best Local Similarity 94.4%; Pred. No. 1.4e+03;
XX Matched 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX
XX 3168 TTACGTTGGGTTTGATA 3185
XX ||| ||| ||| ||| |||
XX 19 TTAGATTGGGTTTGATA 2
XX
XX
XX RESULT 1604
XX AAF28674/C
XX ID AAF28674 standard; DNA; 24 BP.
XX
XX AC
XX AAF28674;
XX

```

DT	05-APR-2001	(first entry)
XX		
DE	Human zacrpf PCR primer #1.	
XX		
KW	Human; zacrpf4; complement factor C1q domain; chromosome 11q11;	
KX	energy balance; cellular metabolic reaction; autocrine factor;	
KW	development; cell proliferation; differentiation; cell survival,	
KM	PCR primer; ss.	
XX		
OS	Homo sapiens.	
PN	WO200102565-A2.	
XX		
PD	11-JAN-2001.	
XX		
PF	28-JUN-2000; 2000WO-US017692.	
XX		
PR	01-JUL-1999; 99US-00346502.	
XX		
PA	(ZYMO) ZYMOGENETICS INC.	
XX		
PI	Holloway JL, Lok S;	
XX		
DR	WPI; 2001-136140/14.	
XX		
PT	Novel secreted protein ZACRP4 polypeptides having tandem C1q globular	
PT	domain, useful for studying cell-cell communication and regulation of	
PT	cellular processes.	
XX		
PS		
XX	Example 1; Page 80; 82pp; English.	
CC	The present sequence is a PCR primer for human ZACRP4 (see AAF28672 and	
CC	AAB61666). ZACRP4 protein has two complement factor C1q domains. The	
CC	ZACRP4 gene is located on human chromosome 11q11. The ZACRP4 coding	
CC	sequence and protein have a number of uses described in the	
CC	specification, including, modulation of energy balance and cellular	
CC	metabolic reactions in mammals. In addition, ZACRP4 protein is useful as	
CC	an autocrine factor, particularly during development, in mediating the	
CC	processes of an organism, in regulating cellular processes such as cell	
CC	proliferation and/or differentiation, cell survival and energy balance	
SQ	Sequence 24 BP; 3 A; 4 C; 8 G; 9 T; 0 U; 0 Other;	
	Query Match 0.2%; Score 16.4; DB 1; Length 24;	
	Best Local Similarity 94.4%; Pred. No. 1.4e+03;	
	Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	2099 TACAGCAGCACGCGCAAG 2116 	
DB	23 TACAGCAACACGCGCAAG 6	
	RESULT 1605	
	AAK99651	
ID	AAK99651 standard; DNA; 24 BP.	
XX		
AC	AAK99651;	
XX		
DT	08-JUL-2002 (first entry)	
XX		
DE	Human alpha 2, 3-sialyltransferase (ST3 GalVI) 9-13 cDNA PCR primer 1.	
XX		
KW	Human alpha 2, 3-sialyltransferase; ST3 GalVI 9-13; DNA recombination;	
KM	immunological deficiency; inflammation; tumour; human; PCR; primer; ss.	
OS	Homo sapiens.	
XX		
PN	CN1329158-A.	
XX		
PD	02-JAN-2002.	
XX		
PF	21-JUN-2000; 2000CN-00116664.	
XX		

PR 21-UTN-2000; 2000CN-00116664.
 XX
 PA (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.
 XX
 PI Mao Y, Xie Y;
 XX
 DR WPI; 2002-292825/34.
 XX
 PT New polypeptide-human alpha 2,3-sialyltransferase (ST3 GalVI) 9.13 for
 PT creating several diseases, such as immunological deficiency, various
 PT inflammations and tumors.
 XX
 PS Example 2; Page 20 Disclosure; 36pp; Chinese.
 XX
 CC The present invention relates to a novel polypeptide-human alpha 2, 3-
 CC sialyltransferase (ST3 GalVI) 9.13, the polynucleotide encoding the
 CC polypeptide and producing the polypeptide by using a DNA recombination
 CC technique. The invention also discloses the method for curing several
 CC diseases, such as immunological deficiency, various inflammations and
 CC tumours by using the polypeptide. The invention also discloses an
 CC antagonist for resisting the polypeptide and its therapeutic action, and
 CC also discloses the application of the polynucleotide encoding the novel
 CC human alpha 2,3-sialyltransferase (ST3 GalVI) 9.13. This polynucleotide
 CC sequence represents a PCR primer of the cDNA encoding the human alpha 2.3
 CC -sialyltransferase (ST3 GalVI) 9.13 protein of the invention
 XX
 SQ Sequence 24 BP; 4 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 16.4; DB 1; Length 24;
 Best Local Similarity 94.4%; Pred. No. 1.4e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 QY 6682 TTATTTTATTTATATAT 6699
 DB 7 TTATTTTATTTATTTAT 24
 XX
 RESULT 1606
 ADCS1227
 ID ADCS1227 standard; DNA; 24 BP.
 XX
 AC ADCS1227;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Brassica defensin gene PCR primer #2.
 XX
 KW antimicrobial protein; defensin; transgenic plant;
 KW composite disease resistance; pathogenic bacteria;
 KW rice white leaf blight; brown-stripe disease; glume blight;
 KW seedling damping-off disease; filamentous fungi; rice blight;
 KW sheath blight disease; leaf blight; gene; ss; PCR.
 XX
 OS Unidentified.
 OS Brassica sp.
 XX
 PN JP2003088379-A.
 XX
 PD 25-MAR-2003.
 XX
 PF 18-SEP-2001; 2001JP-00283117.
 XX
 PR 18-SEP-2001; 2001JP-00283117.
 XX
 PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
 XX
 DR WPI; 2003-621123/59.
 XX
 PT Novel protein from Brassica campestris, useful as antimicrobial against
 PT plant pathogenic filamentous fungi or pathogenic bacteria, especially for
 PT treating e.g. rice white leaf blight and sheath blight disease.
 XX
 PT Example 1; SEQ ID NO 7; 34pp; Japanese.
 PS

XX The invention comprises the amino acid and coding sequences of
 CC antimicrobial (defensin) proteins from Brassica. The DNA and protein
 CC sequences of the invention are useful for producing transformed plants
 CC with composite disease resistance, especially resistant to diseases
 CC caused by pathogenic bacteria, such as: rice white leaf blight, brown-
 CC stripe disease, glume blight, and seedling damping-off disease. As well
 CC as diseases caused by filamentous fungi, such as: rice blight, sheath
 CC blight disease, and leaf blight. The present DNA sequence represents a
 CC PCR primer that was used in the exemplification of the invention.
 XX
 SQ Sequence 24 BP; 1 A; 5 C; 2 G; 16 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 16.4; DB 1; Length 24;
 Best Local Similarity 94.4%; Pred. No. 1.4e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 QY 4463 CTTTTTTTTTTTTTTTTT 4480
 DB 7 CTCCTTTTTTTTTTTTTT 24
 XX
 RESULT 1607
 AAQ57129
 ID AAQ57129 standard; DNA; 25 BP.
 XX
 AC AAQ57129;
 XX
 DT 25-MAR-2003 (revised)
 DT 26-JUL-1994 (first entry)
 XX
 DE Chromosomal translocation detection probe #8.
 XX
 KW probe; detection; chromosomal translocation; leukemia; sarcoma; lymphoma;
 KW chondrodysplasia; Prader-Willi syndrome; trisomy; endocrine dysplasia;
 KW muscular hypotonia; incontinentia pigmenti; rhabdo-myosarcoma;
 KW myelodysplasia; refractory anaemia; balanced X-autosome;
 KW Beckwith-Wiedemann syndrome; ss.
 XX
 OS Synthetic.
 OS
 PN MO9402500-A1.
 XX
 PD 03-FEB-1994.
 XX
 PF 16-JUL-1993; 93WO-US00674.
 XX
 PR 17-JUL-1992; 92US-00915900.
 XX
 PA (APRO-) APROGENEX INC.
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Prashad N, Reading CL, Black M, Weber WD, Cubbage ML, Ju SC;
 PI Asgari M, Bresser J;
 XX
 DR WPI; 1994-048785/06.
 XX
 PT Oligonucleotides for detecting chromosomal translocations - with sequence
 PT complementary to translocation junction-spanning nucleic acid segment.
 XX
 PS Disclosure; Page 59; 75pp; English.
 XX
 CC The sequences given in AAQ57092-150 are probes which were used in the
 CC detection of chromosomal translocations. These oligonucleotides comprise
 CC a nucleotide sequence complementary to that of a translocation junction-
 CC spanning cellular nucleic acid segment where the translocation is inter-
 CC or intra-chromosomal. These probes may also be used as primers for
 CC detecting chromosomal translocations associated with diseases, esp.
 CC leukemia, sarcoma, lymphoma, chondrodysplasia, Prader-Willi syndrome,
 CC muscular hypotonia, incontinentia pigmenti, rhabdo-myosarcoma, trisomy,
 CC myelodysplasia, refractory anaemia, balanced X-autosome, Beckwith-
 CC Wiedemann syndrome or endocrine dysplasia. This sequence is given as
 CC represented in the specification. (Updated on 25-MAR-2003 to correct PN

CC	field.)
XX	
SQ	Sequence 25 BP; 5 A; 6 C; 5 G; 9 T; 0 U; 0 Other;
OY	Query Match 0.2%; Score 16.4; DB 1; Length 25; Best Local Similarity 94.4%; Pred. No. 1.5e+03; Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0
DB	2540 AGCTCCAGATCCTGACGT 2557 2 AGCTCCAGATCCTGACTT 19
RESULT 1608	
ID	AAQ56548 standard; DNA; 25 BP.
XX	
AC	AAQ56548;
XX	
DT	25-MAR-2003 (revised)
DT	22-JUL-1994 (first entry)
XX	
DE	Nucleic acid detection target sequence.
XX	
KW	Nucleic acid; detection; probe; hybridisation assay; complementary; cell;
KW	virus; assay; hybridise; fluorescent dye; kit; ss.
OS	Synthetic.
XX	
PN	WO9402643-A1.
XX	
PD	03-FEB-1994.
XX	
Pf	16-JUL-1993; 93WO-US006715.
XX	
PR	17-JUL-1992; 92US-00915900.
XX	
PA	(APRO-) APPOGENEX INC.
XX	
PI	Prashad N, Bick M, Weber WD, Cubbage ML, Ju SC, Asgari M;
XX	
DR	WPI, 1994-048900/06.
XX	
PT	Detection of double-stranded nucleic acids - by hybridisation assay using
PT	probes complementary to each strand.
XX	
PS	Disclosure; Page 50; 65pp; English.
XX	
CC	Sequences (AAQ56512-539) show various probes used to detect double
CC	stranded nucleic acids using a hybridisation assay. The probes are all
CC	labelled with a fluorescent molecule. Sequences (AAQ56540-562) show target
CC	sequences to which the probes hybridise. The example DNA molecule used
CC	was from a human cervical carcinoma derived cell line. (updated on 25-MAR
CC	-2003 to correct PN field.)
XX	
SQ	Sequence 25 BP; 5 A; 6 C; 5 G; 9 T; 0 U; 0 Other;
OY	Query Match 0.2%; Score 16.4; DB 1; Length 25; Best Local Similarity 94.4%; Pred. No. 1.5e+03; Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0
DB	2540 AGCTCCAGATCCTGACGT 2557 2 AGCTCCAGATCCTGACTT 19
RESULT 1609	
ID	AAA68928/c
XX	AAA68928 standard; DNA; 25 BP.
AC	AAA68928;
XX	
DT	15-SEP-2003 (revised)

DT	06-AUG-2003	(revised)
DT	27-OCT-2000	(first entry)
XX		
DE	Bacteriophage 96 ORF RBS sequence 96ORF320.	
XX		
KW	Bacteriophage; antimicrobial; genome; identification; antibacterial;	
KW	bacterial growth inhibition; PCR primer; RBS; ribosome binding site;	
XX	bacterial infection; ss.	
XX		
OS	Staphylococcus aureus; bacteriophage 96.	
PN	WO20002825-A2.	
XX		
PD	08-JUN-2000.	
XX		
PF	03-DEC-1999; 99WO-IB002040.	
XX		
PR	03-DEC-1999; 98US-0110992P.	
PR	03-JUN-1999; 99US-00326144.	
PR	28-SEP-1999; 99US-00407804.	
PR	30-SEP-1999; 99US-0157218P.	
PR	01-DEC-1999; 99US-0168777P.	
PR	02-DEC-1999; 99US-00454252.	
XX		
PA	(PHAG-) PHAGETECH INC.	
PI	Pelletier J, Gros P, Dubow M;	
XX	WPI, 2000-412361/35.	
DR		
PT	Identifying a bacteriophage coding region for treating bacterial	
PT	infections comprises identifying a nucleic acid encoding a product that	
PT	inhibits bacteria when a bacteriophage infects a bacterium.	
XX		
PS	Disclosure; Page 203; 456pp; English.	
XX		
CC	The present invention describes a method for identifying a bacteriophage	
CC	coding region encoding a product active on an essential bacterial target.	
CC	The method comprises identifying a nucleic acid sequence encoding a gene	
CC	product that provides a bacteria-inhibiting function when an	
CC	uncharacterised bacteriophage infects a pathogenic bacterium. The	
CC	compound active on a target of a bacteriophage inhibitor protein in a	
CC	bacteria is used to treat or prevent a bacterial infection in an animal.	
CC	AA668243 to AA669442 and AAB16523 to AAB16954 represent bacteriophage	
CC	nucleotide and protein sequences which are used in the exemplification of	
CC	the present invention. (Updated on 06-AUG-2003 to correct OS field.)	
CC	(Updated on 15-SEP-2003 to standardise OS field)	
XX		
SO	Sequence 25 BP; 7 A; 5 C; 5 G; 8 T; 0 U; 0 Other;	
XX		
Query Match	0.2%; Score 16.4; DB 1; Length 25;	
Best Local Similarity	94.4%; Pred. No. 1.5e+03;	
Matches 17; Conservative	0; Mismatches 1; Indels 0; Gaps 0	
Oy	6536 CCATAGCATATCTGTAA 6553	
DB	19 CCCTTAGCATATCTGTAA 2	
XX		
RESULT 1610		
AAAC96449		
ID	AAAC96449 standard; DNA; 25 BP.	
XX		
AC	AAAC96449;	
XX		
DT	26-FEB-2001 (first entry)	
XX		
DE	HLA DQB1 gene PCR primer #1.	
XX		
KW	DNA sequence analysis; sequencing; protein sequence; protein structure;	
KW	gene typing; organ donation; bacteria identification; 16S rRNA; HLA;	
XX	human leukocyte antigen; PCR primer; ss.	
XX		

OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 51; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 4 A; 2 C; 4 G; 15 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 16.4; DB 1; Length 25;
Best Local Similarity 94.4%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4472 TTTT TTTT TTTT TTTT GCTTG 4489
DB 1 TTTT TTTT TTTT TTTT TTTT GCTTG 18
XX
RESULT 1611
AAC95730
ID AAC95730 standard; DNA; 25 BP.
XX
AC AAC95730;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA DQB1 gene PCR primer #1.
XX
XX DNA sequence analysis; sequencing; protein sequence; protein structure;
KM gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KM human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or

PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 39; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 4 A; 2 C; 4 G; 15 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 16.4; DB 1; Length 25;
Best Local Similarity 94.4%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4472 TTTT TTTT TTTT TTTT GCTTG 4489
DB 1 TTTT TTTT TTTT TTTT TTTT GCTTG 18
XX
RESULT 1612
AAC95737
ID AAC95737 standard; DNA; 25 BP.
XX
AC AAC95737;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA DQB1 gene PCR primer #8.
XX
XX DNA sequence analysis; sequencing; protein sequence; protein structure;
KM gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KM human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 39; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 3 A; 4 C; 2 G; 16 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 16.4; DB 1; Length 25;

PI uftendahl P, Wong K;
 XX WPI, 2000-679677/66.
 XX
 XX PT Identifying extendible primers for use in identification, or
 PT classification of a nucleic acid of an organism, allele or gene such as
 PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
 PT specific length.
 XX
 XX PS Claim 14; Page 47; 66pp; English.
 XX
 CC The present invention provides a method for identifying a set of
 CC extendible primers which can be used in the identification, typing and
 CC classification of genes. This can then be used to predict protein
 CC sequence and structure, in organ donation to match the organ with the
 CC receiver, and to identify bacteria in a sample. The method can be used to
 CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
 CC particular
 XX
 XX SQ Sequence 25 BP; 1 A; 3 C; 5 G; 16 T; 0 U; 0 Other;
 Query Match 0.2%; Score 16.4; DB 1; Length 25;
 Best Local Similarity 94.4%; Pred. No. 1.5e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4471 TTTT TTTT TTTT TTTT GCTT 4488
 DB 1 TTTT TTTT TTTT TTTT GCTT 18
 RESULT 1616
 ADB05455
 ID ADB05455 standard; DNA; 25 BP.
 XX
 XX ADB05455;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human MD212 scanning oligonucleotide SEQ ID 6441.
 XX
 XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
 KM zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
 KM chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
 KM developmental disorder; ss.
 XX
 XX Homo sapiens.
 OS
 XX
 XX EP1281758-A2.
 PN
 XX
 PD 05-FEB-2003.
 XX
 XX 30-JUL-2002; 2002EP-00016874.
 XX
 XX 02-AUG-2001; 2001US-00922181.
 PR
 XX (AEOM-) AEOMICA INC.
 PA
 XX
 XX Shannon M, Gu Y, Nguyen C;
 PI
 XX
 DR WPI; 2003-423107/40.
 XX
 PT New zinc finger-containing proteins and nucleic acids, useful in
 PT manufacturing a medicament for treating or preventing a disorder
 PT associated with decreased or increased expression or activity of MD23,
 PT MD24, MD27 or MD212, e.g. cancer.
 XX
 XX Example 8; SEQ ID NO 6441; 103pp; English.
 PS
 XX
 CC The present invention relates to novel human zinc finger-containing
 CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
 CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
 CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
 CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
 CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,

CC or in manufacturing a medicament for treating or preventing a disorder
 CC associated with decreased or increased expression or activity of MD23,
 CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
 CC acids and proteins are also useful for diagnosing or monitoring a disease
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
 CC acids can also be used as probes to detect and characterize gross
 CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
 CC useful in constructing microarrays for measuring gene expression. The
 CC proteins are useful as therapeutic agents for gene therapy or as
 CC vaccines. The present sequence was used to illustrate the invention.
 XX
 XX SQ Sequence 25 BP; 4 A; 4 C; 7 G; 10 T; 0 U; 0 Other;
 Query Match 0.2%; Score 16.4; DB 1; Length 25;
 Best Local Similarity 94.4%; Pred. No. 1.5e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5656 CTCATCCTCTAGTGGG 5673
 DB 4 CTCATCCTCTAGTGGG 21
 RESULT 1617
 ADB05451
 ID ADB05451 standard; DNA; 25 BP.
 XX
 XX ADB05451;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human MD212 scanning oligonucleotide SEQ ID 6437.
 XX
 XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
 KM zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
 KM chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
 KM developmental disorder; ss.
 XX
 XX Homo sapiens.
 OS
 XX
 XX EP1281758-A2.
 PN
 XX
 PD 05-FEB-2003.
 XX
 XX 30-JUL-2002; 2002EP-00016874.
 XX
 XX 02-AUG-2001; 2001US-00922181.
 PR
 XX (AEOM-) AEOMICA INC.
 PA
 XX
 XX Shannon M, Gu Y, Nguyen C;
 PI
 XX
 DR WPI; 2003-423107/40.
 XX
 PT New zinc finger-containing proteins and nucleic acids, useful in
 PT manufacturing a medicament for treating or preventing a disorder
 PT associated with decreased or increased expression or activity of MD23,
 PT MD24, MD27 or MD212, e.g. cancer.
 XX
 XX Example 8; SEQ ID NO 6437; 103pp; English.
 PS
 XX
 CC The present invention relates to novel human zinc finger-containing
 CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
 CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
 CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
 CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
 CC or in manufacturing a medicament for treating or preventing a disorder
 CC associated with decreased or increased expression or activity of MD23,
 CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
 CC acids and proteins are also useful for diagnosing or monitoring a disease
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
 CC acids can also be used as probes to detect and characterize gross
 CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
 CC useful in constructing microarrays for measuring gene expression. The


```
ID ADB05457 standard; DNA; 25 BP.
XX
AC ADB05457;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD212 scanning oligonucleotide SEQ ID 6443.
XX
KM Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KM chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KM developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
DR WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
XX
PS Example 8; SEQ ID NO 6443; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 25 BP; 6 A; 4 C; 7 G; 8 T; 0 U; 0 Other;

Query Match      0.2%; Score 16.4; DB 1; Length 25;
Best Local Similarity 94.4%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5656 CTCATCCTCTTAGTGGG 5673
      ||||| ||||| ||||| |||||
DB      2 CTCATCCTCTTAGTGGG 19

RESULT 1621
ADB05453
ID ADB05453 standard; DNA; 25 BP.
XX
AC ADB05453;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD212 scanning oligonucleotide SEQ ID 6439.
XX
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KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
DR WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
XX
PS Example 8; SEQ ID NO 6439; 103pp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 25 BP; 4 A; 5 C; 5 G; 11 T; 0 U; 0 Other;

Query Match      0.2%; Score 16.4; DB 1; Length 25;
Best Local Similarity 94.4%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5656 CTCATCCTCTTAGTGGG 5673
      ||||| ||||| ||||| |||||
DB      6 CTCATCCTCTTAGTGGG 23

RESULT 1622
ADB05456
ID ADB05456 standard; DNA; 25 BP.
XX
AC ADB05456;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD212 scanning oligonucleotide SEQ ID 6442.
XX
KM Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
```

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XX 05-FEB-2003.
PD 30-JUL-2002; 2002EP-00016874.
XX 02-AUG-2001; 2001US-00922181.
XX (AEOM-) AEOMICA INC.
XX Shannon M, Gu Y, Nguyen C;
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 6442; 103bp; English.
XX
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
XX
XX Sequence 25 BP; 5 A; 4 C; 7 G; 9 T; 0 U; 0 Other;
XX
XX
XX Query Match          0.2%; Score 16.4; DB 1; Length 25;
XX Best Local Similarity 94.4%; Pred. No. 1.5e+03;
XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 5656 CTCATCCTCTTAGTGGG 5673
XX ||||| ||||| |||||
XX 3 CTCATCCTCTTAGTGGG 20
XX
XX RESULT 1623
XX ADB05458
XX ID ADB05458 standard; DNA; 25 BP.
XX
XX ADB05458;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human MD212 scanning oligonucleotide SEQ ID 6444.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX
XX Homo sapiens.
XX
XX EPI281758-A2.
XX
XX 05-FEB-2003.
XX
XX 30-JUL-2002; 2002EP-00016874.
XX
XX 02-AUG-2001; 2001US-00922181.
XX
XX (AEOM-) AEOMICA INC.

```

```

XX Shannon M, Gu Y, Nguyen C;
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 6444; 103bp; English.
XX
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
XX
XX Sequence 25 BP; 7 A; 4 C; 7 G; 7 T; 0 U; 0 Other;
XX
XX
XX Query Match          0.2%; Score 16.4; DB 1; Length 25;
XX Best Local Similarity 94.4%; Pred. No. 1.5e+03;
XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 5656 CTCATCCTCTTAGTGGG 5673
XX ||||| ||||| |||||
XX 1 CTCATCCTCTTAGTGGG 18
XX
XX RESULT 1624
XX AB281771/C
XX ID AB281771 standard; DNA; 25 BP.
XX
XX AB281771;
XX
XX 11-JUN-2003 (first entry)
XX
XX Oligonucleotide HD37/25 used to treat Huntington's disease.
XX
XX Huntington's disease; nootropic; anticonvulsant; phosphorothioate;
XX huntingtin; human; gene therapy; ss.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX Key
XX misc_binding
XX
XX Location/Qualifiers
XX 1..13
XX /tag= C
XX /bound_molecule= "HD gene exon 1 triplet repeat region"
XX /note= "hybridises to bases 17-29 of sequence given in
XX AB281770"
XX 1..3
XX /tag= a
XX /mod_base= OTHER
XX /note= "phosphorothioate linkages"
XX 14
XX /tag= d
XX /note= "mismatch with HD gene"
XX 15..25
XX /tag= e
XX /bound_molecule= "HD gene exon 1 triplet repeat region"
XX /note= "hybridises to bases 5-15 of sequence given in
XX AB281771"

```



```
FT modified_base    23..25  
TT      /*tag= b  
TT      /mod_base= OTHER  
XX      /note= "phosphorothioate linkages"  
PN MO2003013437-A2.  
XD  
PD 20-FEB-2003.  
XX  
PF 07-AUG-2002; 2002WO-USO25352.  
XX  
PR 07-AUG-2001; 2001US-0310757P.  
PR 08-AUG-2001; 2001US-0310770P.  
PR 08-AUG-2001; 2001US-0310889P.  
PR 04-DEC-2001; 2001US-0337219P.  
XX  
PA (UYDE ) UNIV DELAWARE.  
XX  
PI Kmiec EB, Parekh-Olmedo H;  
DR WPI ; 2003-256478/25.  
XX  
  
PT New single stranded oligonucleotides comprising a DNA domain having at  
PT least one mismatch with respect to the genetic sequence of the  
PT Huntington's disease gene to be altered, useful for treating or  
PT preventing Huntington's disease.  
XX  
PS Example 4; Fig 13a; 133bp; English.  
XX  
CC The present sequence is that of oligonucleotide HD3T/25, which was  
CC designed for targeted alteration of the Huntington's disease (HD) gene,  
CC converting a CAG triplet to CTG in the poly-glutamine encoding triplet  
CC repeat region of exon 1. The oligonucleotide is modified at each end,  
CC bearing phosphorothioate linkages in the 3 terminal bases. It is an  
CC example of oligonucleotides of the invention that alter the genomic HD  
CC gene sequence, interrupting the triplet repeat region in exon 1, and  
CC reducing the propensity of huntingtin protein to form intracellular  
CC aggregates. The oligonucleotides can be used for the treatment or  
CC prevention of HD  
XX  
SQ Sequence 25 BP; 4 A; 7 C; 9 G; 5 T; 0 U; 0 Other;
```

```
Gy       7413 CAGCAGCAGCACGCACG   7430  
Db          |||||  
         18 CAGCTGCAGCACGCACG   1
```

```
RESULT_1625  
ABZ81755/C  
ID ABZ81755 standard; DNA; 25 BP.  
XX  
Xx ABZ81755;  
DT 11-JUN-2003 (first entry)  
DB Huntington's disease gene targeted oligonucleotide HD3S/25.  
XX  
Xx Huntington's disease; neurotropic; anticonvulsant; huntingtin; human;  
KW gene therapy; phosphorothioate; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT     1..  
FT     /*tag= a  
FT     /mod_base= OTHER  
FT     /note= "phosphorothioate linkages"  
FT modified base    23..25
```

```

FT      /*tag= b
FT      /mod_base= OTHER
FT      /note="phosphorothioate linkages"
XX
XX
XX      WO2003013437-A2.
XX
XX      20-FEB-2003.
XX
XX      07-AUG-2002; 2002WO-US025352.
XX
XX      07-AUG-2001; 2001US-0310757P.
XX
XX      08-AUG-2001; 2001US-0310770P.
XX
XX      08-AUG-2001; 2001US-0310889P.
XX
XX      04-DEC-2001; 2001US-0337219P.
XX
XX      (UYDE ) UNIV DELAWARE.
XX
XX      Kmlec EB, Parekh-Olmedo H;
XX
XX      WPI; 2003-256478/25.
XX
XX
XX      New single stranded oligonucleotides comprising a DNA domain having at
XX      least one mismatch with respect to the genetic sequence of the
XX      Huntington's disease gene to be altered, useful for treating or
XX      preventing Huntington's disease.
XX
XX      Example 7; Fig 19; 133pp; English.
XX
XX
XX      The present sequence is that of HD3S/25, a single-stranded
XX      oligonucleotide that includes phosphorothioate linkages at both its ends.
XX      The 5' end of the oligonucleotide hybridizes to a unique portion of the
XX      first exon of the human Huntington's disease (HD) gene (see AB281778)
XX      with the remainder being complementary to the CAG repeat region of exon
XX      1. It was designed to convert the second CAG repeat triplet of exon 1 to
XX      CTG, thereby creating a restriction fragment length polymorphism that
XX      enabled cleavage by PvuII. PCR was used to analyse for the event in
XX      genomic DNA following transfection of lymphoblastoid cells containing 16
XX      and 20 triplet repeat (CAG) alleles in the HD gene by the
XX      oligonucleotide. Converted clones were found (see AB281779) that
XX      exhibited the CTG codon in the second triplet position. A disruption of
XX      Huntington protein (huntingtin) aggregation was observed following the
XX      treatment. The invention relates to oligonucleotides such as HD3S/25 that
XX      alter the genomic HD gene sequence and/or reduce the propensity of
XX      huntingtin to form intracellular aggregates. Such oligonucleotides can be
XX      used for the treatment or prevention of HD
XX
XX      SEQ
XX
XX      Sequence 25 BP; 4 A; 7 C; 9 G; 5 T; 0 U; 0 Other;
XX
XX      Query Match      0.2%; Score 16.4; DB 1; Length 25;
XX      Best Local Similarity 94.4%; Pred. No. 1.5e+03;
XX      Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0.
XX
XX      QY      7413 CAGCAGCAGCAGCAGCAG 7430
XX      DB      18 CAGCTGCAGCAGCAGCAG 1
XX
XX      ACI99120
XX
XX      ACI99120 standard; DNA; 25 BP.
XX
XX      ACI99120;
XX
XX      DT      14-OCT-2003 (first entry)
XX
XX      DE      Human microarray DNA oligonucleotide SEQ ID NO 99111.
XX
XX      ESF; ss; probe; expressed sequence tag; microarray; gene expression;
XX      KW      genetic variation; diallelic marker; polymorphism; human;
XX      cross-species comparison.
XX
XX      OS      Homo sapiens.
XX

```


XX The present invention describes the human angiomotin-like protein 1
 CC (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene
 CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
 CC compositions of the present invention can be used for treating or
 CC preventing a disorder associated with decreased or increased expression
 CC or activity of AMLP1. The present sequence represents a scanning
 CC oligonucleotide for human AMLP1a, which is used in an example from the
 CC present invention.
 XX
 SQ Sequence 25 BP; 7 A; 7 C; 11 G; 0 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 16.4; DB 1; Length 25;
 Best Local Similarity 94.4%; Pred. No. 1.5e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 7413 CAGCAGCAGCAGCAGCAG 7430
 DB 1 CAGCAGCAACAGCAGCAG 18
 RESULT 1629
 ADC38472
 ID ADC38472 standard; DNA; 25 BP.
 XX
 AC ADC38472;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human AMLP1b scanning 25-mer oligonucleotide SEQ ID NO:821.
 XX
 KM human; angiomotin-like protein 1; AMLP1; cytostatic; gene therapy;
 KM AMLP1b; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN MO2003037931-A2.
 XX
 PS 08-MAY-2003.
 PD
 PF 01-NOV-2002; 2002MO-US035129.
 XX
 PR 01-NOV-2001; 2001US-0334773P.
 XX
 PA (AMSH) AMERSHAM BIOSCIENCES SV CORP.
 XX
 PI Shannon M, Phan T;
 XX
 DR WPI; 2003-430501/40.
 XX
 PT New isolated nucleic acid molecule encoding a human angiomotin-like
 PT protein, useful for treating or preventing a disorder associated with
 PT decreased or increased expression or activity of AMLP1.
 XX
 PS Example 2; SEQ ID NO 821; 172pp; English.
 XX
 CC The present invention describes the human angiomotin-like protein 1
 CC (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene
 CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
 CC compositions of the present invention can be used for treating or
 CC preventing a disorder associated with decreased or increased expression
 CC or activity of AMLP1. The present sequence represents a scanning
 CC oligonucleotide for human AMLP1b, which is used in an example from the
 CC present invention.
 XX
 SQ Sequence 25 BP; 12 A; 2 C; 8 G; 3 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 16.4; DB 1; Length 25;
 Best Local Similarity 94.4%; Pred. No. 1.5e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4015 ATGAGAAAAAGAGAGAA 4032

DB 7 ATGAGAAAAAGAGAGAA 24
 RESULT 1630
 ADC38475
 ID ADC38475 standard; DNA; 25 BP.
 XX
 AC ADC38475;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human AMLP1b scanning 25-mer oligonucleotide SEQ ID NO:824.
 XX
 KM human; angiomotin-like protein 1; AMLP1; cytostatic; gene therapy;
 KM AMLP1b; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN MO2003037931-A2.
 XX
 PS 08-MAY-2003.
 PD
 PF 01-NOV-2002; 2002MO-US035129.
 XX
 PR 01-NOV-2001; 2001US-0334773P.
 XX
 PA (AMSH) AMERSHAM BIOSCIENCES SV CORP.
 XX
 PI Shannon M, Phan T;
 XX
 DR WPI; 2003-430501/40.
 XX
 PT New isolated nucleic acid molecule encoding a human angiomotin-like
 PT protein, useful for treating or preventing a disorder associated with
 PT decreased or increased expression or activity of AMLP1.
 XX
 PS Example 2; SEQ ID NO 824; 172pp; English.
 XX
 CC The present invention describes the human angiomotin-like protein 1
 CC (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene
 CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
 CC compositions of the present invention can be used for treating or
 CC preventing a disorder associated with decreased or increased expression
 CC or activity of AMLP1. The present sequence represents a scanning
 CC oligonucleotide for human AMLP1b, which is used in an example from the
 CC present invention.
 XX
 SQ Sequence 25 BP; 11 A; 2 C; 8 G; 4 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 16.4; DB 1; Length 25;
 Best Local Similarity 94.4%; Pred. No. 1.5e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4015 ATGAGAAAAAGAGAGAA 4032
 DB 4 ATGAGAAAAAGAGAGAA 21
 RESULT 1631
 ADC38478
 ID ADC38478 standard; DNA; 25 BP.
 XX
 AC ADC38478;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human AMLP1b scanning 25-mer oligonucleotide SEQ ID NO:827.
 XX
 KM human; angiomotin-like protein 1; AMLP1; cytostatic; gene therapy;
 KM AMLP1b; ss.
 XX

```
OS Synthetic.
OS Homo sapiens.
XX
XX WO2003037931-A2.
XX
XX PD 08-MAY-2003.
XX
XX PF 01-NOV-2002; 2002WO-US035129.
XX
XX PR 01-NOV-2001; 2001US-0334773P.
XX
XX PA (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
XX
XX PI Shannon M, Phan T;
XX
XX DR WPI; 2003-430501/40.
XX
XX PT New isolated nucleic acid molecule encoding a human angiomin-1-like
XX protein, useful for treating or preventing a disorder associated with
XX decreased or increased expression or activity of AMPL1.
XX
XX PS Example 2; SEQ ID NO 827; 172pp; English.
XX
XX CC The present invention describes the human angiomin-1-like protein 1
XX (AMPL1). human AMPL1 has cytosolic activity, and can be used in gene
XX therapy. The AMPL1 protein, nucleic acid molecules, antibodies, and
XX compositions of the present invention can be used for treating or
XX preventing a disorder associated with decreased or increased expression
XX or activity of AMPL1. The present sequence represents a scanning
XX oligonucleotide for human AMPL1b, which is used in an example from the
XX present invention.
XX
XX SQ Sequence 25 BP; 11 A; 1 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.4; DB 1; Length 25;
Best Local Similarity 94.4%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4015 ATGAGAAAAAGAGAGAA 4032
Db 1 ATGAGAAAAAGAGAGAA 18

RESULT 1632
ADC38471
ID ADC38471 standard; DNA; 25 BP.
XX
XX AC ADC38471;
XX
XX DT 18-DEC-2003 (first entry)
XX
XX DE Human AMPL1b scanning 25-mer oligonucleotide SEQ ID NO:820.
XX
XX KW human; angiomin-1-like protein 1; AMPL1; cytosolic; gene therapy;
XX AMPL1b; ss.
XX
XX OS Synthetic.
XX
XX OS Homo sapiens.
XX
XX PN WO2003037931-A2.
XX
XX PD 08-MAY-2003.
XX
XX PF 01-NOV-2002; 2002WO-US035129.
XX
XX PR 01-NOV-2001; 2001US-0334773P.
XX
XX PA (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
XX
XX PI Shannon M, Phan T;
XX
XX DR WPI; 2003-430501/40.
XX
```

```
PT New isolated nucleic acid molecule encoding a human angiomin-1-like
PT protein, useful for treating or preventing a disorder associated with
PT decreased or increased expression or activity of AMPL1.
XX
XX PS Example 2; SEQ ID NO 820; 172pp; English.
XX
XX CC The present invention describes the human angiomin-1-like protein 1
XX (AMPL1). human AMPL1 has cytosolic activity, and can be used in gene
XX therapy. The AMPL1 protein, nucleic acid molecules, antibodies, and
XX compositions of the present invention can be used for treating or
XX preventing a disorder associated with decreased or increased expression
XX or activity of AMPL1. The present sequence represents a scanning
XX oligonucleotide for human AMPL1b, which is used in an example from the
XX present invention.
XX
XX SQ Sequence 25 BP; 12 A; 2 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.4; DB 1; Length 25;
Best Local Similarity 94.4%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4015 ATGAGAAAAAGAGAGAA 4032
Db 8 ATGAGAAAAAGAGAGAA 25

RESULT 1633
ADC38477
ID ADC38477 standard; DNA; 25 BP.
XX
XX AC ADC38477;
XX
XX DT 18-DEC-2003 (first entry)
XX
XX DE Human AMPL1b scanning 25-mer oligonucleotide SEQ ID NO:826.
XX
XX KW human; angiomin-1-like protein 1; AMPL1; cytosolic; gene therapy;
XX AMPL1b; ss.
XX
XX OS Synthetic.
XX
XX OS Homo sapiens.
XX
XX PN WO2003037931-A2.
XX
XX PD 08-MAY-2003.
XX
XX PF 01-NOV-2002; 2002WO-US035129.
XX
XX PR 01-NOV-2001; 2001US-0334773P.
XX
XX PA (AMSH ) AMERSHAM BIOSCIENCES SV CORP.
XX
XX PI Shannon M, Phan T;
XX
XX DR WPI; 2003-430501/40.
XX
XX PT New isolated nucleic acid molecule encoding a human angiomin-1-like
XX protein, useful for treating or preventing a disorder associated with
XX decreased or increased expression or activity of AMPL1.
XX
XX PS Example 2; SEQ ID NO 826; 172pp; English.
XX
XX CC The present invention describes the human angiomin-1-like protein 1
XX (AMPL1). human AMPL1 has cytosolic activity, and can be used in gene
XX therapy. The AMPL1 protein, nucleic acid molecules, antibodies, and
XX compositions of the present invention can be used for treating or
XX preventing a disorder associated with decreased or increased expression
XX or activity of AMPL1. The present sequence represents a scanning
XX oligonucleotide for human AMPL1b, which is used in an example from the
XX present invention.
XX
XX SQ Sequence 25 BP; 11 A; 1 C; 8 G; 5 T; 0 U; 0 Other;
```

Query Match 0.2%; Score 16.4; DB 1; Length 25;
 Best Local Similarity 94.4%; Pred. No. 1.5e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4015 ATGAGAAAAAGAGAGAA 4032
 |||||
 2 ATGAGAAAGAGAGAGA 19

Db

RESULT 1634
 ADC38182
 ID ADC38182 standard; DNA; 25 BP.
 XX
 AC ADC38182;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human AMLP1a scanning 25-mer oligonucleotide SEQ ID NO:531.
 XX
 KW human; angiotomcin-like protein 1; AMLP1; cytostatic; gene therapy;
 XX AMLP1a; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO2003037931-A2.
 XX
 PS 08-MAY-2003.
 PD
 XX
 PF 01-NOV-2002; 2002WO-US035129.
 XX
 PR 01-NOV-2001; 2001US-0334773P.
 XX
 PA (AMSH) AMERSHAM BIOSCIENCES SV CORP.
 XX
 PI Shannon M, Phan T;
 XX
 DR WPI; 2003-430501/40.
 XX
 DT
 XX
 PT New isolated nucleic acid molecule encoding a human angiotomcin-like
 protein, useful for treating or preventing a disorder associated with
 decreased or increased expression or activity of AMLP1.
 XX
 PS Example 2; SEQ ID NO 531; 172pp; English.
 XX
 CC The present invention describes the human angiotomcin-like protein 1
 (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene
 CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
 CC compositions of the present invention can be used for treating or
 CC preventing a disorder associated with decreased or increased expression
 CC or activity of AMLP1. The present sequence represents a scanning
 CC oligonucleotide for human AMLP1a, which is used in an example from the
 CC present invention.
 XX
 SQ Sequence 25 BP; 8 A; 7 C; 9 G; 1 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.4; DB 1; Length 25;
 Best Local Similarity 94.4%; Pred. No. 1.5e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7415 GCAGCAGCAGCAGCAGCA 7432
 |||||
 8 GCAGCAGCAGCAGCAGCA 25

Db

RESULT 1635
 ADC38476
 ID ADC38476 standard; DNA; 25 BP.
 XX
 AC ADC38476;
 XX
 DT 18-DEC-2003 (first entry)
 XX

DE Human AMLP1b scanning 25-mer oligonucleotide SEQ ID NO:825.
 XX
 KW human; angiotomcin-like protein 1; AMLP1; cytostatic; gene therapy;
 KW AMLP1b; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO2003037931-A2.
 XX
 PS 08-MAY-2003.
 PD
 XX
 PF 01-NOV-2002; 2002WO-US035129.
 XX
 PR 01-NOV-2001; 2001US-0334773P.
 XX
 PA (AMSH) AMERSHAM BIOSCIENCES SV CORP.
 XX
 PI Shannon M, Phan T;
 XX
 DR WPI; 2003-430501/40.
 XX
 DT
 XX
 PT New isolated nucleic acid molecule encoding a human angiotomcin-like
 protein, useful for treating or preventing a disorder associated with
 decreased or increased expression or activity of AMLP1.
 XX
 PS Example 2; SEQ ID NO 825; 172pp; English.
 XX
 CC The present invention describes the human angiotomcin-like protein 1
 (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene
 CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
 CC compositions of the present invention can be used for treating or
 CC preventing a disorder associated with decreased or increased expression
 CC or activity of AMLP1. The present sequence represents a scanning
 CC oligonucleotide for human AMLP1b, which is used in an example from the
 CC present invention.
 XX
 SQ Sequence 25 BP; 11 A; 2 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.4; DB 1; Length 25;
 Best Local Similarity 94.4%; Pred. No. 1.5e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4015 ATGAGAAAAAGAGAGAA 4032
 |||||
 3 ATGAGAAAGAGAGAGA 20

Db

RESULT 1636
 ADC38474
 ID ADC38474 standard; DNA; 25 BP.
 XX
 AC ADC38474;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human AMLP1b scanning 25-mer oligonucleotide SEQ ID NO:823.
 XX
 KW human; angiotomcin-like protein 1; AMLP1; cytostatic; gene therapy;
 KW AMLP1b; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO2003037931-A2.
 XX
 PS 08-MAY-2003.
 PD
 XX
 PF 01-NOV-2002; 2002WO-US035129.
 XX
 PR 01-NOV-2001; 2001US-0334773P.
 XX
 PA (AMSH) AMERSHAM BIOSCIENCES SV CORP.

XX Shannon M, Phan T;
PI
XX WPI; 2003-430501/40.
DR
XX
XX New isolated nucleic acid molecule encoding a human angiogenin-like
PT protein, useful for treating or preventing a disorder associated with
PT decreased or increased expression or activity of AMLP1.
PS
XX Example 2; SEQ ID NO 823; 172bp; English.
XX
XX The present invention describes the human angiogenin-like protein 1
CC (AMLP1). human AMLP1 has cytostatic activity, and can be used in gene
CC therapy. The AMLP1 protein, nucleic acid molecules, antibodies, and
CC compositions of the present invention can be used for treating or
CC preventing a disorder associated with decreased or increased expression
CC or activity of AMLP1. The present sequence represents a scanning
CC oligonucleotide for human AMLP1b, which is used in an example from the
CC present invention.
XX
XX Sequence 25 BP; 11 A; 2 C; 8 G; 4 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 16.4; DB 1; Length 25;
Best Local Similarity 94.4%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CY 4015 ATGAGAAAAAGAGAGAA 4032
|||||
db 5 ATGAGAAAAAGAGAGAA 22

Query Match	Score	DB 1	Length	25
Best Local Similarity	94.4%	Pred No. 1.5e+03		
Sequence 25 BP; 7 A; 2 C; 13 G; 3 T; 0 U; 0 Other;				
Query Match	0.2%	Score 16.4	DB 1	Length 25
Best Local Similarity	94.4%	Pred No. 1.5e+03		

[illegible]

```

DR      WPI; 1999-183822/16.
XX      Peptides having at least two new nucleotides - useful as primers in RT-PCR.
PT
XX
XX
PS      Example 1; Page 12; 19pp; Japanese.
XX
CC      This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or a nucleotide with volatary sequence; m = 0 or 1; alpha = thymine; n = natural number indicating the repetition of alpha; beta, delta = V or N; V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or thymine; gamma, k = thymine; k = natural number of 3 or over indicating the repetition of gamma, in which thymine expressed by gamma is composed of 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are useful as primers for RT-PCR and determination of base sequences. The new sequences allow for reproducible and highly efficient analysis of gene sequences
CC
CC
XX      Sequence 18 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 2 Other;
SQ
Query Match          0.2%; Score 16.2; DB 1; Length 18;
Best Local Similarity 94.1%; Pred.No.1e+03;
Matches    16; Conservative   1; Mismatches     0; Indels      0; Gaps      0;
QY      4468 TTTTTTTTTTTTTTTTGG 4484
           |||
Db       1 TTTTTTTTTTTTTTTTV 17
RESULT 1639
AAQ26592/c
ID      AAQ26592 standard; DNA; 21 BP.
XX
AC      AAQ26592;
XX
DT      24-OCT-2003 (revised)
DT      25-MAR-2003 (revised)
DT      15-JAN-1993 (first entry)
XX
DE      Predicted HIV-1 endogenous triple helix forming sequence #2.
```

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XX detection: hybridisation: probes; primers; target sequence;
KM pathogenic organisms; bacteria; fungi; virus; retrovirus; ss.
XX
XX OS Mycobacterium avium subsp. paratuberculosis.
XX PN MO9211390-A1.
XX
XX PD 09-JUL-1992.
XX
XX PF 11-DEC-1991; 91MO-US009402.
XX PR 17-DEC-1990; 90US-00629601.
XX
XX PA (IDEX-) IDEXX LAB INC.
XX
XX PI Vary CPH;
XX
XX DR WPI; 1992-250109/30.
XX
XX PT Nucleic acid sequence detection by triple helix formation for pathogenic
PT organisms - comprises amplifying in vitro to give product duplex(es) and
PT detecting one duplex by hybridising with a third strand of nucleic acid
PT without denaturation.
XX
XX PS Example 8; Page 50; 80pp; English.
XX
XX CC This sequence represents genomic nucleotides 2250-2270 of HIV-1 that are
CC predicted to form a triple helical structure. (See also AA026591) See
CC also AA026566-614 (Updated on 25-MAR-2003 to correct PN field.) (Updated
CC on 24-OCT-2003 to standardise OS field)
XX
XX SQ Sequence 21 BP; 13 A; 0 C; 7 G; 1 T; 0 U; 0 Other;

Query Match          0.2%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5698 TTTTGCTTCCTTTCTCTCTT 5718
    |||||
DB 21 TTTTCCTTCCTTTCTCATTT 1

RESULT 1640
AA056657
ID AA056657 standard; DNA; 21 BP.
XX
XX AC AA056657;
XX
XX DT 25-MAR-2003 (revised)
XX DT 16-AUG-1994 (first entry)
XX
XX DE Human megakaryocyte differentiation factor PCR primer TP7.
XX
XX KM Human megakaryocyte differentiation factor; MDF; thrombopoietin;
KM haematopoietic stimulating factor; thrombocytopoensis; platelet;
KM bone marrow transplantation; cancer chemotherapy;
KM polymerase chain reaction; primer; ss.
XX
XX OS Synthetic.
XX
XX PN EP583884-A1.
XX PD 23-FEB-1994.
XX
XX PF 19-JUL-1993; 93EP-00305654.
XX
XX PR 17-JUL-1992; 92JP-00212305.
XX PR 04-MAR-1993; 93JP-00067339.
XX
XX PA (SUNR ) SUNTORY LTD.
XX
XX PI Tsujimoto M, Iwasa F, Tsunoka N, Nakazato H, Miura K, Iehida N;

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PI Kurihara T, Yamachi K, Yamaguchi N;
XX
XX DR WPI; 1994-058782/08.
XX
XX PT New megakaryocyte differentiation factor - isolated from human epidermoid
PT carcinoma cells, used to treat conditions involving a decrease in
PT platelets.
XX
XX PS Example 2; Page 26; 47pp; English.
XX
XX CC The cDNA coding for human megakaryocyte differentiation factor (MDF) was
XX isolated from a library prepared using mRNA derived from human epidermoid
XX carcinoma A431 cells. The oligonucleotides AA056647 - AA056667 were used
XX in the isolation and sequence analysis of MDF cDNA by PCR. Oligomer TP7
XX corresponds to nucleotides 683-703 of the human MDF cDNA sequence (see
XX CC AA056670). (Updated on 25-MAR-2003 to correct PN field.)
XX
XX SQ Sequence 21 BP; 4 A; 6 C; 7 G; 4 T; 0 U; 0 Other;

Query Match          0.2%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 694 GATGTGCCATGAGGACCTG 714
    |||||
DB 1 GCTGTGCCATGATGACCAAG 21

RESULT 1641
AA093769
ID AA093769 standard; DNA; 21 BP.
XX
XX AC AA093769;
XX
XX DT 29-JUN-1998 (first entry)
XX
XX DE nNOS exon 3 specific thermal RACE-PCR primer.
XX
XX KM PCR primer; thermal RACE; nNOS; neuronal nitric oxide synthase;
XX diagnosis; muscular dystrophy; skeletal muscle; Huntington's disease;
XX Duchenne muscular dystrophy; Becker muscular dystrophy; dystrophin;
XX sarcolemma; PDZ domain; neurodegenerative disease; Alzheimer's disease;
XX amyotrophic lateral sclerosis; gene therapy; ss.
XX
XX OS Synthetic.
XX OS Mammalia.
XX
XX PN MO9733173-A1.
XX
XX PD 12-SEP-1997.
XX
XX PF 06-MAR-1997; 97WO-US003897.
XX
XX PR 08-MAR-1996; 96US-00613114.
XX
XX PA (REGC ) UNIV CALIFORNIA.
XX
XX PI Bredt DS, Brennan JE, Chao DS;
XX
XX DR WPI; 1997-470555/43.
XX
XX PT Diagnosing muscular dystrophy by detecting absence or decrease of
XX neuronal nitric oxide synthase (nNOS) in skeletal muscle sarcolemma -
XX using new nNOS binding post-synaptic density proteins, PSD-93 and PSD-95;
XX also used for the diagnosis, prophylaxis and treatment of stroke and
XX other neurodegenerative diseases.
XX
XX PS Example 20; Page 77; 124pp; English.
XX
XX CC This sequence represents a PCR primer specific for neuronal nitric oxide
XX synthase (nNOS) used in a thermal RACE reaction. nNOS is detected in the
XX method of the invention. The method is for diagnosing muscular dystrophy
XX (MD) in a mammal by detecting absence or a decrease of nNOS in a skeletal

```


CC cells of the patient are heterozygous for the first gene, the inhibitor
 CC is active on at least one but less than all allelic forms of the gene
 CC present in a population and targets only one allelic form present in the
 CC normal somatic cells, and the first gene. The products and methods can be
 CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.
 CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
 CC lesions, benign tumours, endometriosis, polycystic kidney disease, and
 CC graft versus host disease. The method can also be used to remove
 CC malignant cells from bone marrow transplants. AA225812-Z26825 represent
 CC human polymorphic sites described in the method of the invention
 CC
 SO Sequence 21 BP; 1 A; 14 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.2; DB 1; Length 21;
 Best Local Similarity 85.7%; Pred. No. 1.3e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3384 CCTCCCGCAGCTGCACACCC 3404
 |||||
 DB 1 CCTCTCCGACGCGCTCCCCC 21

RESULT 1644
 AA209196
 ID AA209196 standard; DNA; 21 BP.
 AC AA209196;
 XX
 DT 19-OCT-1999 (first entry)
 XX
 DE Oligonucleotide 8 for DNA analysis.

KW Primer; DNA analysis; amplification; hybridisation; ss.

OS Synthetic.

XX JP11196874-A.

XX 27-JUL-1999.

XX 14-JAN-1998; 98JP-00005399.

XX 14-JAN-1998; 98JP-00005399.

XX (HITA) HITACHI LTD.

XX WPI; 1999-496652/42.

PT Analysis of DNA fragment - comprises addition of known common
 PT oligonucleotide, amplification of resultant DNA fragment and analysis and
 PT labelling of amplified DNA.
 XX
 XX

XX Example 1; Page 12; 17pp; Japanese.

CC This invention describes a novel method for the analysis of a DNA fragment
 CC which comprises: (i) addition of a known common oligonucleotide sequence
 CC to at least one terminal of each DNA fragment; (ii) amplification of the
 CC resultant DNA fragment as a primer using a first common primer containing
 CC a complementary nucleotide sequence to the above mentioned known common
 CC oligonucleotide sequence; a second common primer containing a
 CC complementary nucleotide sequence to the prepared known common
 CC oligonucleotide sequence optionally having been introduced with
 CC complementary nucleotide sequence at a terminal, and a specific primer
 CC capable of hybridisation with a DNA fragment containing whole or part of
 CC the gene having known sequence, to give amplified DNA; (iii) analysis of
 CC the amplified DNA to find the information of the DNA fragment, in which
 CC the specific primer is designed to prepare fragments of the common first
 CC and second primers and to give short fragment of amplified DNA and (iv)
 CC labelling them to make their differentiation. Differentiation of
 CC informations of known and unknown genes readily provides information of
 CC unknown gene and simultaneous monitoring of signals derived from minor
 CC genes. Furthermore, labelling of DNAs according to functions of known
 CC genes can be performed. AA209189-Z09201 represent oligonucleotide primers

CC used to illustrate the method of the invention
 XX
 SO Sequence 21 BP; 0 A; 0 C; 3 G; 18 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.2; DB 1; Length 21;
 Best Local Similarity 85.7%; Pred. No. 1.3e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4459 TCGACTTTTCTTTTCTTTT 4479
 |||||
 DB 1 TGTGGTTTTTTTTTTTTTTT 21

RESULT 1645
 AA27493/C
 ID AA27493 standard; DNA; 21 BP.

AC AA27493;
 XX
 DT 22-JUN-1999 (first entry)
 XX
 DE Human TFIID gene control primer TFIID-F.

KW INSL-4; insulin-like gene; EPIL; early placental insulin-like; antibody;
 KW vector; probe; hybridisation; tumour; hypoglycaemia; hyperglycaemia;
 KW diabetes; cardiovascular; primer; PCR; amplification; ss.

OS Synthetic.

OS Homo sapiens.

XX MO9909172-A1.

XX 25-FEB-1999.

XX 12-AUG-1998; 98WO-FR001799.

XX 14-AUG-1997; 97FR-00010387.

XX 03-NOV-1997; 97FR-00013802.

XX (INSR) INSR ROUSSY GUSTAVE.

XX Bellet D, Trolen F, Bidart J, Mock P;

XX WPI; 1999-181038/15.

PT EPIL polypeptides encoded by insulin-like gene 4 - and corresponding
 PT nucleic acids, antibodies, probes, primers, etc.
 XX
 XX

XX Example 5; Page 52; 11pp; French.

CC The invention relates to a novel INSL-4 (insulin-like gene 4) gene
 CC encoding an EPIL (early placental insulin-like) polypeptide. Primers
 CC AA27493-X27494 were used to PCR amplify a fragment of the TFIID gene
 CC from cytotrophoblast and syncytiotrophoblast cell lines as a control in a
 CC quantitation assay for the level of expression of INSL4 in these cells.
 CC The polypeptide, antibodies to the polypeptide, vectors containing the
 CC coding sequence and probes derived from the coding sequence, can be used
 CC to treat tumours, preferably angio proliferative tumours, especially
 CC Kaposi's sarcoma, tumours of the pancreas, liver, uterus or breast,
 CC angiosarcomas, glioblastomas, neuroblastomas, rhabdomyosarcomas or
 CC leiomyosarcomas; to promote vascularisation of specific tissues; to treat
 CC retinopathy, macular degeneration, psoriasis, endometriosis, rheumatoid
 CC arthritis, atherosclerosis or hyperthyroidism; to treat post-angioplastic
 CC restenosis; to promote or inhibit embryo implantation; to prevent and/or
 CC treat disorders directly or indirectly connected with insulin-like
 CC activity; to prevent and/or treat disorders directly or indirectly
 CC connected with a dysfunction in carbohydrate metabolism, especially
 CC diabetes and diabetic complications, especially cardiovascular
 CC complications
 CC
 SO Sequence 21 BP; 10 A; 3 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.2; DB 1; Length 21;
 Best Local Similarity 85.7%; Pred. No. 1.3e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 3914 TTTTCACTCTTGGCTTCTT 3934
 DB 21 TTCTCAGCTTGGCTCTCT 1

RESULT 1646
 AA24349
 ID AA24349 standard; DNA; 21 BP.
 AC AA24349;
 XX
 DT 04-APR-2000 (first entry)
 DE Protein kinase inhibiting primer #11.
 XX
 KW Antimicrobial; cytostatic; immunosuppressive; protein kinase;
 KW prophylactic; therapy; treatment; cancer; autoimmune disease;
 KW pathogenic microorganism; primer; ss.
 XX
 OS Unidentified.
 XX
 PN US598596-A.
 PD 07-DEC-1999.
 XX
 PF 04-APR-1995; 95US-00416214.
 XX
 PR 04-APR-1995; 95US-00416214.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Bergan R, Neckers L;
 XX
 DR WPI; 2000-104623/09.
 XX
 PT Oligonucleotides inhibiting protein kinase, useful for treating diseases
 PT such as cancer and autoimmune disease.
 XX
 PS Example 3; Col 27-28; 26pp; English.
 XX
 CC This invention describes novel purified aptameric oligonucleotides which
 CC have antimicrobial, cytostatic and immunosuppressive activity. The
 CC oligonucleotides are useful for binding to and preventing or inhibiting
 CC the biological function of a protein kinase or a target molecule and for
 CC detecting the presence or absence of a target molecule in biological
 CC samples. The oligonucleotides are also useful for prophylactic and
 CC therapeutic treatment of diseases such as cancer, autoimmune diseases and
 CC diseases caused by pathogenic microorganisms. This sequence represents a
 CC primer used in the method of the invention
 XX
 SQ Sequence 21 BP; 0 A; 7 C; 14 G; 0 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.2; DB 1; Length 21;
 Best Local Similarity 85.7%; Pred. No. 1.3e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 61 GGAGGCTGCGGCGCGCGC 81
 DB 1 GGCGGCGCGCGCGCGCGC 21

RESULT 1647
 AA27179
 ID AA27179 standard; DNA; 21 BP.
 AC AA27179;
 XX
 DT 10-SEP-2001 (first entry)
 XX

DE Human biallelic marker downstream amplification primer SEQ ID NO:11535.
 XX
 KW Human genome; biallelic marker; high density disequilibrium map;
 KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
 KW haplotyping; hybridisation; identification; characterisation;
 KW amplification; single nucleotide polymorphism; SNP; PCR primer;
 KW diagnosis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO954500-A2.
 PD 28-OCT-1999.
 XX
 PF 21-APR-1999; 99WO-1B000822.
 XX
 PR 21-APR-1998; 98US-0082614P.
 PR 23-NOV-1998; 98US-0109732P.
 XX
 PA (GEST) GENSET.
 XX
 PI Cohen D, Blumenfeld M, Chumakov I;
 XX
 DR WPI; 2000-013267/01.
 XX
 PT Novel biallelic markers used to construct a high density disequilibrium
 PT map of the human genome.
 XX
 PS Claim 9; Page 2689; 2745pp; English.

AA265654 to AA269578 represent human biallelic markers from the present
 CC invention, which contain a polymorphic base at position 24 of their
 CC nucleotide sequences. AA269579 to AA277440 represent amplification
 CC primers for the biallelic markers. The biallelic markers of the invention
 CC have a variety of uses: they can be used for high density mapping of the
 CC human genome, and in complex association studies and haplotyping studies
 CC which are useful in determining the genetic basis for disease states.
 CC Compositions and methods of the invention can also be useful for the
 CC identification of the targets for the development of pharmaceutical
 CC agents and diagnostic methods, as well as the characterisation of the
 CC differential efficacious responses to and side effects from
 CC pharmaceutical agents acting on a disease as well as other treatment.
 CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
 CC 3367, are not actually given a sequence in the Sequence Listing from the
 CC present invention
 XX
 SQ Sequence 21 BP; 7 A; 0 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.2; DB 1; Length 21;
 Best Local Similarity 85.7%; Pred. No. 1.3e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 6192 GAGGAGTGGAGGAGATTG 6212
 DB 1 GAGGAGATGGAGGAGATTGT 21

RESULT 1648
 AAF97156/C
 ID AAF97156 standard; DNA; 21 BP.
 AC AAF97156;
 XX
 DT 06-JUN-2001 (first entry)
 XX

DE Human gene single nucleotide polymorphism #1917.
 XX
 KW Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
 KW polymorphism; vascular disease; coronary artery disease; forensics;
 KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
 KW pulmonary embolism; paternity test; ds.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FT Variation replace(11,A)
 FT /*tag= a
 FT /standard_name= "single nucleotide polymorphism"
 XX
 PN WO200118250-A2.
 XX
 PD 15-MAR-2001.
 XX
 PF 07-SEP-2000; 2000WO-US024503.
 XX
 PR 10-SEP-1999; 99US-0153357P.
 PR 26-JUL-2000; 2000US-0220947P.
 PR 16-AUG-2000; 2000US-0225724P.
 XX
 PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
 PA (MILT-) MILLENNIUM PHARM INC.
 XX
 PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;
 DR WPI; 2001-226749/23.
 XX
 XX Nucleic acids comprising single nucleotide polymorphisms, useful in
 PT applications such as forensics, paternity testing, medicine, genetic
 PT analysis and phenotype correlations to diseases such as diabetes and
 PT atherosclerosis.
 XX
 XX Example; Page 179; 242pp; English.
 XX
 CC The present invention provides a method of diagnosing a vascular disease
 CC in an individual, involving determining the sequence at various
 CC polymorphic sites within the human chromosome 1 and chromosome 4
 CC genes. The sequences at a number of polymorphic sites are also provided
 CC in the specification. In particular, the method can be used in the
 CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
 CC disease, stroke, peripheral vascular diseases, venous thromboembolism and
 CC pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
 CC useful in forensics, paternity testing, genetic analysis and phenotype
 CC correlations to diseases. The present sequence is an example of one of
 CC the human gene SNPs shown in the specification
 XX
 SQ Sequence 21 BP; 6 A; 5 C; 7 G; 3 T; 0 U; 0 Other;
 Query Match 0.2%; Score 16.2; DB 1; Length 21;
 Best Local Similarity 85.7%; Pred. No. 1.3e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 6026 CACCTGTCACCTGCTGGAGC 6046
 Db 21 CAACTGTCACCTGCTGGAGC 1
 RESULT 1649
 ID AAI68508 standard; DNA; 21 BP.
 XX
 AC AAI68508;
 XX
 DT 14-DEC-2001 (first entry)
 XX
 DE L. monocytogenes iap gene competitor probe iap-II-dd-III-R.
 XX
 KM PCR primer; iap gene; p60 protein; detection; infection; ss.
 OS Listeria monocytogenes.
 XX
 PN WO200168900-A2.
 XX
 PD 20-SEP-2001.
 XX
 PF 15-MAR-2001; 2001WO-EP002949.
 XX

PR 15-MAR-2000; 2000DE-01012540.
 XX
 XX (VERM-) VERMICON AG.
 PA
 XX Walcher M, Wagner M, Snaidr J;
 PI
 XX
 DR WPI; 2001-625966/72.
 XX
 PT Specifically detecting microorganisms in a sample, by polymerase chain
 PT reaction with reaction and competitor primers, useful for detecting
 PT subspecies of Listeria, in particular Listeria monocytogenes.
 XX
 PS Claim 11; Page 17; 32pp; German.
 XX
 CC This invention describes a novel method for specifically detecting
 CC microorganisms in a sample by Polymerase Chain Reaction (PCR) where in
 CC addition to reaction primers specific to the target organism, competition
 CC primers specific for non-target organisms are also used. The invention is
 CC used to detect microorganisms in a sample and to distinguish them from
 CC closely related microorganisms, particularly to detect infection by
 CC Listeria below the species level, especially Listeria monocytogenes. The
 CC invention allows detection of different subspecies of Listeria not
 CC provided by prior art. This sequence represents a competitor probe used
 CC in the method of the invention
 XX
 SQ Sequence 21 BP; 1 A; 1 C; 6 G; 13 T; 0 U; 0 Other;
 Query Match 0.2%; Score 16.2; DB 1; Length 21;
 Best Local Similarity 85.7%; Pred. No. 1.3e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 7282 TGTGTACTGTTGTCATTGT 7302
 Db 1 TGTGTCGTGTTGTAATTGT 21
 RESULT 1650
 ID ABL59602 standard; DNA; 21 BP.
 XX
 AC ABL59602;
 XX
 DT 17-JUL-2002 (first entry)
 XX
 DE Human glutathione S-transferase GSTP1 gene PCR primer SEQ ID NO:18.
 XX
 KM Human; glutathione S-transferase; GST; enzyme; differentiation; probe;
 KM PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN JP2002058483-A.
 XX
 PD 26-FEB-2002.
 XX
 PF 14-AUG-2000; 2000JP-00245951.
 XX
 PR 14-AUG-2000; 2000JP-00245951.
 XX
 PA (SAKA) OTSUKA SEIYAKU KOGYO KK.
 XX
 DR WPI; 2002-398775/43.
 XX
 PT Differentiation and quantitative determination of glutathione S-
 PT transferase comprises the use of oligonucleotide probes.
 XX
 PS Claim 8; Page 10; 12pp; Japanese.
 XX
 CC The present invention describes a method for the differentiation and
 CC quantitative determination of glutathione S-transferase using
 CC oligonucleotide probes (ABL59585 to ABL59601). The method allows rapid
 CC and sensitive determination of glutathione S-transferase for
 CC investigation of interaction and incompatibility of proposed drugs. The

CC present sequence represents a PCR primer for a human glutathione S-
transferase gene, which is used in an method for the differentiation and
CC quantitative determination of glutathione S-transferase
XX
SQ Sequence 21 BP; 5 A; 3 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2656 CTGTGTGACAGAGCATGATAC 2676
Db 1 CTGTGTGACATGTGTGATGAC 21
|||||
|||||

RESULT 1651
ABK9279/c
ID ABK9279 standard; RNA; 21 BP.

AC ABK9279;
XX
DT 21-OCT-2002 (first entry)

XX Hepatitis C virus (HCV) NS5B replicase RNA synthesis template #9.

XX Hepatitis C virus; HCV; NS5B replicase; ss; RNA polymerase.

XX Synthetic.

OS US2002064771-A1.

PN 30-MAY-2002.

PD 06-APR-2001; 2001US-00828034.

XX 07-APR-2000; 2000US-0195852P.

PR (ZHON/) ZHONG W.

PA (HONG/) HONG Z.

XX (FERR/) FERRARI E.

PI Zhong W, Hong Z, Ferrari E;

XX WPI; 2002-582330/62.

DR Novel replicase complex comprising hepatitis C virus NS5B replicase, a 3
XX nucleotide-long template to which a 2 nucleotide-long primer is annealed,
PT and template and primer which do not form a stable duplex in the absence
PT of HCV NS5B.

XX Example; Page 6; 17pp; English.

XX The invention relates to a replicase complex comprising a hepatitis C
CC virus (HCV) NS5B replicase protein, a linear nucleic acid template and a
CC complementary nucleic acid primer which is annealed to the 3' terminus of
CC the template, where the template is at least three nucleotides and the
CC primer is two or three nucleotides, and the template and primer do not
CC form a stable duplex in solution in the absence of the HCV NS5B protein.
CC The complex is useful for detecting HCV replicase activity and permits
CC establishment of sensitive RNA-dependent RNA polymerase assays to screen
CC and evaluate antiviral inhibitors and to improve the specificity and
CC efficacy of the inhibitors. The complex is also useful in the development
CC of a reliable system for determining kinetic and thermodynamic constants
CC of HCV NS5B-catalysed nucleotide incorporation and investigation of
CC mechanistic inhibitors for mis-incorporation or chain termination.
CC Specifically, the short RNA template and primer pairs are useful in
CC screening assays which are used for determining kinetic, thermodynamic
CC and mechanistic properties of NS5B replication and ultimately in the
CC development of inhibitors of NS5B. Newly identified inhibitors in the
CC replicase activity may be used for developing anti-HCV pharmaceuticals.
CC Sequences ABK9271-ABK9296 represent HCV NS5B replicase RNA synthesis
XX templates

SQ Sequence 21 BP; 0 A; 14 C; 7 G; 0 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 61 GGAGGCTGCGGCGCGCGC 81
Db 21 GGCGCGCGCGCGCGCGCGC 1
|||||
|||||

RESULT 1652
ABS98508
ID ABS98508 standard; DNA; 21 BP.

AC ABS98508;

XX 23-DEC-2002 (first entry)

XX Human acetyl choline muscarinic receptor 1 polymorphic sequence #2.

XX Human; ss; primer; cytochrome P450 A1; CYP4501A1; UGT2B4; MOR1;

XX cytochrome P450 A2; CYP4501A2; cytochrome P450 02B; CYP45002B1; LTF;

XX adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR112;

XX aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;

XX cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;

XX epoxide hydrolase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;

XX glutathione-S-transferase 12; GSTT2; histamine-N-methyl transferase;

XX HNMT; kallikrein 2; KLR2; nicotinamide-N-methyl transferase; NNMT;

XX NADPH quinone oxidoreductase 2; NQO2; sulfoltransferase thermolabile; STM;

XX UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;

XX UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;

XX multidrug resistance 1; lactotransferrin; orphan nuclear receptor;

XX acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;

XX altered drug metabolism; cardiovascular function; colorectal tumour;

XX central nervous system; pulmonary; immunological; sequencing.

OS Homo sapiens.

PN WO200257410-A2.

PD 25-JUL-2002.

XX 28-NOV-2001; 2001WO-US044838.

XX 28-NOV-2000; 2000US-00724389.

PR (DNAS-) DNA SCI LAB INC.

PA Guida M, Hall J;

XX WPI; 2002-698522/75.

DR Isolated nucleic acid molecules having polymorphisms in known human genes
XX e.g. cytochrome P450 and cathepsin S useful as genetic linkage markers
PT for locating, identifying and characterizing the genes responsible for
PT disorder-related traits.

XX Example 26; Page 157; 714pp; English.

XX This invention relates to the sequence of an isolated nucleic acid
CC molecule comprising at least one base variation from that of a known
CC human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2),
CC cytochrome P450 02B1 (CYP45002B1), adrenergic receptor beta1 (ADBR1),
CC aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator
CC (ARNT), cathepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding
CC inhibitor (DBI), epoxide hydrolase 2 (EPHX2), 5-lipoxygenase activating
CC protein (FLAP), glutathione-S-transferase 12 (GSTT2), histamine-N-methyl
CC transferase (HNMT), (kallikrein 2) KLR2, nicotinamide-N-methyl
CC transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2),
CC sulfoltransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4
CC (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl

CC transferase (UGT2B15), urokinase receptor (uPA), multidrug resistance 1
 CC (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3
 CC (MRP3), orphan nuclear receptor (NR112), or acetylcholine muscarinic
 CC receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence.
 CC The polymorphisms in the human genes cited in the invention are useful as
 CC genetic linkage markers for locating and characterising the genes that
 CC are responsible for specific traits within the genome and eventually
 CC identifying the genes responsible for a variety of disorder-related
 CC traits as a result of their e.g., overexpression, constitutive
 CC expression, mutation or underexpression, which may be used in diagnosing
 CC and/or treating the disorders. The nucleic acid molecules comprising the
 CC polymorphic sequences contained in CYP4501A1, CYP4501A2, CYP4502E1,
 CC AAR1, BPHX2, CSTR2, NNO2, NR12, STM, UGT2B4, UGT2B7, UGT2B15, AHR,
 CC MDR1 and/or MDR3 are useful for screening individuals for altered drug
 CC metabolism. The polymorphic sequences contained in CYP4501A1, CYP4501A2,
 CC AHR, MDR1 and/or MDR3 may also be used to screen individuals for
 CC susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are
 CC used to screen for altered cardiovascular function, in COX2 for altered
 CC susceptibility to colorectal tumours, in DBI or CHMR1 for altered central
 CC nervous system function, in FLAP and HMMT for altered pulmonary,
 CC immunological or haematological function, in KLR2 for altered serine
 CC protease activity in the prostate, in LTF for altered immunological or
 CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
 CC peripheral nervous system function. The present sequence represents a
 CC sequencing primer used to sequence the polymorphic genes of the invention
 XX

Seq Sequence 21 BP; 3 A; 6 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.2; DB 1; Length 21;
 Best Local Similarity 85.7%; Pred. No. 1.3e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5161 TTCTCTGGAGAGTGGGCTC 5181
 |||||
 Db 1 TGCTCATGGAGACTGGGCTC 21

RESULT 1653
 AAD23657/C
 ID AAD23657 standard; DNA; 21 BP.

AC AAD23657;
 XX
 DT 07-MAR-2002 (first entry)

DE Human CYP2C9 358 DNA amplifying downstream PCR primer #8.

KM Human; pharmaceutical agent; mutation; genetic polymorphism; LOT;
 KM long QT; cardiac repolarisation; torsades de Pointe; TDP; CYP2D6;
 KM cytochrome P450; PCR primer; ss.

OS Homo sapiens.

PN WO200179554-A1.

PD 25-OCT-2001.

PF 13-APR-2001; 2001WO-US012087.

PR 13-APR-2000; 2000US-0196916P.

PA (GEU) UNIV GEORGETOWN.

PI Woosley RL;

DR WPI; 2002-034367/04.

PT Determining predisposition for QT interval prolongation when treated with
 PT pharmaceutical agents by identifying genetic polymorphisms or mutations
 PT located in long QT, altered sensitivity or increased exposure genes.

PS Example 1; Page 46; 77pp; English.

CC The invention relates to a method for determining whether a subject has
 CC predisposition for QT interval elongation when treated with one or more
 CC pharmaceutical agents. The method comprises screening a biological sample
 CC from the subject through a nucleic acid array containing probes for at
 CC least two genetic mutations or polymorphisms chosen from long QT (LQT),
 CC altered sensitivity (MRP1) or increased exposure (MDR, P450 cytochrome)
 CC genes. The method is useful for determining whether a subject has a
 CC predisposition for QT interval prolongation when treated with one or more
 CC pharmaceutical agents. The method is useful for screening one or more
 CC pharmaceutical agents in vitro for their ability to induce prolonged
 CC cardiac repolarisation of a cell. The method is also useful for
 CC identifying genetic polymorphisms and mutations which are associated with
 CC an increased risk for prolonged QT intervals or torsades de Pointes
 CC (TdP). The present sequence is a PCR primer used for amplifying human
 CC cytochrome P450 isoform CYP2C9 358 DNA
 XX

Seq Sequence 21 BP; 8 A; 9 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.2; DB 1; Length 21;
 Best Local Similarity 85.7%; Pred. No. 1.3e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6806 TTGGAGAGAGTATTTCTG 6826
 |||||
 Db 21 TTGGGAGAGAGTACTTCTG 1

RESULT 1654
 ACC79938/C
 ID ACC79938 standard; DNA; 21 BP.

AC ACC79938;

DT 09-SEP-2003 (first entry)

DE Thermus oshimai nucleic acid polymerase PCR primer SEQ ID NO:31.

KM Thermus oshimai; nucleic acid polymerase; enzyme; DNA sequencing;

KW amplification; reverse transcription; RNA amplification;

OS Thermus oshimai.

PN WO2003048310-A2.

PD 12-JUN-2003.

PF 22-NOV-2002; 2002WO-US037764.

PR 30-NOV-2001; 2001US-034798P.

PA (APPL-) APPLERA CORP.

PI Bolchakova E, Rozzelle J;

DR WPI; 2003-505286/47.

PT New nucleic acid, useful for DNA sequencing or amplification, reverse
 PT transcription, RNA amplification or primer extension reactions.

PS Example 1; Page 51; 64pp; English.

CC The present invention describes a nucleic acid (1) encoding a nucleic
 CC acid polymerase or a derivative nucleic acid polymerase with a mutation
 CC that decreases 5'-3' exonuclease activity or that reduces discrimination
 CC against dideoxynucleotide triphosphates. Also described: (1) a vector
 CC comprising the nucleic acid (1); (2) a host cell comprising the nucleic
 CC acid (1); (3) a nucleic acid polymerase or its derivative; (4) a kit
 CC comprising a container containing the nucleic acid polymerase of (3); (5)
 CC making the nucleic acid polymerase of (3); (6) synthesising a DNA; (7)
 CC thermocyclic amplification of nucleic acid; and (8) primer extending a
 CC DNA. The nucleic acid (1) is useful for DNA sequencing or amplification.

CC reverse transcription, RNA amplification or primer extension reactions.
CC The present sequence represents a PCR primer for *Thermus oshimai* nucleic
CC acid polymerase, which is used in an example from the present invention
XX
SQ Sequence 21 BP; 3 A; 8 C; 4 G; 6 T; 0 U; 0 Other;
Query Match 0.2%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 992 TCAAGGCGCTGAGTGGAG 1012
Db 21 TCAAGGCGCTGAGGAGAG 1
RESULT 1655
ADD14380
ID ADD14380 standard; DNA; 21 BP.
XX
AC ADD14380;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human src biomarker forward PCR primer SEQ ID NO:569.
XX
KW predictor set; protein tyrosine kinase activity modulator;
KW protein tyrosine kinase pathway; protein tyrosine kinase; cytosolic;
KW gene therapy; drug sensitivity; genetic profile; cancer; human;
KW PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003062395-A2.
XX
PD 31-JUL-2003.
XX
PF 17-JAN-2003; 2003WO-US001981.
XX
PR 18-JAN-2002; 2002US-0350061P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Huang F, Fairchild CR, Lee FY, Shaw P;
XX WPI; 2003-636735/60.
XX
PT New polynucleotides and polypeptides for predicting the activity of
PT compounds that interact with protein tyrosine kinases and/or protein
PT tyrosine kinase pathways.
XX
PS Example 2; SEQ ID NO 569; 139pp; English.
XX
CC The present invention describes a predictor set comprising a plurality of
CC polynucleotides or polypeptides whose expression pattern is predictive of
CC the response of cells to treatment with a compound that modulates protein
CC tyrosine kinase activity or members of the protein tyrosine kinase
CC pathway. Also described: (1) predicting whether a compound is capable of
CC modulating the activity of cells, comprising obtaining a sample of cells,
CC determining whether the cells express a plurality of markers, and
CC correlating the expression of the markers to the compound's ability to
CC modulate the activity of the cells; (2) a plurality of cell lines for
CC identifying polynucleotides and polypeptides whose expression levels
CC correlate with compound sensitivity or resistance of cells associated
CC with a disease state; and (3) identifying polynucleotides and
CC polypeptides that predict compound sensitivity or resistance of cells
CC associated with a disease state, comprising subjecting the plurality of
CC cell lines to one or more compounds, analysing the expression pattern of
CC a microarray of polynucleotides or polypeptides, and selecting
CC polynucleotides or polypeptides that predict the sensitivity or
CC resistance of cells associated with a disease state by using the
CC expression pattern of the microarray. The polynucleotides and
CC polypeptides have cytosolic activities, and can be used in gene therapy.

CC The polynucleotides and polypeptides are useful in predicting the
CC activity of compounds that interact with protein tyrosine kinases and/or
CC protein tyrosine kinase pathways. These may be used in determining drug
CC sensitivity in patients to allow the development of individualized
CC genetic profiles which aid in treating diseases and disorders (e.g.
CC cancer) based on patient response at a molecular level. The present
CC sequence is used in the exemplification of the present invention.
XX
SQ Sequence 21 BP; 7 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 0.2%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2383 AAGAGTGGTAAACATCCAGCT 2403
Db 1 AAGAGGCGTCACATACCACT 21
RESULT 1656
AAQ57211/C
ID AAQ57211 standard; mRNA; 22 BP.
XX
AC AAQ57211;
XX
DT 25-MAR-2003 (revised)
XX
DE 26-JUL-1994 (first entry)
XX
KW Enzymatic RNA molecule streptolysin mRNA target sequence.
XX
KW Specific; cleavage; target RNA; protein; prophylaxis; expression;
KW inhibitor; inhibition; ribozyme; treatment; prevention; psoriasis;
KW asthma; inflammatory diseases; restenosis; cardiovascular condition;
KW hypertension; arthritis; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9402595-A1.
XX
PD 03-FEB-1994.
XX
PF 02-JUL-1993; 93WO-US006316.
XX
PR 17-JUL-1992; 92US-00916763.
PR 07-DEC-1992; 92US-00987132.
PR 07-DEC-1992; 92US-00989848.
PR 07-DEC-1992; 92US-00989849.
PR 19-JAN-1993; 93US-00008895.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Sullivan SM, Draper KG;
XX
XX WPI; 1994-048853/06.
XX
PT Enzymatic RNA molecules which cleave mRNA - used to treat or prevent
PT inflammatory, arthritic, stenotic or cardiovascular diseases or
PT conditions.
XX
PS Claim 3; Page 18; 65pp; English.
XX
CC This is a streptolysin mRNA target sequence (nucleotide no. 327) of an
CC enzymatic RNA molecule (ribozyme) which cleaves mRNA associated with the
CC development or maintenance of osteoarthritis or other pathological
CC conditions which are mediated by metalloproteinase activation. The concn.
CC of the ribozyme necessary to effect a therapeutic treatment is lower than
CC that of an antisense oligonucleotide and the specificity of action is
CC higher. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 22 BP; 5 A; 5 C; 5 G; 7 T; 0 U; 0 Other;
Query Match 0.2%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 1.4e+03;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 7395 TTCTGAAGCAAGCAACATCAG 7415
 |||||
 Db 21 TTCTGAAGTGACCAACATCAG 1

RESULT 1657
 AAQ93468/c
 ID AAQ93468 standard; RNA; 22 BP.
 XX
 AC AAQ93468;
 XX
 DT 25-MAR-2003 (revised)
 XX 06-DEC-1995 (first entry)
 DE Hammerhead ribozyme target sequence #7.
 XX
 KM Hammerhead ribozyme motif; arthritis; cancer; angiogenesis; hairpin;
 KM hepatitis delta virus; group 1 intron; RNase P RNA; stromelysin; ss.
 XX
 OS Synthetic.
 XX
 PN WO9513380-A2.
 XX
 PD 18-MAY-1995.
 XX
 PF 10-NOV-1994; 94WO-US013129.
 XX
 PR 12-NOV-1993; 93US-00152487.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Draper KG, Pavco P, Mcswigen J, Gustofson J;
 XX
 DR WPI; 1995-194099/25.
 XX
 PT New enzymatic RNA molecules - which cleave mRNA of a gene encoding a
 PT matrix metalloproteinase, for treating arthritis, cancer or angiogenesis.
 XX
 PS Disclosure; Page 18; 70pp; English.
 XX
 CC The sequences AAQ93462-Q93494 are examples of target cleavage sequences
 CC for a hammerhead ribozyme with sequence motif AAQ90453. A ribozyme, pref.
 CC hammerhead, hairpin, hepatitis delta virus, group 1 intron or RNase P RNA
 CC motif can be used in a composition for the treatment of arthritis, cancer
 CC or angiogenesis. The ribozyme comprises between 5-45 bases complementary
 CC to the target mRNA. The ribozymes (see AAQ93830-51 for examples) were
 CC synthesised based on putative stromelysin mRNA target cleavage sequences
 CC (AAQ93496-Q93829). (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 22 BP; 5 A; 5 C; 5 G; 0 T; 7 U; 0 Other;
 XX
 QY Query Match 0.2%; Score 16.2; DB 1; Length 22;
 Best Local Similarity 85.7%; Pred. No. 1.4e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 7395 TTCTGAAGCAAGCAACATCAG 7415
 |||||
 Db 21 TTCTGAAGTGACCAACATCAG 1

RESULT 1658
 AAX63375/c
 ID AAX63375 standard; RNA; 22 BP.
 XX
 AC AAX63375;
 XX
 DT 20-JUL-1999 (first entry)
 XX
 DE Human stromelysin hammerhead target SEQ ID NO:7.
 XX
 KM Arthritic condition; graft tolerance; immune response; target; cleavage;

KM hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;
 KM stromelysin; synovial membrane; joint; arthritis; osteoarthritis;
 KM rheumatoid arthritis; autoimmune disease; allergy; inflammation;
 KM diagnosis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9618736-A2.
 XX
 PD 20-JUN-1996.
 XX
 PF 22-NOV-1995; 95WO-US015516.
 XX
 PR 13-DEC-1994; 94US-00354920.
 PR 23-DEC-1994; 94US-00363253.
 PR 23-DEC-1994; 94US-00363254.
 PR 17-FEB-1995; 95US-00390850.
 PR 20-APR-1995; 95US-00426124.
 PR 02-MAY-1995; 95US-00432874.
 PR 04-MAY-1995; 95US-00434509.
 PR 07-JUL-1995; 95US-0000951P.
 PR 07-JUL-1995; 95US-0000974P.
 PR 07-AUG-1995; 95US-00512861.
 PR 05-OCT-1995; 95US-00541365.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Beigelman L, Stinchcomb DT, Jarvis T, Draper K, Pavco P;
 PI Mcswigen J, Gustofson J, Usman N, Wincott F, Matulic-Adamic J;
 PI Karpelsky A, Thompson JD, Modak A, Burgin A;
 XX
 DR WPI; 1996-300653/30.
 XX
 PT Enzymatic nucleic acid molecules having a hammer-head motif - used for
 PT the treatment of arthritis, induction of graft tolerance or treatment of
 PT auto-immune diseases.
 XX
 PS Example 1; Page 139; 307pp; English.
 XX
 CC The present invention describes a novel enzymatic nucleic acid (ENA)
 CC having a hammerhead motif (HM) comprising: (i) at least 5 ribose residues
 CC (ii) a 2'-C-allyl modification at position 4 of the ENA; (iii) at least
 CC ten 2'-O-methyl modifications; and (iv) a 3'-end modification. The ENA's
 CC can inhibit collagenase and stromelysin production in the synovial
 CC membrane of joints for the treatment or prevention of arthritis,
 CC particularly osteoarthritis or rheumatoid arthritis. The ENA's can also
 CC be used to treat antigen presenting cells of a donor to induce tolerance
 CC in a recipient to an alloantigen of a donor. They can also be used for
 CC enhancing graft tolerance or for treating autoimmune disease, and for
 CC treating allergies and other inflammatory conditions. The ENA's can also
 CC be used in diagnosis. Ribozyme therapy impacts on the expression of
 CC stromelysin without introducing the non-specific effects upon gene
 CC expression which accompany treatment with retinoids and dexamethasone.
 CC The concentration of ribozyme required to affect a therapeutic treatment
 CC is lower than that required of antisense molecules, and is highly
 CC specific. The present sequence is used in the exemplification of the
 CC present invention
 XX
 SQ Sequence 22 BP; 5 A; 5 C; 5 G; 0 T; 7 U; 0 Other;
 XX
 QY Query Match 0.2%; Score 16.2; DB 1; Length 22;
 Best Local Similarity 85.7%; Pred. No. 1.4e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 7395 TTCTGAAGCAAGCAACATCAG 7415
 |||||
 Db 21 TTCTGAAGTGACCAACATCAG 1

RESULT 1659
 AAX56196
 ID AAX56196 standard; DNA; 22 BP.
 XX

AC AAX56196;
 XX
 DT 15-JUL-1999 (first entry)
 XX
 DE Human alpha-7 nicotinic receptor PCR primer SEQ ID NO:43.
 XX
 KW Human; alpha-7 nicotinic receptor; neuronal; hybridisation; probe;
 KW alpha-7 neuronal nicotinic acetylcholine receptor; schizophrenia;
 KW small cell lung carcinoma; breast cancer; nicotine-dependent illness;
 KW epilepsy; juvenile myoclonic epilepsy; Prader-Willi syndrome;
 KW Angelman's syndrome; PCR primer; 88.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO920757-A2.
 XX
 PD 29-APR-1999.
 XX
 PF 15-OCT-1998; 98WO-US021762.
 XX
 PR 23-OCT-1997; 97US-00956518.
 XX
 PA (LEON/) LEONARD S.
 PA (FREE/) FREDMAN R.
 XX
 PI Leonard S, Freedman R;
 DR WPI, 1999-288306/24.
 XX
 PT Human alpha-7 neuronal nicotinic acetylcholine receptor and related
 PT polynucleotides.
 XX
 PS Claim 15; Page 66; 104pp; English.
 XX
 CC The present invention describes an isolated nucleotide sequence (I)
 CC encoding at least a portion of the human alpha-7 neuronal nicotinic
 CC acetylcholine receptor (alpha7-hnAChR). Also described are: (1) a peptide
 CC encoded by (1); (2) a vector comprising (1); (3) a host cell transformed
 CC with a vector of (2); (4) a polynucleotide comprising at least 15
 CC nucleotides which hybridises under stringent conditions to at least a
 CC portion of (1); (5) a method for detection of a polynucleotide encoding
 CC alpha 7-hnAChR in a biological sample; and (6) a method for amplification
 CC of nucleic acid from a sample suspected of containing nucleic acid
 CC encoding alpha 7-hnAChR. The primers and probes from the present
 CC invention can be used on brain tissue and blood samples of humans
 CC suspected of suffering from schizophrenia, small cell lung carcinoma,
 CC breast cancer and nicotine-dependent illness. This is particularly useful
 CC for diagnosis of schizophrenia. Other illnesses that can be
 CC studied/diagnosed are epilepsy (e.g. juvenile myoclonic epilepsy) and
 CC Prader-Willi and Angelman's syndromes
 XX
 SQ Sequence 22 BP; 2 A; 7 C; 6 G; 7 T; 0 U; 0 Other;
 QY
 Query Match 0.2%; Score 16.2; DB 1; Length 22;
 Best Local Similarity 85.7%; Pred. No. 1.4e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Db 5161 TTCTCTGGAGACAGTGGCTC 5181
 2 TTCTCTGGAGACTTGGGAC 22
 RESULT 1660
 AA218506/c
 ID AA218506 standard; DNA; 22 BP.
 AC
 XX
 AC AA218506;
 XX
 DT 19-OCT-1999 (first entry)
 XX
 DE Polymorphic fragment in ASTH1J intronic region.
 XX

KW ASTH1; asthma; human; chromosome 11p; ASTH1I; ASTH1J; genetic locus;
 KW therapeutic; immunogen; polymorphism; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO9337809-A1.
 XX
 PD 29-JUL-1999.
 XX
 PF 21-JAN-1998; 98WO-US001260.
 XX
 PR 21-JAN-1998; 98WO-US001260.
 XX
 PA (AXYS-) AXYS PHARM INC.
 XX
 PI Brooks-Wilson AR, Buckler A, Cardon L, Carey AH, Galvin M;
 PI Miller A, North M;
 DR WPI, 1999-479058/40.
 XX
 PT Mammalian asthma related genes, useful for diagnosis of a predisposition
 PT to development of asthma.
 XX
 PS Disclosure; Page 64; 195pp; English.
 XX
 CC The invention identifies a genetic locus ASTH1, associated with asthma,
 CC mapped to human chromosome 11p. ASTH1I and ASTH1J are genes present
 CC within the locus, located close to each other on human chromosome 11p,
 CC and have similar patterns of expression, and common sequence motifs. The
 CC ASTH1 genes and fragments, encoded protein, genomic regulatory regions
 CC and anti-ASTH1 antibodies are useful in the identification of individuals
 CC predisposed to development of asthma, and for the modulation of gene
 CC activity in vivo for prophylactic and therapeutic purposes. The ASTH1
 CC protein is useful as an immunogen to raise specific antibodies, in drug
 CC screening for compositions that mimic or modulate ASTH1 activity, or
 CC expression, including altered forms of ASTH1 protein, and as a
 CC therapeutic. Sequences AA218366-218509 represent polymorphisms in the
 CC ASTH1I and ASTH1J genes
 XX
 SQ Sequence 22 BP; 5 A; 6 C; 2 G; 8 T; 0 U; 1 Other;
 QY
 Query Match 0.2%; Score 16.2; DB 1; Length 22;
 Best Local Similarity 85.7%; Pred. No. 1.4e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Db 6994 AGGTGGAAAGGAGATTTC 7014
 22 AGGTGAGAAAGGACATTTC 2
 RESULT 1661
 AA293694
 ID AA293694 standard; DNA; 22 BP.
 AC
 XX
 AC AA293694;
 XX
 DT 16-AUG-2000 (first entry)
 XX
 DE Primer for amplifying PRO172 cDNA.
 XX
 KW Inhibition; cancer; neoplasia; tumour; breast; ovary; renal; colorectal;
 KW uterus; prostate; lung; bladder; central nervous system; CNS; melanoma;
 KW leukaemia; PRO211; PRO228; PRO536; PRO172; PRO182; human; probe; primer;
 KW 88.
 XX
 OS Homo sapiens.
 XX
 PN WO200021996-A2.
 XX
 PD 20-APR-2000.
 XX
 PF 05-OCT-1999; 99WO-US023089.
 XX

PR 13-OCT-1998; 98US-0104080P.
 XX
 XX (GETH) GENENTECH INC.
 XX
 PI Ashkenazi A, Goddard A, Gurney AL, Klein RD, Napier M, Wood WI,
 XX
 PI Yuan J;
 XX
 DR WPI; 2000-317943/27.
 XX
 PT Composition for inhibiting neoplastic cell growth and treating cancers of
 PT ovary, uterus, prostate, lung and bladder, comprises PRO211, PRO228,
 PT PRO538, PRO172 or PRO182 polypeptide or their agonist.
 XX
 PS Example 1d; Page 81; 122pp; English.
 XX
 CC Compositions comprising a PRO211, PRO228, PRO538, PRO172 or PRO182
 CC polypeptide or their agonists, mixed with a carrier is useful for
 CC inhibiting neoplastic growth and treating tumors such as cancers of
 CC breast, ovary, renal, colorectal, uterus, prostate, lung, bladder,
 CC central nervous system, melanoma and leukemia. Two primers (AA233694,
 CC AA233695) were used to amplify the PRO172 cDNA
 CC
 SQ Sequence 22 BP; 6 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 16.2; DB 1; Length 22;
 Best Local Similarity 85.7%; Pred. No. 1.4e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1725 GCATCTCAGACACCTACTC 1745
 Db 1 GCATCTCAGACACCTACTC 21
 RESULT 1662
 AAC58421
 ID AAC58421 standard; DNA; 22 BP.
 XX
 AC AAC58421;
 XX
 DT 29-JAN-2001 (first entry)
 XX
 DE Human PRO172 (UNQ146) oligonucleotide SEQ ID NO:43.
 XX
 KW Human; immune related diseases; diagnosis; antiinflammatory; cardiant;
 KW dermatological; antiarthritic; antirheumatic; immunosuppressive;
 KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
 KW antineumatic; hepatotropic; virucide; antiprotic; antiallergic;
 KW osteoarthritis; systemic lupus erythematosus; rheumatoid arthritis;
 KW osteoarthritis; spondyloarthritis; systemic sclerosis; sarcoidosis;
 KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
 KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
 KW autoimmune thrombocytopenia; immune-mediated renal disease;
 KW demyelinating disease; hepatobiliary disease; Whipple's disease;
 KW inflammatory bowel disease; gluten-sensitive enteropathy; hydriadsation;
 KW autoimmune disease; immune-mediated skin disease; allergic disease;
 KW immunological disease; transplantation associated disease; PCR primer;
 KW graft rejection; graft-versus-host-disease; probe; ss.
 XX
 OS Homo sapiens.
 OS
 PN WO200053758-A2.
 PD 14-SEP-2000.
 XX
 PF 02-MAR-2000; 2000WO-US005641.
 XX
 PR 08-MAR-1999; 99WO-US005028.
 PR 10-MAR-1999; 99US-0123618P.
 PR 12-MAR-1999; 99US-0123957P.
 PR 23-MAR-1999; 99US-0125775P.
 PR 12-APR-1999; 99US-0128649P.
 PR 20-APR-1999; 99WO-US006615.
 PR 28-APR-1999; 99US-0131445P.

PR 04-MAY-1999; 99US-0132371P.
 PR 14-MAY-1999; 99US-0134287P.
 PR 02-JUN-1999; 99WO-US012252.
 PR 23-JUN-1999; 99US-0141037P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 28-JUL-1999; 99US-0146222P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 29-OCT-1999; 99US-0162506P.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 30-NOV-1999; 99WO-US028409.
 PR 01-DEC-1999; 99WO-US028301.
 PR 01-DEC-1999; 99WO-US028634.
 PR 02-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028564.
 PR 16-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030999.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 XX
 XX (GETH) GENENTECH INC.
 PA
 PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
 PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
 PI Stewart TA, Tumaas D, Watanabe CK, Wood WI, Yan M;
 XX
 DR WPI; 2000-572271/53.
 XX
 PT Sixty four PRO polypeptides, useful in the diagnosis and treatment of
 PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
 PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
 XX
 PS Example 1; Page 95; 309pp; English.
 XX
 CC The present invention describes sixty four human PRO proteins which can
 CC be used in the treatment of immune related diseases. The human PRO
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
 CC treating and diagnosing immune related disorders. The disorders are
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthritis,
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
 CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
 CC immune-mediated renal disease, demyelinating diseases of the central and
 CC peripheral nervous systems, hepatobiliary diseases, inflammatory bowel
 CC disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune
 CC or immune-mediated skin diseases, allergic diseases, immunological
 CC diseases of the lung, and transplantation associated diseases including
 CC graft rejection and graft-versus-host-disease. AAC58397 to AAC58578
 CC represent PCR primers and hybridisation probes used in the isolation of
 CC human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477
 CC represent human PRO polynucleotide and protein sequences given in the
 CC exemplification of the present invention
 XX
 SQ Sequence 22 BP; 6 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 16.2; DB 1; Length 22;
 Best Local Similarity 85.7%; Pred. No. 1.4e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	1725	GCATCTCAAGAACACTACTC	1745
Db	1	GGATCTCGAGAACGCTACTC	21
	RESULT 1663		
	AAA28105		
	AAA28105	standard; DNA; 22 BP.	
AC	AAA28105;		
XX			
DT	01-DEC-2000	(first entry)	
XX			
DE	Human androgen shuttloff gene intron/exon 27 boundary sequence.		
XX			
KM	Androgen-induced tumour suppressor; androgen shuttloff gene 3; AS3;		
KW	chromosome 13q12-13q; cell proliferation inhibitor; prostate cancer;		
KM	diagnosis; treatment; cytostatic; human; ds.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	misc_feature	14..15	
FT		/*tag=	a
FT		/note=	"Intron/exon 27 boundary"
XX			
PN	WO200050454-A1.		
PD	31-AUG-2000.		
XX			
PF	24-FEB-2000; 2000WO-US004732.		
XX			
PR	24-FEB-1999; 99US-0121461P.		
XX			
PA	(TUFT) TUFTS COLLEGE.		
XX			
PI	Soto AM, Sonnenschein C, Geck P, Szelei J;		
DR	WPI; 2000-565451/52.		
XX			
PT	New human androgen-induced tumor suppressor cDNA sequence termed		
PT	'Androgen Shutloff Gene 3' (AS3), useful as a marker for the efficient		
PT	diagnosis and treatment of prostate cancer.		
XX			
PS	Disclosure; Fig 5; 152pp; English.		
XX			
CC	This invention relates to a human androgen-induced tumour suppressor cDNA		
CC	sequence termed "Androgen Shutloff Gene 3" (AS3). The AS3 gene is located		
CC	on chromosome 13 at position 13q12-13q. AS3 has a role in inhibiting cell		
CC	proliferation and use as a marker for the efficient diagnosis and		
CC	treatment of prostate cancer. The invention includes AS3 cDNA and protein		
CC	sequences, a vector comprising the cDNA sequence, a host cell transfected		
CC	with the expression vector, and a method for producing an AS3 polypeptide		
CC	comprising culturing the transfected cells. AS3 has cytosstatic activity,		
CC	and acts to suppress cell proliferation. The AS3 gene is useful as a		
CC	marker for the efficient diagnosis and treatment of prostate cancer. The		
CC	AS3 nucleic acid molecule can be used as a source of antisense agents. The		
CC	sequence specific modulation of gene expression. The AS3 protein may be		
CC	used in the treatment of disorders caused by aberrant modification or		
CC	mutation of a gene encoding an AS3 protein, misregulation of the AS3 gene		
CC	or aberrant post-translational modification of the AS3 protein. This		
CC	sequence represents the boundary between a human AS3 intron and exon		
XX			
SO	Sequence 22 BP; 2 A; 1 C; 2 G; 17 T; 0 U; 0 Other;		
	Query Match	0.2%; Score 16.2; DB 1; Length 22;	
	Best Local Similarity	85.7%; Pred. No. 1.4e+03;	
	Matches 18; Conservative	0; Mismatches 3; Indels 0; Gaps 0;	
QY	4468	TTTTTTTTTTTTTTTGCTT	4468
Db	1	TTTTTTTTTTTTTAAGTCTT	21

RESULT 1664
 AAA77513
 ID AAA77513 standard; DNA; 22 BP.
 XX
 AC AAA77513;
 XX
 DT 07-NOV-2000 (first entry)
 XX
 DE Human PRO172 PCR primer SEQ ID NO:5.
 XX
 OS Homo sapiens.
 KW Human; PRO; promotion; inhibition; angiogenesis; cardiovascularity;
 KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
 KW angiogenic; proliferative; cardiac; cardiovascular; antiatherosclerotic;
 KW cyostatic; gene therapy; vaccine; hybridisation; probe; PCR primer; ss.
 XX
 MO WO200032221-A2.
 PN 08-JUN-2000.
 XX
 PF 30-NOV-1999; 99WO-US028313.
 XX
 PR 01-DEC-1998; 98WO-US025108;
 PR 16-DEC-1998; 98US-0112850P;
 PR 12-JAN-1999; 99US-011554P;
 PR 08-MAR-1999; 99WO-US005028;
 PR 12-MAR-1999; 99US-0123957P;
 PR 28-APR-1999; 99US-0131445P;
 PR 14-MAY-1999; 99US-0134287P;
 PR 02-JUN-1999; 99WO-US012252;
 PR 23-JUN-1999; 99US-0141037P;
 PR 20-JUL-1999; 99US-0144758P;
 PR 26-JUL-1999; 99US-0145698P;
 PR 01-SEP-1999; 99WO-US020111;
 PR 08-SEP-1999; 99WO-US020594;
 PR 13-SEP-1999; 99WO-US020944;
 PR 15-SEP-1999; 99WO-US02109P;
 PR 15-SEP-1999; 99WO-US02154P;
 PR 05-OCT-1999; 99WO-US023089;
 PR 29-OCT-1999; 99US-0162506P.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Aeshkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ,
 PI Goddard A, Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF,
 PI Smith V, Watanabe CK, Williams PM, Wood WI;
 XX
 DR WPI; 2000-412154/35.
 XX
 PT Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing
 PT and treating disorders in cardiovascular, endothelial or angiogenic
 PT disorders in mammals.
 XX
 PS Example 4; Page 111; 315pp; English.
 XX
 CC The present invention describes nucleic acids encoding PRO polypeptides
 CC useful for preventing, diagnosing and treating disorders in mammals by
 CC cardiovascular, endothelial or angiogenic disorder in mammals by
 CC modulating cell proliferation, angiogenesis and cardiovascularisation,
 CC and for identifying agonists and antagonists of these processes. The
 CC nucleic acids and the proteins they encode may be used in the prevention,
 CC treatment and diagnosis of diseases associated with inappropriate PRO
 CC expression such as cardiovascular, endothelial or angiogenic disorders in
 CC mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For
 CC example, the nucleic acids (NGs) and vectors containing them and the PRO
 CC polypeptide may be used to treat disorders associated with decreased PRO
 CC expression. AAA77510 to AAA77721 and AAB2438 to AAB24435 represent
 CC nucleotide and protein sequences used in the exemplification of the
 CC present invention
 XX
 XX Sequence 22 BP; 6 A; 7 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.2; DB 1; Length 22;
 Best Local Similarity 85.7%; Pred. No. 1.4e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1725 GCATCTCAAGAACCTACTC 1745
 |||||
 1 GGATCTCGAGACGCTACTC 21

RESULT 1665
 ID AAA54102 standard; cDNA; 22 BP.
 AC AAA54102;
 DT 08-FEB-2001 (first entry)
 DE Primer for amplifying PRO172 cDNA.
 XX PRO211; PRO228; PRO538; PRO172; PRO182; neoplasia; inhibition; tumour;
 KM treatment; therapy; agonist; antibody; breast cancer; ovarian cancer;
 KM renal cancer; colorectal cancer; uterine cancer; prostate cancer;
 KM lung cancer; bladder cancer; melanoma; leukaemia; inflammatory disorder;
 KM angiogenic disorder; immunologic disorder; human; primer; ss.
 OS Homo sapiens.
 XX MO200055319-A1.
 XX 21-SEP-2000.
 PD 02-DEC-1999; 99MO-US028564.
 PF 12-MAR-1999; 99US-0123957P.
 PR 28-APR-1999; 99US-0131445P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 08-SEP-1999; 99MO-US020594.
 PR 15-SEP-1999; 99MO-US021090.
 PR 05-OCT-1999; 99MO-US023089.
 PR 30-NOV-1999; 99MO-US028313.
 XX (GETH) GENENTECH INC.
 PA Ashkenazi AJ, Goddard A, Gurney AL, Klein RD, Napier MA, Wood WI,
 PI Yuan J,
 XX WPI; 2000-638201/61.
 DR PRO211, PRO228, PRO538, PRO172 and PRO182 polypeptides useful for
 PT treating tumors including cancers of the breast and lung, leukemia and
 PT for identifying compounds capable of inhibiting growth of neoplastic
 PT cells.
 XX Example 1; Page 86; 133pp; English.
 XX Isolated (PRO211, PRO228, PRO538, PRO172 or PRO182 polypeptides or their
 CC agonists (preferably anti-PRO agonist antibody or a small molecule
 CC mimicking the biological activity of PRO polypeptide) are useful in vitro
 CC or in vivo for inhibiting the growth of a tumor cell. Compositions
 CC comprising the PRO polypeptides are useful for inhibiting neoplastic cell
 CC growth and for treating cancer including breast, ovarian, renal,
 CC colorectal, uterine, prostate, lung, bladder, central nervous system
 CC cancer, melanoma and leukemia in a mammal. The PRO polypeptides are also
 CC useful for treating other disorders such as neuronal, glial, astrocytal,
 CC hypothalamic and other glandular, macrophagal, epithelial, stromal,
 CC blastococic disorders and inflammatory, angiogenic and immunologic
 CC disorders as well as being useful for identifying agonists to PRO
 CC polypeptides by contacting the polypeptide with a candidate molecule and
 CC monitoring biological activity mediated by the polypeptide. Two primers
 CC (AAA54102, AAA54103) were used to amplify the PRO172 cDNA sequence

Sequence 22 BP; 6 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
 Query Match 0.2%; Score 16.2; DB 1; Length 22;
 Best Local Similarity 85.7%; Pred. No. 1.4e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1725 GCATCTCAAGAACCTACTC 1745
 |||||
 1 GGATCTCGAGACGCTACTC 21

RESULT 1666
 ID AAA80413 standard; DNA; 22 BP.
 AC AAA80413;
 DT 22-NOV-2000 (first entry)
 DE Human ASTHJ intron a polymorphic site, SEQ ID NO:156.
 XX ASTH1 locus; ASTH1I; ASTH1J; human; chromosome 11p; asthma;
 KM bronchial hyperreactivity; ets family; transcription factor;
 KM splice variant; genetic predisposition; polymorphism; antibody;
 KM drug screening; prophylaxis; therapy; diagnosis;
 KM single nucleotide polymorphism; SNP; ss.
 OS Homo sapiens.
 XX US6087485-A.
 XX 11-JUL-2000.
 PD 21-JAN-1998; 98US-00009913.
 PF 21-JAN-1997; 97US-0035663P.
 PR 01-JUL-1997; 97US-0051432P.
 XX (AXYS-) AXYS PHARM INC.
 PA Galvin M, Miller A, North M, Cardon L, Buckler A,
 PI Brooks-Wilson AR, Carey AH;
 XX WPI; 2000-505109/45.
 DR New nucleic acids other than naturally occurring chromosomes encoding
 PT ASTH1 protein, for e.g. screening compositions that modulate expression
 PT or function of ASTH1 proteins or as diagnostics for genetic
 PT predisposition to asthma.
 XX Example; Col 43-44; 131pp; English.
 XX The invention relates to the ASTH1 locus on the short arm of human
 CC chromosome (11p). This locus comprises the ASTH1 and ASTH1J genes, which
 CC are associated with a genetic predisposition to asthma and bronchial
 CC hyperreactivity. The ASTH1I and ASTH1J genes are oriented in opposite
 CC directions with the ASTH1 locus, and have similar patterns of expression
 CC and common sequence motifs. They are both expressed in trachea, lung and
 CC several other tissues. ASTH1I and ASTH1J are novel members of the ets
 CC family of transcription factors, which have been implicated in the
 CC activation of a variety of genes including the TCRA gene and cytokine
 CC genes known to be important in the aetiology of asthma. Both ASTH1I and
 CC ASTH1J mRNAs are alternatively spliced. Alternative splicing of
 CC transcripts has no effect on the open reading frame of ASTH1J, as the
 CC exons involved are all 5' to the start codon in exon b. In contrast,
 CC alternative splicing of ASTH1I transcripts results in 3 different ASTH1I
 CC isoforms. The invention also encompasses mouse asth1j protein. The ASTH1
 CC nucleic acids are useful as diagnostics to identify a hereditary
 CC predisposition to asthma, as probes for identifying ASTH1 related genes,
 CC for identifying expression of the gene in a biological specimen, and for
 CC generating genetically modified non-human animals or site specific gene
 CC modifications in cell lines. The encoded ASTH1 proteins are useful as
 CC immunogens to raise specific antibodies; in drug screening for

CC compositions that mimic or modulate activity or expression of ASTH11
 CC and/or ASTH1J (including altered forms of these proteins); and as a
 CC therapeutic. The ASTH1 genes or fragments thereof, encoded proteins,
 CC ASTH1 genomic regulatory regions, and anti-ASTH1 and anti-ASTH1J
 CC antibodies are useful in the identification of individuals predisposed to
 CC development of asthma, and for modulation of gene activity in vivo for
 CC prophylactic and therapeutic purposes. The intact ASTH1 or ASTH1J
 CC proteins or active fragments thereof may be used to modulate or reduce
 CC bronchial hyperreactivity. Sequences AA80260-AA80261 and AA80264-AA80416
 CC represent polymorphic sites within the ASTH1J or ASTH1 genes

XX
 SQ Sequence 22 BP; 5 A; 6 C; 2 G; 8 T; 0 U; 1 Other;

Query Match 0.2%; Score 16.2; DB 1; Length 22;
 Best Local Similarity 85.7%; Pred. No. 1.4e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6994 AGGTGCGAAGGAGCATTTTC 7014
 DB 22 AGGTGAGAAAGACATTTTC 2

RESULT 1667
 AAC97372
 ID AAC97372 standard; DNA; 22 BP.

XX
 AC AAC97372;
 XX
 DT 28-FEB-2001 (first entry)

XX
 DE Human PRO172 PCR primer, SEQ ID NO:6.

XX
 KW Human; angiogenesis-associated protein; PRO; endothelial cell growth;
 KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;
 KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;
 KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;
 KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;
 KW Alzheimer's disease; Huntington's disease; stroke; drug screening;
 KW gene therapy; transgenic animal; PCR primer; ss.

XX
 OS Homo sapiens.
 XX
 PN WO200053753-A2.

XX
 PD 14-SEP-2000.
 XX
 PF 05-JAN-2000; 2000WO-US000219.

XX
 PR 08-MAR-1999; 99WO-US005028.
 PR 12-MAR-1999; 99US-0123957P.
 PR 14-MAY-1999; 99US-0134287P.
 PR 02-JUN-1999; 99WO-US012252.
 PR 23-JUN-1999; 99US-0141037P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 30-NOV-1999; 99WO-US028313.
 PR 30-NOV-1999; 99WO-US028409.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.

XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;
 PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;
 XX
 DR WPI; 2001-090793/10.
 XX

PT New isolated nucleic acid for producing a PRO polypeptide, analyzing
 PT genetic disorders and treating cardiovascular, endothelial or angiogenic
 PT disorders, such as atherosclerosis, wounds or cancer.

XX
 PS Example 4; Page 119; 293pp; English.

XX
 CC The invention relates to novel human angiogenesis-associated proteins
 CC designated PRO proteins (AA853064-B53097), and to nucleic acids encoding
 CC PRO proteins. The invention also relates to vectors and host cells
 CC comprising a PRO nucleic acid, the recombinant production of a PRO
 CC protein, PRO antibodies specific for a PRO protein, fusion proteins
 CC comprising a PRO protein, agonists or antagonists of a PRO protein, and
 CC compounds which inhibit the expression of a PRO gene. The invention
 CC additionally encompasses methods of identifying modulators of PRO
 CC expression or activity; diagnosing a cardiovascular, endothelial or
 CC angiogenic disorder, or a susceptibility to such a disorder by detecting
 CC mutations in a PRO gene, or the expression level of a PRO gene within a
 CC particular tissue; treating a cardiovascular, endothelial or angiogenic
 CC disorder via the administration of a PRO protein, PRO nucleic acid, or
 CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a
 CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial
 CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the
 CC administration of a PRO protein, or an agonist or antagonist thereof. PRO
 CC nucleic acids, PRO proteins, antibodies against PRO proteins, PRO
 CC agonists and PRO antagonists may be used as therapeutic agents to treat
 CC cardiovascular, endothelial or angiogenic disorders, such as
 CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,
 CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,
 CC endometriosis, ulcers, cancer, Alzheimer's disease, Huntington's
 CC disease, or stroke. PRO nucleic acids are additionally useful in the
 CC recombinant production of PRO proteins, as hybridisation probes to screen
 CC libraries to isolate cDNAs with sequence identity to PRO proteins, to map
 CC genes encoding PRO proteins, to analyse genetic disorders, and in gene
 CC therapy. PRO nucleic acids can also be used to produce transgenic animals
 CC useful for the development and screening of potential therapeutic agents.
 CC The present sequence represents a PCR primer used in the isolation of a
 CC cDNA encoding a PRO protein of the invention

XX
 SQ Sequence 22 BP; 6 A; 7 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.2; DB 1; Length 22;
 Best Local Similarity 85.7%; Pred. No. 1.4e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1725 GCATCTCAAGAACCTACTC 1745
 DB 1 GCATCTCAAGAACCTACTC 21

RESULT 1668
 AA168502
 ID AA168502 standard; DNA; 22 BP.

XX
 AC AA168502;
 XX
 DT 14-DEC-2001 (first entry)

XX
 DE L. monocytogenes iap gene cluster III PCR primer iap-1047-III-R.

XX
 KW PCR primer; iap gene; p60 protein; detection; infection; ss.

XX
 OS *Listeria monocytogenes*.

XX
 PN WO200168900-A2.

XX
 PD 20-SEP-2001.
 XX
 PF 15-MAR-2001; 2001WO-EP002949.
 XX
 PR 15-MAR-2000; 2000DE-01012540.
 XX
 PA (VERM-) VERMICON AG.
 XX

PI Walcher M, Wagner M, Snaidr J;
XX
XX WPI; 2001-625966/72.
XX Specifically detecting microorganisms in a sample, by polymerase chain
PT reaction with reaction and competitor primers, useful for detecting
PT subspecies of *Listeria*, in particular *Listeria monocytogenes*.
XX
XX Claim 10; Page 16; 32pp; German.
XX This invention describes a novel method for specifically detecting
CC microorganisms in a sample by Polymerase Chain Reaction (PCR) where in
CC addition to reaction primers specific to the target organism, competition
CC primers specific for non-target organisms are also used. The invention is
CC used to detect microorganisms in a sample and to distinguish them from
CC closely related microorganisms, particularly to detect infection by
CC *Listeria* below the species level, especially *Listeria monocytogenes*. The
CC invention allows detection of different subspecies of *Listeria* not
CC provided by prior art. This sequence represents a PCR primer used in the
CC amplification of the *Listeria monocytogenes* iap gene associated with the
CC p60 protein described in the method of the invention
XX
XX Sequence 22 BP; 1 A; 1 C; 7 G; 13 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 7282 TGTGTACTTGTGTCATTGT 7302
Db 1 TGTGTCTGCTTGTATTGT 21
RESULT 1669
ABZ84314/c
ID ABZ84314 standard; DNA; 22 BP.
XX
AC ABZ84314;
DT 14-MAY-2003 (first entry)
XX
DE Toxicologically relevant rat PCR primer #1473.
XX
KM Toxicologically relevant gene; toxicological response; PCR primer: ss.
XX
OS Rattus sp.
OS Synthetic.
XX
PN MO2003016500-A2.
XX
XX 27-FEB-2003.
PD
XX
PF 16-AUG-2002; 2002MO-US026514.
XX
PR 16-AUG-2001; 2001US-0313080P.
XX
PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
XX
PI Neft RE, Dunn RT, Adkins K, Pickett GG, Kier LD, Schweisler K;
PI Allen P;
XX
XX WPI; 2003-268322/26.
DR
XX
XX Determining a toxicological response to an agent, useful for screening of
PT drugs, comprises comparing the expression profile of one or more human
PT toxic response genes to a reference gene expression profile indicative of
PT toxicity.
XX
PS Claim 1; Page 341; 455pp; English.
XX
XX The present invention describes a method (M1) for determining a
CC toxicological response to an agent, which comprises comparing the
CC expression profile of one or more human toxic response genes to a

CC reference gene expression profile indicative of toxicity, and so
CC determining the presence of a toxic response to the agent. Also
CC described: (1) an array comprising one or more polynucleotides selected
CC from the genes corresponding to the partial sequences given in ABZ82842
CC to ABZ84764, or their fragments of at least 20 nucleotides, or homologues
CC; and (2) determining if a gene putatively identified to be a toxic
CC response gene plays a role on toxic response pathways by determining the
CC expression profile of the gene after exposure of cells or a human subject
CC to a known toxic pharmaceutical or industrial agent, comprising: (a)
CC exposing cells to an agent; (b) obtaining the test gene expression profile
CC for a putatively identified toxic response gene after exposure to a known
CC toxic pharmaceutical or industrial agent; and (c) comparing the test
CC profile to the expression profile of a gene with a similar function or
CC comparing the test profile to the expression profile of that gene after
CC exposure to other known toxic compounds. The methods are useful for
CC predicting and determining toxicological responses on a cellular, organ
CC or system level. The arrays comprising the human genes are useful for
CC toxicological screening of drugs, pharmaceutical compounds and chemicals
XX
XX Sequence 22 BP; 5 A; 6 C; 3 G; 8 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 831 TGGCATGTGAAAGATGATCT 851
Db 21 TGGCAAAAGGAAGATGATCT 1
RESULT 1670
ABX94818
ID ABX94818 standard; DNA; 22 BP.
XX
XX
AC ABX94818;
DT 11-UTL-2003 (first entry)
XX
DE Human cysteine-rich FGF receptor (CFR) PCR primer CFR-For1.
XX
XX
KM Human; antibody; murine antibody NM58-49/69; cysteine-rich FGF receptor;
KM glycoprotein receptor; proliferating cell; stomach carcinoma; vaccine;
KM CFR-1 protein; human antibody 103/51; immunoglobulin M; cytostatic; gut;
KM antibacterial; antiinflammatory; receptor antagonism; cancer; stomach;
KM oesophagus; rectum; liver; gall bladder; pancreas; lung; bronchus;
KM breast; cervix; prostate; heart; ovary; uterus; metaplasia of oesophagus;
KM Helicobacter pylori-associated gastritis; tubular adenoma; tumour marker;
KM villous adenoma; Barrett dysplasia; cervical intraepithelial neoplasia;
KM anticancer agent; PCR; primer; ss.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH modified_base 1 /+tag= a
FT /mod_base= OTHER
FT /note= "This nucleotide is depicted as o in the
specification"
XX
XX MO2003011907-A2.
PN
XX
XX 13-FEB-2003.
PD
XX
XX 23-JUL-2002; 2002MO-DE002699.
PF
XX
XX 24-UTL-2001; 2001DE-01036009.
PR
XX
XX 09-MAR-2002; 2002DE-01010425.
PR
XX
XX (MUEL/) MUELLER-HERMELINK H K.
PA (VOL/) VOLLMERS H.
PA (HENS/) HENSEL F.
XX

PI Mueller-Hermelink HK, Vollmers H, Hensel F;
 XX WPI; 2003-256436/25.
 XX
 PT New glycoprotein receptor on surface of cancer cells, useful for
 PT treatment and diagnosis of cancer and for drug screening, also new
 PT specific antibody.
 XX
 PS Disclosure; Page 21; 49pp; German.
 XX
 CC This invention describes a novel glycoprotein receptor, present on the
 CC surface membrane of strongly proliferating cells, especially stomach
 CC carcinoma, having at least one determinant that corresponds with a
 CC determinant of CCR-1 protein and binding specifically to human antibody
 CC 103/51 and/or the murine antibody 58/47-69 (immunoglobulin M). The
 CC products of the invention have cytostatic, antibacterial and
 CC antiinflammatory activity and can be used in a vaccine or for receptor
 CC antagonism. The novel receptor is used for therapeutic in vivo generation
 CC of antibodies, for treatment and prevention of cancer (of oesophagus,
 CC stomach, gut, rectum, liver, gall bladder, pancreas, lung, bronchi,
 CC breast, cervix, prostate, heart, ovary and/or uterus), for treating a
 CC wide range of precancerous states (e.g. Helicobacter pylori-associated
 CC gastritis, tubular or villous adenoma, Barrett dysplasia/metaplasia of
 CC oesophagus, cervical intraepithelial neoplasia etc.), for diagnosis (as a
 CC tumour marker) and for identifying potential anticancer agents from their
 CC ability to bind selectively to the glycoprotein receptor. This sequence
 CC represents a PCR primer used to amplify the human cysteine-rich FGF
 CC receptor (CRR) described in the disclosure of the invention
 XX
 SQ Sequence 22 BP; 7 A; 7 C; 5 G; 2 T; 0 U; 1 Other;
 XX
 Query Match 0.2%; Score 16.2; DB 1; Length 22;
 Best Local Similarity 85.7%; Pred. No. 1.4e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 XX
 QY 7406 GCACATCAGCAGCAGCAGCA 7426
 DB 2 GCAGCTTCAGCAGCAGCAGCA 22
 XX
 RESULT 1671
 ABZ80010
 ID ABZ80010 standard; DNA; 22 BP.
 XX
 AC ABZ80010;
 XX
 DT 20-MAY-2003 (first entry)
 XX
 DE Mantle histiocyte retrovirus gag PCR primer HERV-10 SEQ ID NO:4.
 XX
 KW Mantle histiocyte retrovirus; MHRV; gag; mantle cell lymphoma;
 KW retrovirus; lymphoma; cytosstatic; immunosuppressive; antineumatic;
 KW neuroprotective; neuroleptic; MHRV-associated disorder; infection;
 KW teratocarcinoma; multiple sclerosis; autoimmune rheumatic disease;
 KW schizoprenia; PCR primer; ss.
 XX
 OS Retroviridae.
 XX
 PN WO2003016491-A2.
 XX
 PD 27-FEB-2003.
 XX
 PF 15-AUG-2002; 2002MO-US026249.
 XX
 PR 15-AUG-2001; 2001US-0312686P.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI McGrath MS, Herndler B;
 XX
 DR WPI; 2003-256702/25.
 XX
 PT New isolated mantle histiocyte retrovirus (MHRV) particle, useful for the

PT diagnosis and treatment of MHRV-associated disorders, such as lymphoma,
 PT teratocarcinoma, multiple sclerosis, rheumatic diseases, and
 PT schizoprenia.
 XX
 PS Example 3; Fig 1; 85pp; English.
 XX
 CC The present invention describes an isolated mantle histiocyte retrovirus
 CC (MHRV) particle (I). MHRV is isolated from human lymphoma, more
 CC specifically from mantle cell lymphoma. (I) has cytosstatic, neuroleptic,
 CC antineumatic, immunosuppressive and neuroprotective activities. Methods
 CC and compositions from the present invention can be used for the diagnosis
 CC and treatment of MHRV-associated disorders, such as lymphoma,
 CC teratocarcinoma, multiple sclerosis, autoimmune rheumatic diseases, and
 CC schizoprenia. The present sequence represents a PCR primer for MHRV gag,
 CC which is used in the exemplification of the present invention
 XX
 SQ Sequence 22 BP; 10 A; 3 C; 6 G; 3 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 16.2; DB 1; Length 22;
 Best Local Similarity 85.7%; Pred. No. 1.4e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 XX
 QY 1194 AGTTGCCAGGAACTMAAGCA 1214
 DB 2 AATTGGCAAGAACTMAAGCA 22
 XX
 RESULT 1672
 ADD26412/C
 ID ADD26412 standard; DNA; 22 BP.
 XX
 AC ADD26412;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Human abl intron 1b primer 3-4.
 XX
 KW conjugate; bcr; abl; fusion gene; transport mediator; cell membrane; PNA;
 KW Philadelphia chromosome; triple helix; cytosstatic;
 KW chronic myeloid leukaemia; chromosome 22; ss; primer.
 XX
 OS Homo sapiens.
 XX
 PN WO2003039438-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 08-NOV-2002; 2002MO-DE004154.
 XX
 PR 08-NOV-2001; 2001DE-01054827.
 XX
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 XX
 PI Braun K, Waldeck W, Pipkorn R, Braun I, Debuss J;
 XX
 DR WPI; 2003-441456/41.
 XX
 PT New peptide nucleic acid conjugate, useful for treating chronic myeloid
 PT leukemia, targets the Philadelphia chromosome and includes transport
 PT peptides.
 XX
 PS Example 2; Fig 4B; 30pp; German.
 XX
 CC This invention describes a novel conjugate for specifically inhibiting
 CC expression of a bcr/abl fusion gene comprising a transport mediator for
 CC the cell membrane, a protein or peptide for importation into the cell
 CC nucleus, and a peptide nucleic acid (PNA) that hybridizes specifically to
 CC the bcr/abl fusion gene, inhibiting its expression. The transport
 CC mediator is a protein or peptide that can overcome the plasma membrane,
 CC especially the transmembrane peptide part(43-58) or peptides designated
 CC TPDECO, TPORHIV-1/TRAT and TRUHAM. The conjugate may include a spacer,
 CC especially between protein and PNA, and it has the structure transport
 CC mediator-disulfide-protein-spacer-PNA. Spacers are preferably polylysine,

CC polyethylene glycol, derivatives of polymethacrylic acid and polyvinyl
 CC pyrrolidone. The conjugate of the invention binds to the fusion region of
 CC the bcr/abl genes in the Philadelphia chromosome, forming a triple helix
 CC and thus inhibiting expression of the corresponding fusion protein (a
 CC tyrosine kinase). The products of the invention are cytostatic and are
 CC used to treat chronic myeloid leukaemia. Treatment with the conjugate is
 CC non-invasive and combining the PNA with a transport mediator ensures
 CC efficient, rapid and directed transport of PNA to its target site
 CC (nucleus). The PNA is resistant to both protease and nuclease, so
 CC produces stable blockade of transcription of target genes. The conjugate
 CC can discriminate between the gene fusion and unused bcr and abl genes
 CC and is effective at very low concentrations (below 100 pM), so side
 CC effects should not be significant. This sequence represents a primer
 CC capable of binding to a fragment of the human abl gene intron 1b (see
 CC Genbank U07562).

XX
 CC Sequence 22 BP, 5 A, 8 C, 4 G, 5 T, 0 U, 0 Other;
 SQ

Query Match 0.2%; Score 16.2; DB 1; Length 22;
 Best Local Similarity 85.7%; Pred. No. 1.4e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 685 CAAGCCTGATGTGGCATG 705
 DB 22 CAAGTCCTGAATGTGGCATG 2

RESULT 1673
 AAZ06740/c
 ID AAZ06740 standard; cDNA; 23 BP.
 XX
 AC AAZ06740;
 XX
 DT 26-NOV-1999 (first entry)
 XX
 DE PCR primer FR-Ndr-299 for ndr1 mutation S20D generation.
 XX
 XX Non-specific disease resistance gene; ndr1; hypersensitive response;
 KM Ca2+ dependent protein kinase; CDPK; protein kinase C; PKC; pesticide;
 KM Inducible promoter; signal transduction; transgenic plant; paper;
 KM pulp manufacture; pathogen resistant; PCR primer; FR-Ndr-299; ss.
 XX
 OS Synthetic.
 OS Arabidopsis thaliana.
 XX
 PN WO945129-A1.
 XX
 PD 10-SEP-1999.
 XX
 PP 08-MAR-1999; 99WO-EP001672.
 XX
 PR 06-MAR-1998; 98EP-00104076.
 XX
 PA (MOGE-) MOGEN INT NV.
 XX
 PI Stuijver MH, Custers J, Simons LH;
 XX
 DR WPI; 1999-540854/45.
 XX
 PT New promoter sequence useful for generating pathogen resistant transgenic
 PT plants - to prevent need for pesticides.
 XX
 PS Example 2; Page 18; 43pp; English.
 XX
 CC PCR primers AAZ06740-206741 are used to create a mutation in the non-
 CC specific disease resistance (ndr1) protein. These primers cause a
 CC substitution of the Ser at position 20 in the wild-type ndr1 protein
 CC (AA19278) for Asp. This mutation and a substitution of wild-type Ser at
 CC position 207 for Asp result in the production of a mutant ndr1 gene
 CC AAZ06737. The NDR1 protein (AA19278) plays a role in the hypersensitive
 CC response, and has 2 putative Ca2+ dependent protein kinase (CDPK)
 CC phosphorylation sites, and 3 putative protein kinase C (PKC)
 CC phosphorylation sites. Mutant versions of the ndr1 gene (AAZ06736-206737)

CC can be used in a method for the induction of pathogen resistance in
 CC plants by transforming the plant with a polynucleotide sequence which is
 CC made from a pathogen inducible promoter, which regulates the expression
 CC of a plant signal transduction protein e.g. ndr1. Alternatively the
 CC promoter can regulate the expression of a compound which alleviates the
 CC inhibitory effect of a protein on the signal transduction pathway,
 CC causing a hypersensitive response. The new methods are useful for
 CC generating transgenic plants at least partially resistant to pathogens.
 CC These plants are especially useful in the plant industry, paper and pulp
 CC manufacturing industries. The method prevents the need for pesticide
 CC treatment

XX
 CC Sequence 23 BP, 5 A, 6 C, 3 G, 9 T, 0 U, 0 Other;
 SQ

Query Match 0.2%; Score 16.2; DB 1; Length 23;
 Best Local Similarity 85.7%; Pred. No. 1.4e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5819 TGTGATGATGAATCTGTCA 5839
 DB 21 TGTGAAGATGAATCTTAACA 1

RESULT 1674
 AAZ99839
 ID AAZ99839 standard; DNA; 23 BP.
 XX
 AC AAZ99839;
 XX
 DT 12-JUL-2000 (first entry)
 XX
 DE Nucleotide sequence of reverse transcription primer.
 XX
 KM Mono-length cDNA library; differential display; gene expression;
 KM gene identification; drug response; primer; ss.
 XX
 OS Synthetic.
 OS WO200014273-A2.
 XX
 PD 16-MAR-2000.
 XX
 PP 26-AUG-1999; 99WO-CA000789.
 XX
 PR 03-SEP-1998; 98US-00145936.
 XX
 PA (SIGW-) SIGNALGENE INC.
 XX
 PI Belouchi AM, Fournier H, Gee M, Gauvreau D;
 XX
 DR WPI; 2000-257012/22.
 XX
 PT Determining differential display of gene expression, useful for
 PT monitoring drug responses at the gene expression level and locating genes
 PT involved in a particular response, by comparisons between mono-length
 PT cRNA libraries.
 XX
 PS Example 3; Page 48; 73pp; English.
 XX
 CC The present sequence represents a primer used for reverse transcription
 CC of mRNA to produce cDNA. The cDNA is used for cDNA library production, in
 CC the course of the invention. The specification describes a method of
 CC determining differential display of gene expression, by comparison of
 CC mono-length cRNA libraries. These libraries are probe hybridised to
 CC accessible ordered arrays to determine differential hybridisation display
 CC sites between mono-length segment libraries and to locate genes of
 CC expression differential. The methods are useful for determining
 CC differential hybridisation display sites between mono-length segment
 CC libraries and to locate genes of expression differential. The methods are
 CC also useful in gene identification related to complex traits. The methods
 CC also permit monitoring drug responses at the gene expression level and
 CC locating genes involved in a particular response. The methods are also
 CC useful for pharmacogenomic research in evaluating how variability in

CC The invention relates to novel isolated polypeptides, mature form of the
 CC polypeptide, a sequence that is 95% identical to the polypeptide or the
 CC polypeptide comprising one or more conservative substitutions. The NOVX
 CC polypeptide is useful for treating or preventing a pathology associated
 CC with the polypeptide e.g. disorders associated with aberrant expression
 CC or activity of the polypeptide, such as cancer, diabetes, obesity, and
 CC endocrine, CNS and inflammatory disorders. They can also be used in
 CC various detection and screening assays, chromosome mapping, tissue typing
 CC and predictive medicine. This sequence corresponds to a probe used to
 CC isolate the coding sequence for one of the polypeptides of the invention.

XX
 SQ Sequence 23 BP; 7 A; 8 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.2; DB 1; Length 23;
 Best Local Similarity 85.7%; Pred. No. 1.4e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2408 CCACAGTGGACCAACATCA 2428
 DB 1 CCAGGTGGCCACCAACATCA 21

RESULT 1679

AAV52547/C
 ID AAV52547 standard; DNA; 24 BP.

AC AAV52547;

XX 20-NOV-1998 (first entry)

DE Unmethylated CpG dinucleotide 1776.

XX Unmethylated CpG dinucleotide; immune response; bacterial meningitis;
 KW natural killer cell activation; NK cell; Th2 response; neonatal sepsis;
 KW pulmonary disorder; asthma; environmentally induced airway disease;
 KW bacterial infection; endotoxaemia; therapy; cystic fibrosis;
 KW inflammatory bowel disease; ss.

XX Synthetic.

XX WO9837919-A1.

XX 03-SEP-1998.

XX 25-FEB-1998; 98WO-US003678.

XX 28-FEB-1997; 97US-0039405P.

XX (IOWA) UNIV IOWA RES FOUND.

XX Schwartz DA, Krieg AM;

XX WPI; 1998-480941/41.

XX Use of nucleic acids containing an unmethylated CpG - for treating a
 PT subject having or at risk of having an acute decrement in air flow or
 PT inhibiting an inflammatory response.

XX Example 4; Page 35; 65pp; English.

XX This sequence represents an unmethylated CpG dinucleotide, and can be
 CC used in the method of the invention. The method is for treating a subject
 CC having, or at risk of having an acute decrement in air flow, comprising
 CC administering a nucleic acid sequence containing at least one
 CC unmethylated CpG. The nucleic acid containing an unmethylated CpG
 CC dinucleotide affect an immune response in a subject by activating natural
 CC killer cells (NK) or redirecting a subject's immune response from a Th2
 CC to a Th1 response by inducing monocytic and other cells to produce Th1
 CC cytokines. They can be used to treat pulmonary disorders having an
 CC immunologic component, such as asthma or environmentally induced airway
 CC disease. They can also be used to treat diseases associated with Gram-
 CC positive bacterial infections or endotoxaemia including bacterial
 CC meningitis, neonatal sepsis, cystic fibrosis, inflammatory bowel disease

CC and liver cirrhosis, Gram-negative pneumonia, Gram-negative abdominal
 CC abscess, haemorrhagic shock, disseminated intravascular coagulation, or
 CC an inflammatory response to lipopolysaccharide

XX Sequence 24 BP; 5 A; 9 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.2; DB 1; Length 24;
 Best Local Similarity 85.7%; Pred. No. 1.5e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1521 GGGGAAACGTTCTACATGG 1541
 DB 22 GGGGAAACGTTCTCATGG 2

RESULT 1680

AAV67059/C
 ID AAV67059 standard; CDNA; 24 BP.

AC AAV67059;

XX 14-JAN-1999 (first entry)

DE Mouse Ikaros oligonucleotide Ik3-20.

XX CD3-delta gene; Ikaros gene; T cell; progenitor stem cell; leukaemia;
 KW differentiation marker; immune system; corpus striatum; AIDS;
 KW Alzheimer's disease; ss.

XX Mus sp.
 OS Synthetic.

XX US5824770-A.

XX 20-OCT-1998.

XX 05-JUN-1995; 95US-00465590.

XX 14-SEP-1992; 92US-00946233.

XX 14-SEP-1993; 93US-00121438.

XX 02-MAY-1994; 94US-00238212.

XX (GEHO) GEN HOSPITAL CORP.

XX Georgopoulos K;

XX WPI; 1998-582621/49.

XX Ikaros poly:peptide(s) - useful for treating disorders of immune system
 PT or corpus striatum.

XX Disclosure; Col 26; 111pp; English.

XX The present invention describes a purified peptide having at least one of
 CC the following properties: (a) it stimulates transcription of a DNA
 CC sequence under the control of a delta A element, an NFkB element or an
 CC Ikaros binding oligonucleotide consensus sequence; (b) it binds to any of
 CC a delta A element, an NFkB element or an Ikaros binding oligonucleotide
 CC consensus sequence; (c) it competitively inhibits the binding of a
 CC naturally occurring Ikaros isoform to any of a delta A element, an NFkB
 CC element or an Ikaros binding oligonucleotide consensus sequence; (d) it
 CC competitively inhibits Ikaros binding to Ikaros responsive elements; or
 CC (e) it inhibits protein-protein interactions of transcriptional complexes
 CC formed with naturally occurring Ikaros isoforms. The proteins, provided
 CC that they stimulate gene transcription under the control of delta A
 CC elements, NFkB elements and/or Ikaros-binding oligonucleotides, bind to
 CC delta A elements, NFkB elements and/or Ikaros-binding oligonucleotides,
 CC competitively inhibit binding of naturally occurring Ikaros isoforms to
 CC delta A elements, NFkB elements and/or Ikaros-binding oligonucleotides,
 CC competitively inhibit Ikaros binding to Ikaros-responsive elements and/or
 CC inhibit protein-protein interactions of transcriptional complexes with
 CC naturally occurring Ikaros isoforms, can be used to treat immune system
 CC disorders, e.g. leukaemia or AIDS, or corpus striatum disorders, e.g.

CC Alzheimer's disease. AAV66975 to AAV67118 represent oligonucleotides
CC given in the present invention
XX
SQ Sequence 24 BP; 8 A; 5 C; 8 G; 3 T; 0 U; 0 Other;
Query Match 0.2%; Score 16.2; DB 1; Length 24;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1170 GATCCCATCTGCTGCT 1190
DB 21 GATCCCGATATCTCTGCT 1
RESULT 1681
AAV27721/c
ID AAV27721 standard; DNA; 24 BP.
XX
AC AAV27721;
XX
DT 01-OCT-1998 (first entry)
XX
DE Immunostimulatory oligodeoxyribonucleotide of the invention.
XX
KM Immunostimulatory; oligodeoxyribonucleotide; ODN;
KM unethylated CPG dinucleotide; activator; lymphocyte; immune response;
KM Th2; Th1; cytokine; treatment; prevention; asthma; autoimmune disease;
KM desensitisation therapy; artificial adjuvant; antibody generation; ss.
XX
OS Synthetic.
XX
PN WO918810-A1.
XX
PD 07-MAY-1998.
XX
PF 30-OCT-1997; 97WO-US019791.
XX
PR 30-OCT-1996; 96US-00738652.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PI Krieg AM, Kline JN;
XX
DR WPI; 1998-27127/24.
XX
PT New immunostimulatory nucleic acid molecules - which contain at least one
PT unethylated CPG dinucleotide, used for treating e.g. tumours, infections
PT or autoimmune disease.
XX
PS Disclosure; Page 49; 10pp; English.
XX
AAV27641-751 represent immunostimulatory oligodeoxyribonucleotides (ODNs)
CC of the invention. The ODNs contain at least one unethylated CPG
CC dinucleotide, and have the formula: 5' N1X1CGX2N 3', where at least one
CC nucleotide separates consecutive CPGs, X1 is adenine, guanine, or
CC thymine, X2 is cytosine or thymine, N is any nucleotide and N1+N2 is 0-26
CC bases with the provision that N1 and N2 does not contain a CCGG tetramer
CC or more than one CCG or CCG trimer OR 5' NX1X2CGX3X4N 3', where at least
CC one nucleotide separates consecutive CPGs, X1 and X2 are selected from
CC GPT, GPG, GGA, APT and APA, X3 and X4 are selected from TPT or CPT. N is
CC any nucleotide, and N1+N2 is 0-26 bases with the provision that N1 and N2
CC does not contain a CCGG tetramer or more than one CCG or CCG trimer. The
CC ODNs activate lymphocytes in a subject and redirect a subject's immune
CC response from a Th2 to a Th1 (e.g. by inducing monocyte cells and other
CC cells to produce Th1 cytokines, including IL-12, IFN-gamma and GM-CSF).
CC The ODNs can be used to treat or prevent an asthmatic disorder,
CC autoimmune disease, in desensitisation therapy, as an artificial
CC adjuvant during antibody generation in a mammal such as a mouse or a
CC human
XX
SQ Sequence 24 BP; 5 A; 9 C; 4 G; 6 T; 0 U; 0 Other;
Query Match 0.2%; Score 16.2; DB 1; Length 24;

Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1521 GGGGAAACAGTTCTACAAATGG 1541
DB 22 GGGGAAACAGTTCTGTCATGG 2
RESULT 1682
AAZ41907/c
ID AAZ41907 standard; DNA; 24 BP.
XX
AC AAZ41907;
XX
DT 24-JAN-2000 (first entry)
XX
DE IL-12 secretion inducing Cpg oligonucleotide 52.
XX
KM Cpg oligonucleotide; phosphorothioate; interleukin-12; IL-12; secretion;
KM human PBMC; immune response; cancer; HIV; bacterial disease; asthma;
KM neoplastic disorder; jaagsiekte; B cell; NK cell; ss; cytokine;
KM antigen presenting cell; infection; allergic disease.
XX
OS Synthetic.
XX
PN WO951259-A2.
XX
PD 14-OCT-1999.
XX
PF 02-APR-1999; 99WO-US007335.
XX
PR 03-APR-1998; 98US-0080729P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PI Krieg AM, Weiner G;
XX
DR WPI; 1999-620169/53.
XX
PT Novel synergistic combinations of immunostimulatory oligonucleotides and
PT immunopotentiating cytokines are useful for stimulating the immune
PT system.
XX
PS Example 8; Page 80; 91pp; English.
XX
CC Sequences AAZ41856-241949 are phosphorothioate Cpg oligonucleotides which
CC are used in the invention to induce interleukin-12 (IL-12) secretion from
CC human PBMC. The invention comprises stimulating an immune response in a
CC subject comprising administering to a subject exposed to an antigen, an
CC immunopotentiating cytokine and an immunostimulatory Cpg oligonucleotide
CC to induce a synergistic antigen specific immune response. The methods are
CC useful for treating cancer by stimulating an antigen specific immune
CC response against a cancer antigen. The methods can also be used to treat
CC neoplastic disorders in humans, including but not limited to: sarcoma,
CC carcinoma, fibroma, lymphoma, melanoma, neuroblastoma, retinoblastoma,
CC and glioma. The methods are also useful for treating infectious diseases,
CC e.g. viral diseases such as HIV, bacterial diseases, and fungal diseases.
CC The methods may also be used to treat allergic diseases, e.g. asthma. The
CC methods and compositions may also be applied to treat cancer and tumours
CC in non human subjects, e.g. cats and dogs. Neoplasias affecting
CC agricultural livestock may also be treated and include leukaemia,
CC haemangioepithelioma and bovine ocular neoplasia. Chronic, infectious,
CC contagious diseases of sheep and goats caused by the bacterium
CC Corynebacterium pseudotuberculosis, and contagious lung tumour of sheep
CC caused by jaagsiekte may also be treated. Cpg oligonucleotides can be
CC useful in activating B cells, NK cells, and antigen presenting cells,
CC such as monocytes and macrophages. Cpg oligonucleotides enhance antibody
CC dependent cellular cytotoxicity and can be used as an adjuvant in
CC conjunction with tumour antigens to protect against a tumour challenge
XX
SQ Sequence 24 BP; 5 A; 9 C; 4 G; 6 T; 0 U; 0 Other;
Query Match 0.2%; Score 16.2; DB 1; Length 24;

Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1521 GGGGAACAGCTCTACATGG 1541

Db 22 GGGGAACAGCTCTACATGG 2

RESULT 1683

AAZ24998/C
ID AAZ24998 standard; DNA; 24 BP.

AC AAZ24998;

DT 24-DEC-1999 (first entry)

DE Antisense probe to Fragile X syndrome gene.

KW Trinucleotide repeat; myotonic-protein kinase; myotonic dystrophy; probe;
in situ hybridisation; detection; expansion; Fragile X syndrome; ss.

OS Synthetic.

OS Homo sapiens.

PN US962332-A.

PD 05-OCT-1999.

PF 11-DEC-1995; 95US-00570155.

PR 17-MAR-1994; 94US-00214823.

PR 07-MAR-1995; 95US-00399499.

PA (UYMA-) UNIV MASSACHUSETTS.

PI Taneja KL, Singer RH;

DR WPI; 1999-579615/49.

PT Detection of trinucleotide repeats.

PS Disclosure; Col 20; 18pp; English.

CC This oligonucleotide is targeted to the CGG trinucleotide repeats found

CC in the FMR1 gene. Excessive numbers of the trinucleotide repeats in the

CC FMR1 gene leads to the disease Fragile X syndrome. This sequence is used

CC as an antisense oligonucleotide probe for the hybridisation reaction. The

CC invention relates to a method for the detection of trinucleotide repeat

CC expansion, e.g. in the FMR1 gene or Mc-PK gene (leading to myotonic

CC dystrophy) by in situ hybridization

CC SQ Sequence 24 BP; 0 A; 14 C; 6 G; 2 T; 0 U; 2 Other;

QY Query Match 0.2%; Score 16.2; DB 1; Length 24;

Best Local Similarity 81.8%; Pred. No. 1.5e+03;

Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 59 ACGGAGGCTGCGGCGCGCGG 80

24 AAGGCGCGCGCGCGCGCGG 3

RESULT 1684

AAZ78982
ID AAZ78982 standard; DNA; 24 BP.

AC AAZ78982;

DT 17-AUG-1999 (first entry)

DE Oligonucleotide #48 for recombination and cloning method.

KW Cloning; donor; recombination site; vector; chimeric; ss.

XX Synthetic.

OS WO921977-A1.

PN 06-MAY-1999.

PD 26-OCT-1998; 98WO-US022589.

PF 24-OCT-1997; 97US-0065930P.

PR 23-OCT-1998; 98US-00177387.

PA (LIFE-) LIFE TECHNOLOGIES INC.

PI Harley JL, Braach MA, Temple GF, Fox DK;

DR WPI; 1999-303011/25.

PT New nucleic acid cloning methods.

PS Disclosure; Page 172; 185pp; English.

CC The invention relates to novel methods for cloning or subcloning one or

CC more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or

CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one or

CC more desired nucleic acid segments flanked by at least 2 recombination

CC sites which do not recombine with each other; (2) one or more vector

CC donor molecules (VDMs) comprising at least 2 recombination sites which do

CC not recombine with each other; and (3) one or more site-specific

CC recombination proteins; (b) incubating the combination to transfer one or

CC more of the desired segments into one or more of the VDMs, thereby

CC producing one or more desired product molecules (PDMs). The methods can be

CC used for the efficient and specific recombination of NAM segments. They

CC can be used to generate chimeric DNA or RNA molecules that have the

CC desired characteristics and/or nucleic acid segments. The methods can

CC also be used for changing vectors. The oligonucleotides AAZ7895-X78994

CC XX SQ Sequence 24 BP; 6 A; 5 C; 3 G; 10 T; 0 U; 0 Other;

QY Query Match 0.2%; Score 16.2; DB 1; Length 24;

Best Local Similarity 85.7%; Pred. No. 1.5e+03;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 3109 AAGACTGCTGTCAGCAGCTT 3129

1 AATTCATGTTTACACAGCTT 21

RESULT 1685

AAZ60976/C
ID AAZ60976 standard; DNA; 24 BP.

AC AAZ60976;

DT 30-MAY-2000 (first entry)

DE Nucleotide sequence of an immunostimulatory Cpg oligonucleotide.

KW Immunostimulatory; stereoisomer; Cpg oligonucleotide; Th2; Th1; asthma;

KW allergic reaction; allergen; cancer antigen; cancer; immunoinhibitory;

KW inflammatory disease; inflammatory bowel disease; autoimmune disease;

KW gingivitis; psoriasis; sepsis; ss.

OS Synthetic.

OS WO200006588-A1.

PN 10-FEB-2000.

PD 27-JUL-1999; 99WO-US017100.

PF 27-JUL-1998; 98US-0094370P.

XX (IOWA) UNIV IOWA RES FOUND.
PA (CPGI-) CPG IMMUNOPHARMACEUTICALS INC.
XX Krieger AM;
PI WPI; 2000-195254/17.
XX
DR
XX Immunostimulatory and immunoinhibitory stereoisomers of Cpg
PT oligonucleotides useful for immunotherapy of cancer.
XX
XX Disclosure; Page 11; 88pp; English.
XX
XX AA260933-261015 represent immunostimulatory stereoisomers of Cpg
CC oligonucleotides. The sequences are derived from generic nucleic acid
CC sequence, from which immunoinhibitory sequences may also be derived. The
CC immunostimulatory nucleic acids can be co-administered with an antigen to
CC induce an antigen-specific immune response. The immunostimulatory nucleic
CC acids can also be used in methods for redirecting a subject's immune
CC response from a Th2 to a Th1, for treating asthma, for desensitising a
CC subject against the occurrence of an allergic reaction in response to
CC contact with an allergen, for activating an immune cell, especially a
CC lymphocyte or a dendritic cell expressing a cancer antigen or for
CC treating cancer. The immunoinhibitory nucleic acid can be used to prevent
CC an immune response, especially where the immune response in the subject
CC is excessive due to having received an immune stimulating compound. The
CC immunoinhibitory nucleic acid can be used to treat a subject having or at
CC risk of an inflammatory disease, especially inflammatory bowel disease,
CC autoimmune disease, gingivitis, psoriasis and sepsis
XX
SQ Sequence 24 BP; 5 A; 9 C; 4 G; 6 T; 0 U; 0 Other;
Query Match 0.2%; Score 16.2; DB 1; Length 24;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1521 GGGGAAACAGTCTACATCG 1541
Db 22 GGGGAAACAGTCTGTCATCG 2
RESULT 1686
AA247983/c
ID AA247983 standard; DNA; 24 BP.
XX
AC AA247983;
XX
DT 08-MAR-2000 (first entry)
XX
DE Immune remodeling inducing Cpg oligonucleotide SEQ ID NO:61.
XX
KW Haematopoiesis; regulation; Cpg oligonucleotide; phosphorothioate;
KW immune remodeling; thrombopoiesis; anaemia; immune system; cancer;
KW immune response; allergic reaction; infectious disease; asthma;
KW thrombocytopaenia; immunohaemolytic disorder; genetic disorder;
KW haemoglobinopathy; kidney failure; chronic inflammatory disorder;
KW rheumatoid arthritis; ss.
XX
OS Synthetic.
XX
PN WO958118-A2.
XX
PD 18-NOV-1999.
XX
XX 14-MAY-1999; 99WO-IB001285.
XX
XX 14-MAY-1998; 98US-0085516P.
PR 02-FEB-1999; 99US-00241653.
XX
PA (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.
PA (CPGI-) CPG IMMUNOPHARMACEUTICALS INC.
XX
PI Wagner H, Liford G;

XX WPI; 2000-062261/05.
DR
XX Use of Cpg containing oligonucleotides for, e.g. inducing an antigen-
PT specific immune response.
XX
XX Example 1; Page 66; 116pp; English.
XX
CC The present invention describes a method using Cpg containing
CC oligonucleotides (ONs) for regulating immune system remodeling and for
CC regulating haematopoiesis. The method for inducing an antigen-specific
CC immune response comprises: (1) administering an ON having a sequence
CC including at least the formula (1); and (2) exposing the subject to an
CC antigen at least 3 days after the ON is administered to the subject to
CC produce an antigen-specific immune response: 5' X1GCGX 3' (1), where the
CC ON = includes at least 8 nucleotides; C and G = unmethylated, and X1 and
CC X2 = nucleotides. The method can be used for inducing an immune response
CC against an antigen such as cells, cell extracts, proteins,
CC polysaccharides, polysaccharide conjugates, lipids, glycolipids,
CC carbohydrate, viral extracts, viruses, bacteria, fungi, parasites and
CC allergens. It can be used in a subject at risk of developing cancer or an
CC allergic reaction. It can also be used for treating an infectious
CC disease, allergic diseases and asthma, as well as thrombocytopaenia which
CC is drug-induced, due to an autoimmune disorder such as idiopathic
CC thrombocytopenic purpura, or resulting from accidental or therapeutic
CC radiation exposure. It can also be used for treating anaemia such as drug
CC induced anaemia, immunohaemolytic disorder, genetic disorders such as
CC haemoglobinopathy and inherited haemolytic anaemia, inadequate production
CC despite adequate iron stores, chronic disease such as kidney failure, and
CC chronic inflammatory disorder such as rheumatoid arthritis, or anaemia
CC resulting from accidental or therapeutic radiation exposure. AA247932 to
CC AA248029 represent phosphorothioate Cpg oligonucleotides used in the
CC exemplification of the present invention
XX
SQ Sequence 24 BP; 5 A; 9 C; 4 G; 6 T; 0 U; 0 Other;
Query Match 0.2%; Score 16.2; DB 1; Length 24;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1521 GGGGAAACAGTCTACATCG 1541
Db 22 GGGGAAACAGTCTGTCATCG 2
RESULT 1687
AA250099
ID AA250099 standard; DNA; 24 BP.
XX
AC AA250099;
XX
DT 17-MAY-2000 (first entry)
XX
DE Nested PCR primer PNHsp6 to identify mRNA transcripts for human enovin.
XX
KW Enovin; EVN; neutrotrophic growth factor; chromosome 1p31.3-32;
KW glial cell-line derived neutrotrophic factor; GDNF; neuroprotective;
KW GDNF family receptor alpha-3; GFR alpha 3; neurotrophic; analgesic;
KW antirheumatic; cerebroprotective; antiparkinsonian; antiinflammatory;
KW antidiarrhoeal; laxative; antiemetic; neurological disorder; Parkinson's;
KW Alzheimer's; Huntington's; neuropathy; multiple sclerosis; stroke; pain;
KW endocrine neoplasia; prion; rheumatic; inflammation; gastrointestinal;
KW dyspepsia; constipation; intestinal atony; emesis; diarrhoea;
KW Crohn's disease; bowel hypersensitivity; gene therapy; PCR primer; ss.
XX
XX Homo sapiens.
XX
PN WO200004050-A2.
XX
PD 27-JAN-2000.
XX
XX 14-JUL-1999; 99WO-EP005031.
XX

PR 14-JUL-1998; 98GB-00015283.
PR 12-FEB-1999; 99US-00248772.
PR 08-JUN-1999; 99US-00327668.
XX
XX
XX (JANNC) JANSSEN PHARM NV.
XX
XX
XX Geerts HA, Maure SLJ, Meert TF, Clik M, Ver Donck LAL,
XX
XX WPI; 2000-182404/16.
XX
XX
XX Novel human neurotrophic growth factor designated enovin used to treat
PT neurological disorders, neuronal disorders, peripheral neuropathy, brain
PT injury, nervous system disorders, prion associated and gastrointestinal
PT diseases.
XX
XX
XX Disclosure; Page 41; 125pp; English.
XX
XX
XX The present sequence is nested PCR primer PNHsp6, used in RT-PCR to
CC identify different mRNA transcripts for Enovin from human multiple tissue
CC CDNA. Enovin (EVN) is a neurotrophic growth factor, that belongs to glial
CC cell-line derived neurotrophic factor (GDNF) family; it binds to GDNF
CC family receptor alpha-3 (GFR alpha 3). Enovin gene is located on
CC chromosome 1p31.3-32. It is predominantly expressed in heart, skeletal
CC muscle, pancreas and prostate. It has neurotrophic, analgesic,
CC neuroprotective, antirheumatic, cerebroprotective, antiparkinsonian,
CC antiinflammatory, antidiarrhoeal, laxative and antiemetic activity. It
CC can be used to treat neurological disorders like Parkinson's, Alzheimer's
CC and Huntington's disease, neuropathy, multiple sclerosis, endocrine
CC neoplasia, prion associated diseases, stroke, pain, rheumatic/
CC inflammatory diseases and gastrointestinal disorders like dyspepsia,
CC constipation, intestinal atony, emesis, diarrhoea, Crohn's disease and
CC bowel hypersensitivity. EVN polynucleotide can be used in gene therapy
XX
XX
XX Sequence 24 BP; 7 A; 4 C; 10 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.2; DB 1; Length 24;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1521 GGGGAACAGTTCTACAAATGG 1541
DB 4 GGGGAACAGTTCTACAAATGG 24

RESULT 1689
AAZ47851/C
ID AAZ47851 standard; DNA; 24 BP.
XX
XX AAZ47851;
XX
XX
XX 07-MAR-2000 (first entry)
XX
XX Immunostimulatory oligonucleotide sequence SEQ ID NO:52.
XX
XX Mucosal immunity; immunostimulatory; Cpg motif; immune response; antigen;
XX allergic reaction; cancer; infectious disease; asthma; eczema;
XX allergic rhinitis; coryza; hay fever; conjunctivitis; bronchial asthma;
XX urticaria; food allergy; atopic condition; mucosal delivery; ss.
XX
XX
XX Synthetic.
XX
XX
XX WO9961056-A2.
XX
XX 02-DEC-1999.
XX
XX 21-MAY-1999; 99WO-US011359.
XX
XX 22-MAY-1998; 98US-0086393P.
XX
XX (LOBB-) LOBB HEALTH RES INST AT OTTAWA HOSPITAL.
XX (CPG-) CPG IMMUNOPHARMACEUTICALS INC.
XX
XX
XX Mccluskie MJ, Davis HL;

XX
XX WPI; 2000-062585/05.
XX
XX
XX Use of CG containing oligonucleotides as adjuvants for inducing an immune
PT response.
XX
XX
XX Disclosure; Page 25; 116pp; English.
XX
XX
XX

CC The present invention describes a method using Cpg containing
CC oligonucleotides (ONs) as adjuvants for inducing an immune response. The
CC method for inducing a mucosal immune response (MIR) comprises: (1)
CC administering to a mucosal surface of a subject an ON, having a sequence
CC including at least the formula (1); and (2) exposing the subject to an
CC antigen to induce the MIR, where the antigen is not encoded in a nucleic
CC acid vector; 5'X1X2CGX3X43' (1), where C and G = unmethylated, and X1,
CC X2, X3 and X4 = nucleotides. The method can be used for treating a
CC subject at risk of developing an allergic reaction, cancer or infectious
CC disease. It can be used for treating asthmatic subjects, eczema, allergic
CC rhinitis or coryza, hay fever, conjunctivitis, bronchial asthma,
CC urticaria, food allergies or other atopic conditions. The antigen may be
CC derived from infectious organisms such as infectious bacteria, viruses,
CC parasites or fungi. It can be used in humans or animals, e.g. bovine,
CC equine, feline, swine, aquatic or avian species. The ONs act as potent
CC mucosal adjuvants to induce immune responses at both local and remote
CC sites against an antigen administered to the mucosal tissue. Both
CC systemic and mucosal immunity are induced by mucosal delivery of the ONs.
CC AAZ47808 to AAZ47891 represent examples of immunostimulatory
CC oligonucleotides given in the present invention
XX
XX
XX Sequence 24 BP; 5 A; 9 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.2; DB 1; Length 24;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1521 GGGGAACAGTTCTACAAATGG 1541
DB 22 GGGGAACAGTTCTACAAATGG 2

RESULT 1689
AAZ61245/C
ID AAZ61245 standard; DNA; 24 BP.
XX
XX AAZ61245;
XX
XX
XX 30-MAY-2000 (first entry)
XX
XX
XX Primer Acr-02-RG used to amplify DNA encoding phenol oxidising enzyme.
XX
XX
XX Phenol oxidizing enzyme; fungus; redox reaction; detergent; bleaching;
XX fabric; pulp; paper; decolourisation; plant-derived food product;
XX coloured compound; porphyrin; tannin; polyphenol; carotenoid;
XX anthocyanin; Mallard reaction product; PCR primer; ss.
XX
XX
XX Acremonium murorum.
XX
XX
XX WO200005349-A1.
XX
XX
XX 03-FEB-2000.
XX
XX 13-JUL-1999; 99WO-EP004922.
XX
XX 21-JUL-1998; 98EP-00202454.
XX
XX (UNIL) UNILEVER NV.
XX (UNIL) UNILEVER PLC.
XX (HIND-) HINDUSTAN LEVER LTD.
XX
XX Convents D, Gouka RJ, Van Der Heiden M, Swarthoff T, Verrips CT,
XX WPI; 2000-195101/17.
XX
XX
XX

PT Phenol-oxidizing enzyme from *Acromonium*, used in detergent compositions
PT for bleaching stains on fabrics.
XX
PS Example 3; Page 26; 45pp; English.
XX
CC PCR primers AA261244-45 were used to amplify a DNA fragment encoding a
CC phenol oxidizing enzyme from the fungus *Acromonium mucronum*. The enzyme
CC has the CBS accession number 157.72. The enzyme catalyses redox reactions
CC and is specific for molecular oxygen as the electron acceptor. The phenol
CC oxidizing enzyme is specifically used in detergents for bleaching stains
CC on fabrics, but also for bleaching pulp and paper and for decolourisation
CC of plant-derived food products. The enzyme has a pH optimum in the
CC alkaline to neutral range and can bleach a wide variety of coloured
CC compounds, e.g. porphyrins, tanning, polypheols, carotenoids,
CC anthocyanins and Maillard reaction products
XX
SQ Sequence 24 BP; 5 A; 5 C; 5 G; 9 T; 0 U; 0 Other;
Query Match 0.2%; Score 16.2; DB 1; Length 24;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1533 CTACATGGAGTTGAGATCAA 1553
Db 23 CTACTATGAGATGAGATCAA 3
|||||
AAZ47645/c
ID AAZ47645 standard; DNA; 24 BP.
XX
XX AAZ47645;
XX
DT 01-MAR-2000 (first entry)
XX
XX Parasitic infection preventing exemplary oligonucleotide SEQ ID NO:51.
DE
XX Immune system; immunostimulatory; parasitic infection; parasite;
KM Cpg oligonucleotide; antigen presenting cell; natural killer cell;
KM granulocyte; malaria; helminth disease; tick; mite; ss.
XX
OS Synthetic.
XX
XX WO9956755-A1.
XX
XX 11-NOV-1999.
XX
XX 06-MAY-1999; 99MO-US009863.
XX
XX 06-MAY-1998; 98US-0084512P.
XX
XX (IOWA) UNIV IOWA RES FOUND.
XX (OTTA-) OTTAMA CIVIC LOEB RES INST.
XX (USNA) US SEC OF NAVY.
XX
XX Graminaki RA, Krieg AM, Davis HL, Hoffman SL;
PI
DR WPI; 2000-062123/05.
XX
XX
XX Treating and preventing parasitic infections using Cpg oligonucleotides.
PT
XX
XX Disclosure; Page 20; 74pp; English.
PS
XX The present invention describes a method for treating and preventing
CC parasitic infection by administration of unmethylated Cpg
CC oligonucleotides. The Cpg oligonucleotides are able to stimulate the
CC innate immune system via the activation of immune cells, such as antigen
CC presenting cells, natural killer cells and granulocytes. The Cpg
CC oligonucleotides, and the method can be used to treat and prevent
CC parasitic diseases, such as malaria, helminth diseases, tick and mites in
CC humans, animals and poultry. The oligonucleotides may be administered in
CC conjunction with parasitocides or other therapeutic compounds after an
CC organism has been diagnosed to be infected with parasites. Diseases which

CC can be treated or prevented include those caused by Plasmodium
CC falciparum, P. ovale, P. malariae, P. vivax, P. knowlesi, Babesia
CC microti, B. divergens, Trypanosoma cruzi, T. gambiense, T. rhodesiense,
CC Schistosoma mansoni, Toxoplasma gondii, Trichinella spiralis, Leishmania
CC major, L. donovani, L. braziliensis, and L. tropica. The parasite is
CC especially capable of causing malaria. The present sequence represents a
CC parasitic infection preventing exemplary oligonucleotide sequence from
CC the present invention
XX
SQ Sequence 24 BP; 5 A; 9 C; 4 G; 6 T; 0 U; 0 Other;
Query Match 0.2%; Score 16.2; DB 1; Length 24;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1521 GGGGAAACAGTTCTACATG 1541
Db 22 GGGGAAACAGTTCTGTCATG 2
|||||
AAH50629/c
ID AAH50629 standard; DNA; 24 BP.
XX
XX AAH50629;
XX
XX 22-AUG-2001 (first entry)
XX
XX
XX Natural killer cell lytic activity inducing oligonucleotide SEQ ID NO:61.
DE
XX Immunoestimulatory; inducing; natural killer cell; lytic activity;
KM unmethylated Cpg dinucleotide; immune response; B cell proliferation;
KM Th1; immune activation; interleukin 6; IL-6; interferon gamma; IFN-gamma;
KM cytokine; ss.
XX
XX Homo sapiens.
OS
XX Synthetic.
XX
XX US6239116-B1.
XX
XX 29-MAY-2001.
XX
XX 30-OCT-1997; 97US-00960774.
XX
XX 30-OCT-1996; 96US-00738652.
XX
XX (IOWA) UNIV IOWA RES FOUND.
XX (COLE-) COLEY PHARM GROUP INC.
XX (USSR) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Krieg AM, Kline JN;
PI
DR WPI; 2001-380456/40.
XX
XX
XX Methods for inducing IL-6, interferon-gamma or IL-12, or stimulating
PT natural killer cell lytic activity in a human, comprise administering to
PT the subject or exposing a natural killer cell to immunostimulatory
PT nucleic acids.
XX
XX
XX Disclosure; Col 32; 74pp; English.
PS
XX The present invention describes methods for inducing interleukin 6 (IL-
XX 6), interferon-gamma (IFN-gamma) or IL-12, or for stimulating natural
XX killer cell lytic activity. The methods comprise administering to the
XX subject or exposing a natural killer cell to an immunostimulatory nucleic
XX acid. Also described are: (1) inducing IL-6 in a subject comprising
XX administering to the subject to induce IL-6 in the subject the
XX immunoestimulatory nucleic acid; (2) stimulating natural killer cell lytic
XX activity comprising exposing a natural killer cell to the
XX immunoestimulatory nucleic acid to stimulate natural killer cell lytic
XX activity; (3) inducing interferon-gamma in a subject to treat an immune
XX system deficiency comprising administering to the subject to induce
XX interferon-gamma production, the immunoestimulatory nucleic acid; and (4)

CC inducing IL-12 in a subject comprising administering to the subject the
 CC immunostimulatory nucleic acid. The methods are useful for inducing IL-6,
 CC interferon-gamma or IL-12, or stimulating natural killer cell lytic
 CC activity in a subject, particularly a human. The methods are particularly
 CC useful for modulating an immune response. AAH50571 to AAH50671 represent
 CC oligonucleotide sequences used in the exemplification of the present
 CC invention
 XX
 SQ Sequence 24 BP; 5 A; 9 C; 4 G; 6 T; 0 U; 0 Other;
 Query Match 0.2%; Score 16.2; DB 1; Length 24;
 Best Local Similarity 85.7%; Pred. No. 1.5e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1521 GGGGAACAGTCTACATGG 1541
 DB 22 GGGGAACAGTCTGCATGG 2
 RESULT 1692
 ID AAH44680 standard; DNA; 24 BP.
 XX
 AC AAH44680;
 XX
 DT 07-DEC-2001 (first entry)
 XX
 DE Human Kazal type inhibitory factor 35 PCR primer 2 SEQ ID NO:4.
 XX
 XX Human; Kazal type inhibitory factor 35; malignant tumour; haemopathy;
 KW human immunodeficiency virus; HIV infection; immunological disease;
 KW inflammation; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN CN1301765-A.
 XX
 PD 04-JUL-2001.
 XX
 PF 29-DEC-1999; 99CN-00127224.
 XX
 PR 29-DEC-1999; 99CN-00127224.
 XX
 PA (UYFU-) UNIV FUDAN.
 XX
 PI Mao Y, Xie Y;
 XX
 DR WPI; 2001-550471/62.
 XX
 PT New polypeptide-human kazal type inhibitory factor 35 for treating
 PT malignant tumor, hemopathy, human immunodeficiency virus infection,
 PT immunological diseases and various inflammations.
 XX
 PS Example 3; Page 17 (disclosure); 31pp; Chinese.
 XX
 CC The present invention discloses a new kind of polypeptide designated
 CC human kazal type inhibitory factor 35. Also described are polynucleotides
 CC encoding this polypeptide, and a DNA recombination process to produce the
 CC polypeptide. The present invention also describes a method of applying
 CC the polypeptide to treat various diseases, such as malignant tumour,
 CC haemopathy, human immunodeficiency virus (HIV) infection, immunological
 CC diseases and various inflammations. The present sequence represents a PCR
 CC primer used in the isolation of human kazal type inhibitory factor 35,
 CC which is used in an example from the present invention
 XX
 SQ Sequence 24 BP; 1 A; 0 C; 4 G; 19 T; 0 U; 0 Other;
 Query Match 0.2%; Score 16.2; DB 1; Length 24;
 Best Local Similarity 85.7%; Pred. No. 1.5e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 4459 TGGACTTTTTTTTTTTTTTT 4479
 III IIIIIIIIIIIIIIIIIIIIIII

DB 4 TGGGTTTTTTTTTTTTTTTATT 24
 RESULT 1693
 ID AAF98768 standard; DNA; 24 BP.
 XX
 AC AAF98768;
 XX
 DT 11-JUN-2001 (first entry)
 XX
 DE Cpg immunostimulatory nucleic acid SEQ ID NO: 39.
 XX
 KW Immunostimulatory nucleic acid; ISNA; human; interferon alpha; IFN-alpha;
 KW viral infection; phosphorothioate backbone; palindrome; cancer; ds.
 XX
 OS Synthetic.
 XX
 PN WO200122990-A2.
 XX
 PD 05-APR-2001.
 XX
 PF 27-SEP-2000; 2000WO-US026527.
 XX
 PR 27-SEP-1999; 99US-0156147P.
 XX
 PA (COLE-) COLEY PHARM GROUP INC.
 XX
 PI (IOWA) UNIV IOWA RES FOUND.
 XX
 PI Hartmann G, Bratzler RL, Krieg A;
 DR WPI; 2001-290487/30.
 XX
 PT Improving the efficacy of treatments involving the administration of
 PT interferon-alpha by co-administering an isolated immunostimulatory
 PT nucleic acid.
 XX
 PS Disclosure; Page 21; 168pp; English.
 XX
 CC The present invention describes an improvement to a method requiring the
 CC administration of interferon alpha (IFN-alpha), involving administering
 CC an immunostimulatory nucleic acid (ISNA). The sequences of a number of
 CC such nucleic acids are also provided. These may comprise oligonucleotides
 CC with phosphorothioate backbones, palindromes, or G-rich sequences. The
 CC sequences of the invention are useful in the treatment of proliferative
 CC diseases, such as cancers, and viral infections. The present sequence is
 CC an example of an immunostimulatory oligonucleotide
 XX
 SQ Sequence 24 BP; 5 A; 9 C; 4 G; 6 T; 0 U; 0 Other;
 Query Match 0.2%; Score 16.2; DB 1; Length 24;
 Best Local Similarity 85.7%; Pred. No. 1.5e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1521 GGGGAACAGTCTACATGG 1541
 DB 22 GGGGAACAGTCTGCATGG 2
 RESULT 1694
 ID AAF98900 standard; DNA; 24 BP.
 XX
 AC AAF98900;
 XX
 DT 12-JUN-2001 (first entry)
 XX
 DE Immunostimulatory nucleic acid #16.
 XX
 KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
 KW immunostimulatory; tumour; viral infection; bacterial infection;
 KW fungal infection; parasitic infection; cancer; asthma;
 KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.


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XX OS Synthetic.
XX PN WO200122972-A2.
XX PD 05-APR-2001.
XX PF 25-SEP-2000; 2000WO-US026383.
XX PR 25-SEP-1999; 99US-0156113P.
XX PR 27-SEP-1999; 99US-0156135P.
XX PR 23-AUG-2000; 2000US-0227436P.
XX PA (IOWA ) UNIV IOWA RES FOUND.
XX PA (COLE-) COLEY PHARM GMBH.
XX PI Krieg AM, Schetter C, Volmer J;
XX DR WPI; 2001-273485/28.
XX PT Vaccinating against tumors, infectious diseases, allergies and asthma
XX PT using immunostimulatory Py-rich and TG nucleic acids.
XX PS Disclosure; Page 38; 338pp; English.
XX CC The present invention relates to a method for stimulating an immune
XX CC response. The method comprises administering an immunostimulatory nucleic
XX CC acid to a non-todent subject in sufficient quantity to stimulate an
XX CC immune response. The present sequence is one such immunostimulatory
XX CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
XX CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
XX CC against tumor antigens, viral antigens (e.g. herpesviridae, retroviridae
XX CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
XX CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
XX CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
XX CC also useful for preventing cancer, asthma, infectious disease, allergy or
XX CC immune deficiency. The present sequence can also be used to redirect a
XX CC Th2 to a Th1 immune response and to activate immune cells. Note: the
XX CC present sequence may have a phosphorothioate backbone
XX SQ Sequence 24 BP; 5 A; 9 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.2; DB 1; Length 24;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1521 GGGGAAACAGTCTACATG 1541
    |||||
Db 22 GGGGAAACAGTCTGTCATG 2

RESULT 1695
AAH46484
ID AAH46484 standard; DNA; 24 BP.
XX AC AAH46484;
XX DT 17-SEP-2001 (first entry)
XX DE Human ribosomal phosphoprotein 16 PCR primer #2.
XX KM Human; ribosomal phosphoprotein 16; cytosolic; haemostatic; virucide;
XX KM immunomodulatory; antiinflammatory; gene therapy; malignant tumour;
XX KM haemopathy; HIV infection; immunological disease; inflammation;
XX KM PCR primer; ss.
XX OS Homo sapiens.
XX PN WO200145729-A1.
XX PD 28-JUN-2001.
XX PF 18-DEC-2000; 2000WO-CN000603.

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XX PR 22-DEC-1999; 99CN-00125676.
XX PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX PI Mao Y, Xie Y;
XX DR WPI; 2001-408543/43.
XX PT Human ribosomal phosphoprotein 16 and encoded polynucleotide, used in
XX PT diagnosis and treatment of malignant tumors, hemopathy, human
XX PT immunodeficiency virus infection, immunological diseases and
XX PT inflammation.
XX PS Example 3; Page 14; 41pp; Chinese.
XX CC The present invention relates to human ribosomal phosphoprotein 16 and
XX CC coding sequence (see AAH46482 and AAB9298). The phosphoprotein and
XX CC coding sequence are useful in the diagnosis and treatment of malignant
XX CC tumour, haemopathy, human immunodeficiency virus (HIV) infection,
XX CC immunological diseases and various inflammations. The present sequence is
XX CC a PCR primer, which was used in an example from the present invention
XX SQ Sequence 24 BP; 5 A; 3 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.2; DB 1; Length 24;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 4461 GACTTTTTTTTTTTTTTTT 4481
    |||||
Db 4 GACTAATTTTTTTTATTTT 24

RESULT 1696
ABK12118
ID ABK12118 standard; DNA; 24 BP.
XX AC ABK12118;
XX DT 05-JUN-2002 (first entry)
XX DE Human hRDRI RT-PCR primer #1.
XX KM Human; ss; PCR; ribonucleotide dephosphatase reductase inhibitor 10.23;
XX KM hRDRI; malignant tumour; haemopathy; HIV; immunological disease;
XX KM human immunodeficiency virus infection; inflammation; cytostatic;
XX KM haemostatic; virucide; immunomodulatory; antiinflammatory; primer.
XX OS Homo sapiens.
XX PN WO200212303-A1.
XX PD 14-FEB-2002.
XX PF 18-JUN-2001; 2001WO-CN000983.
XX PR 19-JUN-2000; 2000CN-00116569.
XX PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX PI Mao Y, Xie Y;
XX DR WPI; 2002-172133/22.
XX PT Human ribosomal diphosphate reductase inhibitor 10.23 polypeptide and
XX PT encoding polynucleotide, used in diagnosis and treatment of malignant
XX PT tumors, hemopathy, human immunodeficiency virus infection, immunological
XX PS diseases and inflammation.
XX PS Example 2; Page 12; 37pp; Chinese.
XX CC The invention relates to an isolated polypeptide of ribonucleotide

```

CC dephosphatase reductase inhibitor 10.23 (hrdri) the cDNA encoding it, and
 CC its fragment, analogue or derivative. Also included are vectors
 CC expressing the protein, a host cell comprising the vector, the isolation
 CC of modulators of the protein and an anti-hrdri antibody. The protein and
 CC nucleic acid are used in diagnosis and treatment of a malignant tumour,
 CC haemopathy, human immunodeficiency virus (HIV) infection, immunological
 CC diseases and various inflammations. The present sequence is a reverse
 CC transcriptase (RT)-PCR primer used to isolate the cDNA encoding the
 CC ribonucleotide dephosphatase reductase inhibitor 10.23
 XX

SO Sequence 24 BP; 7 A; 5 C; 12 G; 0 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.2; DB 1; Length 24;
 Best Local Similarity 85.7%; Pred. No. 1.5e+03;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7414 AGCAGCAGCAGCAGCAGCAGC 7434

DB 3 AGGAGAGAGAGCAGCAGCAGC 23

RESULT 1697

ABR04964
 ID ABA04964 standard; DNA; 24 BP.

AC ABA04964;

DT 01-MAR-2002 (first entry)

DE Human FD14 PCR primer #1.

XX Human; FD14; tumour; embryo maldevelopment; tissue; cytostatic;

KW immunodeficiency disease; immune disease; immunomodulatory; gene therapy;

KW PCR primer; ss.

XX Homo sapiens.

OS CN1312286-A.

PN 12-SEP-2001.

PF 07-MAR-2000; 2000CN-0011937.

XX 07-MAR-2000; 2000CN-0011937.

PR (BODE-) BODE GENE DEV CO LTD SHANGHAI.

XX Mao Y, Xie Y;

PI WPI; 2002-018504/03.

DR Human FD14 polypeptides and polynucleotides encoding it.

XX Example 2; Page 16 (disclosure); 32pp; Chinese.

XX The present invention relates to human FD14 (AAW47799). FD14 and its

CC coding sequence are useful for treating several diseases, such as

CC malignant tumours, embryo and tissue maldevelopment, immunodeficiency

CC diseases, various acquired and hereditary disease and immune disease. The

CC present sequence is a PCR primer, which was used in an example from the

CC present invention

XX Sequence 24 BP; 0 A; 6 C; 16 G; 2 T; 0 U; 0 Other;

SO Query Match 0.2%; Score 16.2; DB 1; Length 24;
 Best Local Similarity 85.7%; Pred. No. 1.5e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 61 GGAGGCTGGCGGCGCGCGC 81

DB 2 GGTGGCGCGCGCGCGCGC 22

RESULT 1698

ABST7535/C
 ID ABST7535 standard; DNA; 24 BP.

AC ABST7535;

DT 13-DEC-2002 (first entry)

DE Angiogenesis inhibitory oligonucleotide #19.

XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;

KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;

KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;

KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;

KW rubosis; Osler-Weber Syndrome; myocardial angiogenesis;

KW plaque neovascularisation; telangiectasia; haemophilic joint;

KW angiodioma; wound granulation; intestinal adhesion; atherosclerosis;

KW scleroderma; hypertrophic scar.

XX Synthetic.

OS WO200253141-A2.

PN 11-JUL-2002.

PD 14-DEC-2001; 2001WO-US048458.

PF 14-DEC-2000; 2000US-0255534P.

PR (COLE-) COLEY PHARM GROUP INC.

XX Bratzler RL;

PI WPI; 2002-566690/60.

DR Inhibiting angiogenesis in a subject, involves administering at least one

XX antitumorigenic nucleic acid molecule to the subject.

XX Claim 2; Page 20; 276pp; English.

XX The invention relates to inhibiting angiogenesis in a subject, comprising

CC administering at least one antitumorigenic nucleic acid molecule. Also

CC included is a kit comprising a first container housing the antitumorigenic

CC nucleic acids, and instructions for administering them to a subject

CC having a condition characterised by unwanted angiogenesis. The method is

CC useful for inhibiting angiogenesis associated with solid tumour growth,

CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,

CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,

CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,

CC rubosis, Osler-Weber Syndrome, myocardial angiogenesis, plaque

CC neovascularisation, telangiectasia, haemophilic joints, angiodioma,

CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and

CC hypertrophic scars. The present sequence is an antitumorigenic nucleic

CC acid of the invention

XX Sequence 24 BP; 5 A; 9 C; 4 G; 6 T; 0 U; 0 Other;

SO Query Match 0.2%; Score 16.2; DB 1; Length 24;
 Best Local Similarity 85.7%; Pred. No. 1.5e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1521 GGGGAAACAGTTCACATG 1541

DB 22 GGGGAAACAGTTCATG 2

RESULT 1699

ABV76657/C
 ID ABV76657 standard; DNA; 24 BP.

AC ABV76657;

DT 21-FEB-2003 (first entry)

```

XX DE Human EGF receptor protein 10.12 RT-PCR primer, SEQ ID NO:3.
XX XX
XX XX Human; epidermal growth factor receptor protein 10.12;
XX KM EGF receptor protein 10.12; recombinant production; gene therapy;
XX KM malignant tumour; cancer; blood disease; human immunodeficiency virus;
XX KM HIV infection; immune disorder; inflammatory condition; cytostatic;
XX KM antiinflammatory; immunomodulator; reverse transcription-PCR; RT-PCR;
XX KM primer; ss.
XX XX
XX OS Homo sapiens.
XX PN CN1358749-A.
XX PD 17-JUL-2002.
XX PF 13-DEC-2000; 2000CN-00127861.
XX PR 13-DEC-2000; 2000CN-00127861.
XX PA (SHAN-) SHANGHAI BIOWINDOM GENE DEV INC.
XX PI Mao Y, Xie Y;
XX DR WPI; 2002-733538/80.
XX PT Novel polypeptide-human epidermal growth factor 10.12 the polynucleotide
XX PS for encoding the polypeptide.
XX XX
XX PS Example 2; Page 16 (Disclosure); 32pp; Chinese.
XX CC The invention relates to human epidermal growth factor (EGF) receptor
XX CC protein 10.12 (AB89979) and nucleic acids encoding it (ABV76656). The
XX CC protein has a molecular weight of 10.12 kD. The invention also relates to
XX CC a method for the recombinant production of the protein, an antagonist of
XX CC the protein, and the use of the protein, gene and antagonist in
XX CC therapeutic applications. EGF receptor protein 10.12 can be used in the
XX CC treatment of a variety of diseases such as malignant tumours, blood
XX CC diseases, HIV (human immunodeficiency virus) infection, immune disorders
XX CC and inflammatory conditions. Sequences ABV76657-ABV76658 represent
XX CC reverse transcription-PCR (RT-PCR) primers used in an exemplification of
XX CC the invention to isolate human EGF receptor protein 10.12 cDNA
XX SQ
XX Query Match 0.2%; Score 16.2; DB 1; Length 24;
XX Best Local Similarity 85.7%; Pred. No. 1.5e+03;
XX Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4207 GTCCAGGCTCCATCTTCTTC 4227
DB 21 GTCCAGGCTCCCTCTGCCCC 1

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```

FT XX /note= "phosphorothioate backbone"
XX XX
XX PN WO200197843-A2.
XX PD 27-DEC-2001.
XX XX
XX PF 22-JUN-2001; 2001WO-US020154.
XX PR 22-JUN-2000; 2000US-0213346P.
XX PA (IOWA ) UNIV IOWA RES FOUND.
XX PI Weiner G, Hartmann G;
XX DR WPI; 2002-154611/20.
XX PT Treating or preventing cancer, such as basal cell carcinoma, comprises
XX PT administering immunostimulatory nucleic acids that induce expression of
XX PT cell surface antigens and antibodies to a subject having or at risk of
XX PS developing cancer.
XX PS Disclosure; Page 104; 312pp; English.
XX CC
XX CC The present invention relates to methods for treating or preventing
XX CC cancer, involving administering to a subject having or at risk of
XX CC developing cancer immunostimulatory nucleic acids that induce expression
XX CC of cell surface antigens and antibodies. The methods are useful for
XX CC treating or preventing cancer such as basal cell carcinoma, bladder
XX CC cancer, bone cancer, brain and central nervous system (CNS) cancer,
XX CC breast cancer, cervical cancer, colon and rectum cancer, connective
XX CC tissue cancer, esophageal cancer, eye cancer, kidney cancer, larynx
XX CC cancer, leukemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
XX CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
XX CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
XX CC cancer, stomach cancer, testicular cancer, and uterine cancer. The
XX CC present sequence is an immunostimulatory oligonucleotide described in the
XX CC exemplification of the invention
XX SQ
XX Query Match 0.2%; Score 16.2; DB 1; Length 24;
XX Best Local Similarity 85.7%; Pred. No. 1.5e+03;
XX Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1521 GGGGAAACAGTTCTACATGG 1541
DB 22 GGGGAAACAGTTCTGTCATGG 2

```

```

RESULT 1700
ABL38675/c
ID ABL38675 standard; DNA; 24 BP.
XX
XX ABL38675;
AC
XX
XX 16-APR-2002 (first entry)
DT
XX
XX Immunostimulatory nucleic acid SEQ ID NO: 35.
DS
XX
XX Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
KM angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
XX FT modified_base 1..24
XX FT /*tag= a
XX FT /mod_base= OTHER

```

```

RESULT 1701
ABV74361
ID ABV74361 standard; DNA; 24 BP.
XX
XX ABV74361;
AC
XX
XX 05-FEB-2003 (first entry)
DT
XX
XX Signalase 10.01 PCR primer SEQ ID NO 4.
DE
XX
XX Signalase 10.01; enzyme; tumour; haemopathy; cytostatic; HIV; infection;
KM human immunodeficiency virus; immunological disease; inflammation; PCR;
KM primer; ss.
XX
XX Unidentified.
OS
XX
XX CN1345975-A.
PN
XX
XX 24-APR-2002.
PD
XX
XX 22-SEP-2000; 2000CN-00125348.
PF
XX
XX 22-SEP-2000; 2000CN-00125348.
PR
XX

```

PA (SHAN-) SHANGHAI BIOWINDOM GENE DEV INC.
XX
PI Mao Y, Xie Y;
XX
XX
DR WPI; 2002-539373/58.
XX
PT New polypeptide-signalase 10.01 for treating malignant tumor, hemopathy,
PT human immunodeficiency virus infection, immunological disease and various
PT inflammations.
XX
PS Example 2; Page 16 (Disclosure); 32pp; Chinese.
XX
CC The invention relates to signalase 10.01, a polynucleotide encoding the
CC polypeptide and producing the polypeptide by DNA recombinant technology.
CC The invention also discloses curing several diseases, such as malignant
CC tumour, haemopathy, human immunodeficiency virus (HIV) infection,
CC immunological disease and various inflammations using the polypeptide.
CC The invention also discloses an antagonist for resisting the polypeptide
CC and its therapeutic action and application of the polynucleotide encoding
CC the new signalase 10.01. The present sequence is that of a signalase
CC 10.01 PCR primer, useful in examples of the invention
XX
SQ Sequence 24 BP; 1 A; 3 C; 1 G; 19 T; 0 U; 0 Other;
Query Match 0.2%; Score 16.2; DB 1; Length 24;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4470 TTTTCTTTTCTTCTCTGA 4490
DB 1 TTTTCTTTCTTTCTCTGA 21
RESULT 1702
ABQ05218/C
ID ABQ05218 strand; DNA; 24 BP.
XX
AC ABQ05218;
XX
XX
DT 11-JUN-2002 (first entry)
XX
DE Oligonucleotide adapter/capture probe 5209.
XX
KW Oligonucleotide array; adapter sequence; probe; ss.
XX
OS Synthetic.
XX
XX WO200216649-A2.
XX
XX
PD 28-FEB-2002.
XX
XX
PF 27-AUG-2001; 2001WO-US026519.
XX
XX
PR 25-AUG-2000; 2000US-0227948P.
PR 29-AUG-2000; 2000US-0228854P.
XX
XX
PA (ILLU-) ILLUMINA INC.
XX
PI Gunderson K;
XX
XX WPI; 2002-292068/33.
DR
XX
PT Array comprising adapter sequences useful for immobilizing or detecting a
PT target nucleic acid sequence, has different addresses comprising
PT different specific capture probes.
XX
PS Claim 1; Page 154; 261pp; English.
XX
XX The invention relates to an oligonucleotide array (I) comprising at least
CC 25 different addresses (adapter sequences) with each comprising a
CC different capture probe selected from a group consisting of the sequences
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
CC and contacting the modified target nucleic acid with (I). The steps of
CC above method is useful for detecting a target nucleic acid, which further
CC comprises detecting the presence of the modified target nucleic acid
XX
SQ Sequence 24 BP; 1 A; 3 C; 1 G; 19 T; 0 U; 0 Other;
Query Match 0.2%; Score 16.2; DB 1; Length 24;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4470 TTTTCTTTTCTTCTCTGA 4490
DB 1 TTTTCTTTCTTTCTCTGA 21
RESULT 1704

CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
CC and contacting the modified target nucleic acid with (I). The steps of
CC above method is useful for detecting a target nucleic acid, which further
CC comprises detecting the presence of the modified target nucleic acid
XX
SQ Sequence 24 BP; 4 A; 6 C; 6 G; 8 T; 0 U; 0 Other;
Query Match 0.2%; Score 16.2; DB 1; Length 24;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 433 GAATACATGCTCCAGCATTTTC 453
DB 21 GAATACATGCTCCAGCATTTTC 1
RESULT 1703
ABQ11505/C
ID ABQ11505 strand; DNA; 24 BP.
XX
AC ABQ11505;
XX
XX
DT 11-JUN-2002 (first entry)
XX
DE Oligonucleotide adapter/capture probe 11496.
XX
KW Oligonucleotide array; adapter sequence; probe; ss.
XX
OS Synthetic.
XX
XX WO200216649-A2.
XX
XX
PD 28-FEB-2002.
XX
XX
PF 27-AUG-2001; 2001WO-US026519.
XX
XX
PR 25-AUG-2000; 2000US-0227948P.
PR 29-AUG-2000; 2000US-0228854P.
XX
XX
PA (ILLU-) ILLUMINA INC.
XX
PI Gunderson K;
XX
XX WPI; 2002-292068/33.
DR
XX
PT Array comprising adapter sequences useful for immobilizing or detecting a
PT target nucleic acid sequence, has different addresses comprising
PT different specific capture probes.
XX
PS Claim 1; Page 231; 261pp; English.
XX
XX The invention relates to an oligonucleotide array (I) comprising at least
CC 25 different addresses (adapter sequences) with each comprising a
CC different capture probe selected from a group consisting of the sequences
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
CC and contacting the modified target nucleic acid with (I). The steps of
CC above method is useful for detecting a target nucleic acid, which further
CC comprises detecting the presence of the modified target nucleic acid
XX
SQ Sequence 24 BP; 4 A; 6 C; 6 G; 8 T; 0 U; 0 Other;
Query Match 0.2%; Score 16.2; DB 1; Length 24;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 433 GAATACATGCTCCAGCATTTTC 453
DB 21 GAATACATGCTCCAGCATTTTC 1
RESULT 1704

ABQ00624/c
ID ABQ00624 standard; DNA; 24 BP.
XX
AC ABQ00624;
XX
DT 11-JUN-2002 (first entry)
XX
DE Oligonucleotide adapter/capture probe 615.
XX
KM Oligonucleotide array; adapter sequence; probe; ss.
XX
OS Synthetic.
XX
PN WO200216649-A2.
XX
PD 28-FEB-2002.
XX
PF 27-AUG-2001; 2001WO-US026519.
XX
PR 25-AUG-2000; 2000US-0227948P.
PR 29-AUG-2000; 2000US-0228854P.
XX
PA (ILLU-) ILLUMINA INC.
XX
PI Gunderson K;
XX
DR WPI; 2002-292068/33.
XX
PT Array comprising adapter sequences useful for immobilizing or detecting a
PT target nucleic acid sequence, has different addresses comprising
PT different specific capture probes.
XX
PS Claim 1; Page 58; 261pp; English.
XX
CC The invention relates to an oligonucleotide array (I) comprising at least
CC 25 different addresses (adapter sequences) with each comprising a
CC different capture probe selected from a group consisting of the sequences
CC given in ABQ00010-ABQ13409. (I) is useful for immobilizing a target
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
CC and contacting the modified target nucleic acid with (I). The steps of
CC above method is useful for detecting a target nucleic acid, which further
CC comprises detecting the presence of the modified target nucleic acid
XX
SQ Sequence 24 BP; 4 A; 6 C; 6 G; 8 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 16.2; DB 1; Length 24;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 433 GAATACATGTCGACGATTTC 453
DB 21 GAATACATGTCGACGATTTC 1
XX
RESULT 1705
ABQ11546
ID ABQ11546 standard; DNA; 24 BP.
XX
AC ABQ11546;
XX
DT 11-JUN-2002 (first entry)
XX
DE Oligonucleotide adapter/capture probe 11537.
XX
KM Oligonucleotide array; adapter sequence; probe; ss.
XX
OS Synthetic.
XX
PN WO200216649-A2.
XX
PD 28-FEB-2002.
XX

PF 27-AUG-2001; 2001WO-US026519.
XX
PR 25-AUG-2000; 2000US-0227948P.
PR 29-AUG-2000; 2000US-0228854P.
XX
PA (ILLU-) ILLUMINA INC.
XX
PI Gunderson K;
XX
DR WPI; 2002-292068/33.
XX
PT Array comprising adapter sequences useful for immobilizing or detecting a
PT target nucleic acid sequence, has different addresses comprising
PT different specific capture probes.
XX
PS Claim 1; Page 231; 261pp; English.
XX
CC The invention relates to an oligonucleotide array (I) comprising at least
CC 25 different addresses (adapter sequences) with each comprising a
CC different capture probe selected from a group consisting of the sequences
CC given in ABQ00010-ABQ13409. (I) is useful for immobilizing a target
CC nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
CC ABQ13409) to a target nucleic acid to form a modified target nucleic acid
CC and contacting the modified target nucleic acid with (I). The steps of
CC above method is useful for detecting a target nucleic acid, which further
CC comprises detecting the presence of the modified target nucleic acid
XX
SQ Sequence 24 BP; 8 A; 6 C; 6 G; 4 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 16.2; DB 1; Length 24;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 433 GAATACATGTCGACGATTTC 453
DB 4 GAATACATGTCGACGATTTC 24
XX
RESULT 1706
ABQ05259
ID ABQ05259 standard; DNA; 24 BP.
XX
AC ABQ05259;
XX
DT 11-JUN-2002 (first entry)
XX
DE Oligonucleotide adapter/capture probe 5250.
XX
KM Oligonucleotide array; adapter sequence; probe; ss.
XX
OS Synthetic.
XX
PN WO200216649-A2.
XX
PD 28-FEB-2002.
XX
PF 27-AUG-2001; 2001WO-US026519.
XX
PR 25-AUG-2000; 2000US-0227948P.
PR 29-AUG-2000; 2000US-0228854P.
XX
PA (ILLU-) ILLUMINA INC.
XX
PI Gunderson K;
XX
DR WPI; 2002-292068/33.
XX
PT Array comprising adapter sequences useful for immobilizing or detecting a
PT target nucleic acid sequence, has different addresses comprising
PT different specific capture probes.
XX
PS Claim 1; Page 154; 261pp; English.
XX

Query Match	0.2%	Score 16.2	DB 1	Length 24
Best Local Similarity	85.7%	Pred. No. 1.5e+03		
Matches 18	Conservative	0	Mismatches 3	Indels 0
			Gaps	0

KW Human; succinate dehydrogenase 11.66; digestive ulcer; abortion;
KM succinate; dehydrogenase; enzyme; PCR; primer; 88.

XX Homo sapiens.
OS
XX
XX CN1360035-A.
PN
XX
XX 24-JUL-2002.
PD
XX
XX 20-DEC-2000; 2000CN-00135151.
PF
XX
XX 20-DEC-2000; 2000CN-00135151.
PR
XX
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
PA
XX
XX Mao Y, Xie Y;
PI
XX
XX WPI; 2002-733660/80.
DR
XX
XX Polypeptide-human succinate dehydrogenase 11.66 and polynucleotide for
PT coding it.
XX
XX Example 3; Page 18 (Disclosure); 31pp; Chinese.
PS
XX
XX The invention relates to the novel human succinate dehydrogenase 11.66
CC polypeptide and the polynucleotide encoding it. The polypeptide is useful
CC in treating diseases such as digestive ulcer and abortion. The antagonist
CC of the polypeptide and its medical action, and the application of the
CC polynucleotide are also disclosed. The present sequence represents a PCR
CC primer used to amplify the human succinate dehydrogenase 11.66 cDNA of
CC the invention
XX
XX Sequence 24 BP; 17 A; 1 C; 2 G; 4 T; 0 U; 0 Other;
SQ
XX
XX Query Match 0.2%; Score 16.2; DB 1; Length 24;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 6455 TTTTGATCTTTTCTTCT 6475
Db 24 TTTAAATCTTTTCTTGT 4
XX
XX RESULT 1710
ABS62162
ID ABS62162 standard; DNA; 24 BP.
XX
XX AC ABS62162;
XX
XX DT 05-NOV-2002 (first entry)
XX
XX DE Analyte sorting tag sequence #634.
XX
XX KW Analyte sorting oligonucleotide tag; ss.
XX
XX OS Synthetic.
XX
XX PN WO200259355-A2.
XX
XX PD 01-AUG-2002.
XX
XX PF 25-JAN-2002; 2002WO-CA000089.
XX
XX PR 25-JAN-2001; 2001US-0263710P.
XX
XX PR 10-JUL-2001; 2001US-0303799P.
XX
XX PA (TMBI-) TM BIOSCIENCE CORP.
XX
XX PI Kohler D, Fieldhouse D;
XX
XX WPI; 2002-619176/66.
XX
XX Polynucleotides comprising minimally cross-hybridizing nucleotide
PT sequences, useful as tags or tag complements for use in a wide variety of
PT research, medical or industrial applications, e.g. in diagnostic assays

PT or DNA sequencing.
XX
XX Example 2; Page 69; 120pp; English.
PS
XX
XX The invention relates to a composition, which comprises molecules for use
CC as tags or tag complements. Each molecule comprises an oligonucleotide
CC selected from a set of oligonucleotides based on numeric identifiers
CC (numerals 1-3) corresponding to the pattern of nucleotide bases present
CC in 1168 nucleotide sequences fully defined in the specification. These
CC oligonucleotides were found to be non-cross hybridizing. The composition
CC is useful as a tag or tag complement, in analysing a biological sample
CC for the presence of a mutation or polymorphism at a locus in a nucleic
CC acid, and in determining the presence of a target suspected of being
CC contained in a mixture. Also for use in a wide variety of research,
CC medical, or industrial applications, e.g. identification of disease-
CC related polynucleotides in diagnostic assays, screening for clones of
CC novel target polynucleotides, identification of specific polynucleotide
CC in biots of mixtures of polynucleotides, therapeutic blocking of
CC inappropriately expressed genes or DNA sequencing. The polynucleotides of
CC the composition are particularly useful in methods involving highly
CC parallel processing of analytes. The use of the polynucleotides provides
CC minimal cross-hybridisation or cross-talk during the sorting process.
CC Thus, any sequence within the family of sequences will not significantly
CC cross-hybridise with any other sequence derived from that family, making
CC it suitable for highly parallel processing of analytes. ABS61525-ABS62636
CC represent oligonucleotide tags of the invention
XX
XX Sequence 24 BP; 14 A; 0 C; 6 G; 4 T; 0 U; 0 Other;
SQ
XX
XX Query Match 0.2%; Score 16.2; DB 1; Length 24;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4013 AAATGAGAAAAAGAGAGAA 4033
Db 1 AAATAAGATAGAGAGAGAA 21
XX
XX RESULT 1711
AAL39148/c
ID AAL39148 standard; DNA; 24 BP.
XX
XX AC AAL39148;
XX
XX DT 05-SEP-2002 (first entry)
XX
XX DE Murine Toll-like receptor related Cpg DNA SEQ ID No 23.
XX
XX KW Murine Toll-like receptor; TLR5; TLR7; TLR8; ISNA; ds.
XX
XX OS Unidentified.
XX
XX PN WO200222809-A2.
XX
XX PD 21-MAR-2002.
XX
XX PF 17-SEP-2001; 2001WO-US029229.
XX
XX PR 15-SEP-2000; 2000US-0233035P.
XX
XX PR 23-JAN-2001; 2001US-0263657P.
XX
XX PR 17-MAY-2001; 2001US-0291726P.
XX
XX PR 22-JUN-2001; 2001US-0300210P.
XX
XX PA (COLE-) COLEY PHARM GMBH.
XX
XX PI Bauer S, Lipford G, Wagner H;
XX
XX WPI; 2002-393964/42.
XX
XX New isolated murine Toll-like receptor (TLR)9, TLR7, TLR8 polypeptides,
PT useful for identifying species specificity of immunostimulatory nucleic
PT acid and identifying immunostimulatory nucleic acids.

PS Disclosure; Page 76; 195pp; English.

CC The invention relates to isolated murine Toll-like receptors (TLR) 9, TLR7
CC and TLR8 polypeptides. These polypeptides comprise fully defined
CC sequences of 1032, 1050 or 1032 amino acids as given in specification, or
CC their fragments, where TLR9, TLR7 and TLR8 polypeptides or their
CC fragments have an amino acid sequence which is identical to human TLR9,
CC TLR7 or TLR8 polypeptides or their fragment except for at least one amino
CC acid of a murine TLR polypeptide. The isolated nucleic acids of the
CC invention are useful for inhibiting TLR9 signalling activity in a cell.
CC TLR7, TLR8 and TLR9 polypeptides are useful for identifying nucleic acid
CC molecules which interact with a TLR polypeptide or its fragment. The
CC TLR7, TLR8 or TLR9 polypeptides are also useful for identifying ISNA. The
CC TLR7, TLR8 and TLR9 polypeptides are also useful for comparing TLR9
CC signalling activity of a test compound (that is not a nucleic acid, and
CC is a polypeptide or a part of a combinatorial library of compounds) with
CC an ISNA. The TLR7, TLR8 and TLR9 polypeptides are also useful for
CC identifying species specificity of an ISNA. The isolated nucleic acids of
CC the invention are useful as probes or primers. This polynucleotide
CC sequence represents DNA relating to the isolated Toll-like receptors of
CC the invention

SQ Sequence 24 BP; 5 A; 9 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.2; DB 1; Length 24;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1521 GGGGAACAGTCTTACATGG 1541
|||||
DB 22 GGGGAACAGTCTTACATGG 2

RESULT 1712
ABV75621
ID ABV75621 standard; DNA; 24 BP.

AC ABV75621;
XX
XX
DT 23-JAN-2003 (first entry)
XX
DE Argininoacyl tRNA synthetase 12.87 PCR primer 1.
XX
KW Argininoacyl tRNA synthetase 12.87; malignant tumour; inflammation;
KM immunological disease; haemopathy; human immunodeficiency virus; HIV;
XX enzyme; PCR; primer; 88.
XX
XX Unidentified.
OS
XX
XX CN1347985-A.
PN
XX
PD 08-MAY-2002.
XX
PF 11-OCT-2000; 2000CN-00125646.
XX
PR 11-OCT-2000; 2000CN-00125646.
XX
PR 11-OCT-2000; 2000CN-00125646.
XX
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
XX Mao Y, Xie Y;
XX
XX WPI; 2002-548992/59.
DR
XX
XX
PT New polypeptide argininoacyl tRNA synthetase 12.87 and encoding
PT polynucleotides, useful for treating malignant tumors, inflammations,
PT immunological diseases, hemopathy and human immunodeficiency virus
XX infection.
XX
XX Example 2; Page 17 (Disclosure); 32pp; Chinese.
PS
XX The invention relates to a novel polypeptide, argininoacyl tRNA
CC synthetase 12.87, and the polynucleotide encoding it. The polypeptide is
CC useful for treating various diseases, such as malignant tumours,

CC inflammations, immunological diseases, haemopathy and human
CC immunodeficiency virus (HIV) infection. The invention also discloses the
CC antagonist resisting the polypeptide and its treatment effect, and
CC application of the polynucleotide. The present sequence represents a PCR
CC primer used to amplify the argininoacyl tRNA synthetase 12.87 gene of the
CC invention

SQ Sequence 24 BP; 6 A; 4 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.2; DB 1; Length 24;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2865 AGCAGGAGGAGGAGGTGG 2885
|||||
DB 2 AGCAGGAGGAGGAGGTGG 22

RESULT 1713
AB870566/C
ID AB870566 standard; DNA; 24 BP.

AC AB870566;
XX
XX
DT 25-NOV-2002 (first entry)
XX
DE Dendritic cell stimulating Cpg oligodeoxynucleotide #55.
XX
XX Cpg; ss; dendritic cell; dendritic cell activation; cytostatic;
KM anti-allergic; cancer; immunotherapy; infectious disease; allergy.
XX
XX Synthetic.
OS
XX
XX US6429199-B1.
PN
XX
PD 06-AUG-2002.
XX
PF 13-NOV-1998; 98US-00191170.
XX
PR 15-JUL-1994; 94US-00276358.
PR 07-FEB-1995; 95US-00386063.
PR 30-OCT-1996; 96US-00738652.
PR 30-OCT-1997; 97US-00960774.
XX
XX (IOWA) UNIV IOWA RBS FOUND.
PA
XX
XX Krieg AM, Hartmann G;
PI
XX
XX WPI; 2002-689667/74.
DR
XX
XX
PT Activating a dendritic cell for cancer immunotherapy or for treating
PT infectious or allergy disease, by contacting a dendritic cell with an
PT isolated nucleic acid containing at least one unmethylated Cpg
XX dinucleotide.
XX
XX
PS Example 6; Col 32; 52pp; English.
XX
XX This invention relates to a novel method for activating or causing
CC maturation of a dendritic cell. The method comprises contacting a
CC dendritic cell with an isolated nucleic acid containing at least one
CC unmethylated Cpg dinucleotide in an amount effective to activate or cause
CC maturation of the dendritic cell, where the activation is performed ex
CC vivo. The method of the invention may have cyostatic or anti-allergic
CC activities. The method of the invention is useful for cancer
CC immunotherapy or for treating an infectious disease or allergy, by
CC administering an activated dendritic cell that expresses a specific cancer,
CC microbial or allergy causing antigen, to a subject having a cancer
CC including the cancer antigen, to a subject having an infection with a
CC microorganism including the microbial antigen or to a subject having an
CC allergic reaction to the allergy causing antigen, where the activated
CC dendritic cell is prepared using the method of the invention. The method
CC is useful for generating a high yield of dendritic cells by administering
CC an isolated nucleic acid containing at least one unmethylated Cpg

CC dinucleotide, where the nucleic acid is 8-80 bases in length in an amount effective to activate the dendritic cells to a subject, and isolating CC dendritic cells from the subject. The use of Cpg allows the generation of CC mature dendritic cells from peripheral blood within two days in a well defined system. The application of Cpg for this purpose is superior to CC granulocyte macrophage-colony stimulating factor (GM-CSF), which is CC currently used for this purpose. Cpg oligonucleotides have a longer half CC life, are less expensive, and show a greater magnitude of immune effects. CC The present sequence represents a Cpg oligonucleotide used in the method CC of the invention XX

XX Sequence 24 BP; 5 A; 9 C; 4 G; 6 T; 0 U; 0 Other;

QY Query Match 0.2%; Score 16.2; DB 1; Length 24;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 1521 GGGGAACAGTTCTACATCG 1541
22 GGGGAACAGTTCTCATTG 2

RESULT 1714
ID ABX03813/C
ABX03813 standard; cDNA; 24 BP.

XX AC ABX03813;
XX
XX 09-JAN-2003 (first entry)
XX
XX

DE DNA encoding secreted protein signal peptide sequence #22.

KW Differential display method; leucine-rich motif; transmembrane protein;
KM secreted protein; secreted protein signal peptide; ss.

XX Unidentified.
OS
XX MO200259259-A2.
XX
XX 01-AUG-2002.
XX
XX 23-JAN-2002; 2002MO-IL000071.
XX
XX 23-JAN-2001; 2001US-0263158P.
XX
XX (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
XX
XX Wreschner DH;
XX
XX WPI; 2002-599769/64.
XX
XX P-PSDB; ABG98342.
XX
XX

PT Differential display method for identifying secreted or transmembrane
PT protein, comprising contacting a DNA with a first primer that hybridizes
PT to a sequence coding for a leucine-rich motif and with a second
PT oligonucleotide primer.
XX
XX
XX Disclosure; Fig 2; 37pp; English.
XX
XX PS
XX CC The invention relates to a differential display comprising contacting
CC cDNA with a first primer that hybridizes to an oligonucleotide sequence
CC coding for a leucine-rich motif, and with a second oligonucleotide primer
CC to form a cDNA-hybrid molecule. The method comprises obtaining mRNA from
CC at least 2 samples, synthesizing cDNA from the RNA of each sample,
CC contacting the cDNA with a first primer that hybridizes to an
CC oligonucleotide sequence coding for a leucine-rich motif, and with a second
CC oligonucleotide primer to form cDNA-hybrid molecules, amplifying the cDNA
CC -hybrid molecules, detecting amplified products, and comparing the
CC amplified products from each sample to identify distinctive amplified
CC products coding for at least one secreted or transmembrane protein. The
CC method is useful for discovering novel secreted and/or transmembrane
CC proteins which are important for cell processes and play an important
CC role in determining its phenotype, and which act as mediators for the

CC transfer of signals from external environment into the cell itself, thus
CC modulating gene expression. Sequences ABX03792-ABX03869 represent DNA
CC encoding secreted protein signal peptide sequences
XX
XX

XX Sequence 24 BP; 1 A; 9 C; 7 G; 7 T; 0 U; 0 Other;

QY Query Match 0.2%; Score 16.2; DB 1; Length 24;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 7413 CAGCAGCAGCAGCAGCAGCAG 7433
21 CAGCAGCAGCAGCAGCAGCAG 1

RESULT 1715
ID ACF36745/C
ACF36745 standard; DNA; 24 BP.

XX AC ACF36745;
XX
XX 06-NOV-2003 (first entry)
XX
XX

DE Immunostimulatory Cpg oligonucleotide, SEQ ID NO:40.

KW Human TLR3; Toll-like receptor 3; TLR3 signal transduction pathway;
KM Immunostimulant; drug screening; Cpg oligonucleotide; ss.

XX Synthetic.
OS
XX MO2003031573-A2.
XX
XX 17-APR-2003.
XX
XX 03-OCT-2002; 2002MO-US031460.
XX
XX 05-OCT-2001; 2001US-0327520P.
XX
XX (COLE-) COLEY PHARM GMBH.
XX
XX Lipford G;
XX
XX WPI; 2003-393438/37.
XX
XX

PT Identifying an immunostimulatory compound by contacting a functional Toll
PT -like receptor (TLR) 3 with a test compound, and detecting a test
PT response mediated by the TLR3 signal transduction pathway.
XX
XX
XX Disclosure; Page 17; 104pp; English.
XX
XX PS
XX CC The invention relates to a method for identifying an immunostimulatory
CC compound which comprises contacting a functional Toll-like receptor 3
CC (TLR3) with a test compound, and detecting a test response mediated by
CC the TLR3 signal transduction pathway. A test compound is deemed to be
CC immunostimulatory when the test response exceeds the negative control
CC sequence, or equals or exceeds the reference response. The method is
CC useful for identifying compounds that modulate TLR3 signalling activity,
CC particularly immunostimulatory compounds. The method may also be used in
CC screening for species specificity of an immunostimulatory compound.
CC Sequences ACF36744-ACF36822 represent exemplary immunostimulatory Cpg
CC oligonucleotides which may be used to stimulate TLR3 signalling activity
CC according to the invention XX

XX Sequence 24 BP; 5 A; 9 C; 4 G; 6 T; 0 U; 0 Other;

QY Query Match 0.2%; Score 16.2; DB 1; Length 24;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 1521 GGGGAACAGTTCTACATCG 1541
22 GGGGAACAGTTCTCATTG 2

```
RESULT 1716
ABX76041/c
ID ABX76041 standard; DNA; 24 BP.
XX
AC ABX76041;
XX
DT 31-MAR-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #52.
XX
KW ss; immunostimulatory nucleic acid; anaemia; thrombocytopenia;
KW neutropenia; methylated CpG nucleic acid; T-rich nucleic acid;
KW poly-G nucleic acid; phosphorothioate backbone; chemotherapy;
KW radiation treatment; stress; red blood cell; haematopoiesis; synergistic.
XX
OS Synthetic.
XX
PN US2002165178-A1.
XX
PD 07-NOV-2002.
XX
PF 28-JUN-2001; 2001US-00895007.
XX
PR 28-JUN-2000; 2000US-0214368P.
XX
PA (SCHE/) SCHETTER C.
PA (BRAT/) BRATZLER R L.
PA (PETE/) PETERSEN D M.
XX
PI Schetter C, Bratzler RL, Petersen DM,
XX
DR WPI; 2003-166150/16.
XX
PT Pharmaceutical composition for treatment of anemia, thrombocytopenia and
PT neutropenia comprises an immunostimulatory nucleic acid and a medicament
PT for the respective disease.
XX
PS Claim 18; Page 8; 27pp; English.
XX
CC The invention discloses a pharmaceutical composition comprising an
CC immunostimulatory nucleic acid and either an anaemia medicament,
CC thrombocytopenia medicament or a neutropenia medicament formulated in a
CC carrier. The immunostimulatory nucleic acid can be selected from a
CC methylated CpG nucleic acid, a T-rich nucleic acid, a poly-G nucleic acid
CC and/or a nucleic acid having a phosphorothioate backbone. The
CC compositions can be used for the treatment or prevention of anaemia,
CC thrombocytopenia and neutropenia in a subject preparing to undergo
CC chemotherapy, radiation treatment, and has received at least one dose of
CC chemotherapy or radiation treatment. The treatment is required due to the
CC effect of stress, including chemotherapy, on the formation of red blood
CC cells, haematopoiesis. The composition provides a synergistic effect
CC which permits a lower dose of the medicament to be used, thus providing
CC lower costs associated with using lower doses of the medicament, and
CC reduced chances of inducing side effects. The efficacy of the combination
CC is profoundly improved over the use of each of the medicaments alone. The
CC sequences presented in ABX75990-ABX76123 are the immunostimulatory
CC nucleic acids disclosed in the invention
XX
SQ Sequence 24 BP; 5 A; 9 C; 4 G; 6 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 16.2; DB 1; Length 24;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
XX
AC ACA58706;
XX
DT 10-JUN-2003 (first entry)
XX
DE Gastric ulcer treatment immunostimulatory nucleic acid #52.
XX
KW Gastric ulcer; ss; immunostimulant; equine gastric ulcer syndrome; EGUS;
KW Helicobacter pylori.
XX
OS Synthetic.
XX
PN US2002198165-A1.
XX
PD 26-DEC-2002.
XX
PF 01-AUG-2001; 2001US-00920313.
XX
PR 01-AUG-2000; 2000US-0222248P.
XX
PA (BRAT/) BRATZLER R L.
PA (PETE/) PETERSEN D M.
XX
PI Bratzler RL, Petersen DM,
XX
DR WPI; 2003-370798/35.
XX
PT Prevention or treatment of gastric ulcer involves administering nucleic
PT acid.
XX
PS Disclosure; Page 13; 45pp; English.
XX
CC The invention relates to a method of prevention or treatment of gastric
CC ulcer comprising administering a nucleic acid to a subject in need for
CC treatment of gastric ulcer. A nucleic acid sample comprising
CC oligonucleotide 2006 was administered to a mouse model by an oral route
CC or a vehicle control. Colonisation of mice by Helicobacter pylori was
CC assessed at time points from 1 day to 1 month after treatment. The
CC ability of the nucleic acid to reduce H. pylori colonisation was
CC assessed. The method is useful for preventing or treating a gastric ulcer
CC on a subject e.g. human or non-human vertebrate animal including dog,
CC cat, horse (equine gastric ulcer syndrome, EGUS), cow, goat, sheep, pig,
CC rabbit, turkey, chicken, primate, rat and mouse. The method effectively
CC treats or prevents gastric ulcers. The present sequence represents an
CC immunostimulatory nucleic acid for the treatment of gastric ulcers
XX
SQ Sequence 24 BP; 5 A; 9 C; 4 G; 6 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 16.2; DB 1; Length 24;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
XX
QY 1521 GGGGAAACAGTTCTTACATGG 1541
   |||||
DB 22 GGGGAAACAGTTCTTACATGG 2
   |||||

RESULT 1718
AB257482
ID AB257482 standard; DNA; 24 BP.
XX
AC AB257482;
XX
DT 05-APR-2003 (first entry)
XX
DE GALV receptor 2-14.63 RT-PCR primer, SEQ ID NO:3.
XX
KW Gibbon ape leukaemia virus (GALV) receptor 2-14.63;
KW GALV receptor 2-14.63; recombinant production; gene therapy;
KW reverse transcription-PCR; RT-PCR; primer; ss.
XX
OS Unidentified.
XX
```

PN CN1355196-A.
 XX
 PD 26-JUN-2002.
 XX
 PF 01-DEC-2000; 2000CN-00127672.
 XX
 PR 01-DEC-2000; 2000CN-00127672.
 XX
 PA (UYFU-) UNIV FUDAN.
 XX
 PI Mao Y, Xie Y;
 XX
 DR WPI; 2003-000133/01.
 XX
 PT Polypeptide-Jibon ape leukovirus receptor 2-14.63 and polynucleotide for
 PT coding it.
 XX
 PS Example 2; Page 16 (Disclosure); 31pp; Chinese.
 XX
 CC The invention relates to gibbon ape leukaemia virus (GALV) receptor 2-
 CC 14.63 (ABP5848) and nucleic acids encoding it (AB257481). The protein
 CC has a molecular weight of 15 kD. The invention also relates to a method
 CC for the recombinant production of the protein, an antagonist of the
 CC protein, and the use of the protein, gene and antagonist in therapeutic
 CC applications. GALV receptor 2-14.63 can be used in gene therapy.
 CC Sequences AB257482-AB257483 represent reverse transcription-PCR (RT-PCR)
 CC primers used in an exemplification of the invention to isolate GALV
 CC receptor 2-14.63 cDNA
 XX
 SQ Sequence 24 BP; 3 A; 10 C; 2 G; 9 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 16.2; DB 1; Length 24;
 Best Local Similarity 85.7%; Pred. No. 1.5e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 XX
 QY 5100 CCCTGTCATGCGCTTCATAT 5120
 DB 4 CCCTGTCCTCTCTTCATAT 24
 XX
 RESULT 1719
 AB258439/c
 ID AB258439 standard; DNA; 24 BP.
 XX
 AC AB258439;
 XX
 DT 08-MAY-2003 (first entry)
 XX
 DE Sheep galectin-14 PCR primer galectin-143'UTR.
 XX
 KW Sheep; galectin-14; antiinflammatory; antiallergic; cytostatic;
 KW gene therapy; PCR; primer; ss.
 XX
 OS Ovis aries.
 XX
 PN WO2003008580-A1.
 XX
 PD 30-JAN-2003.
 XX
 PF 19-JUL-2002; 2002WO-AU000965.
 XX
 PR 19-JUL-2001; 2001AU-00006474.
 XX
 PA (UYME) UNIV MELBOURNE.
 XX
 PI Nash A, Dunphy JL, Barcham G, Young AR, Meusen ENT;
 XX
 DR WPI; 2003-239335/23.
 XX
 PT New nucleic acid molecule comprising one carbohydrate recognition domain,
 PT useful for treating a condition characterized by aberrant, unwanted or
 PT inappropriate inflammatory response, e.g. allergic condition or cellular
 PT apoptosis.

XX
 PS Example 1; Page 83; 137pp; English.
 XX
 CC The present sequence is that of PCR primer galectin-143'UTR, which is
 CC designed from the putative 3' untranslated region of sheep galectin cDNA.
 CC The primer was used in an RT-PCR amplification to obtain a full-length
 CC clone (see AB258435) encoding sheep galectin-14 (see ABP72306) from a
 CC mammary lavage fluid cell cDNA library. The isolation of ovine galectin-
 CC 14 permits the identification and design of products for use in therapy,
 CC diagnosis and antibody generation. These therapeutic molecules may also
 CC act as antagonists or agonists of galectin function, especially for the
 CC modification of inflammation, e.g. in allergic reactions or cellular
 CC apoptosis
 XX
 SQ Sequence 24 BP; 6 A; 6 C; 7 G; 5 T; 0 U; 0 Other;
 XX
 Query Match 0.2%; Score 16.2; DB 1; Length 24;
 Best Local Similarity 85.7%; Pred. No. 1.5e+03;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 XX
 QY 828 CCCTGCCATGTGGAAGATGAT 848
 DB 22 CCTACCGGTGGAAGATGTT 2
 XX
 RESULT 1720
 ABX89853/c
 ID ABX89853 standard; DNA; 24 BP.
 XX
 AC ABX89853;
 XX
 DT 30-APR-2003 (first entry)
 XX
 DE Cancer medicament related immunostimulatory nucleic acid #52.
 XX
 KW Immunostimulatory nucleic acid; cancer; cancer vaccine; hormone therapy;
 KW bone cancer; brain cancer; central nervous system cancer; CNS cancer;
 KW connective tissue cancer; oesophageal cancer; eye cancer;
 KW Hodgkin's lymphoma; larynx cancer; oral cavity cancer; skin cancer;
 KW testicular cancer; allergic response; blood transfusion; infection; ss.
 XX
 OS Unidentified.
 XX
 PN US2002156033-A1.
 XX
 PD 24-OCT-2002.
 XX
 PF 05-MAR-2001; 2001US-00800266.
 XX
 PR 03-MAR-2000; 2000US-0187214P.
 XX
 PA (BRAT/) BRATZLER R L.
 PA (PETE/) PETERSEN D M.
 XX
 PI Bratzler RL, Petersen DM;
 XX
 DR WPI; 2003-275279/27.
 XX
 PT Treatment of a subject having, or at risk of developing cancer, involves
 PT the use of an immunostimulatory nucleic acid having a modified backbone
 PT in combination with a cancer medicament.
 XX
 PS Disclosure; Page 6; 32pp; English.
 XX
 CC The invention describes a method of treating (T1) a subject having cancer
 CC involving administering an immunostimulatory nucleic acid (1) having
 CC modified backbone and a cancer medicament (M1) selected from
 CC chemotherapeutic agent, immunotherapeutic agent, cancer vaccine or
 CC hormone therapy. The poly-G nucleic acid is not conjugated to (M1) and is
 CC free of CpG and T-rich motifs. The composition is for the treatment of
 CC cancer (e.g. bone cancer, brain and CNS cancer, connective tissue cancer,
 CC oesophageal cancer, eye cancer, Hodgkin's lymphoma, larynx cancer, oral
 CC cavity cancer, skin cancer, and testicular cancer), and for preventing

CC allergic responses in those receiving blood transfusions. It is also
CC useful for the treatment of fungal, bacterial, parasitic and viral
CC infections. The combination of the immunostimulatory nucleic acids and
CC the cancer medicament is synergistic. The combination allows for the
CC administration of higher doses of cancer medicaments without as many side
CC effects, and allows for the administration of lower, sub-therapeutic
CC doses of either compound, but with higher efficacy than would otherwise
CC be achieved using such low doses. The immunostimulatory nucleic acids
CC function by enhancement of anti-body dependent cell cytotoxicity. This
CC mechanism provides long lasting effects of nucleic acids, thus reducing
CC dosing regimens, improving compliance and maintenance therapy, reducing
CC emergency situations and improving quality of life. This sequence
CC represents an immunostimulatory nucleic acid used in the method of
CC treating cancer described in the invention
XX
SQ Sequence 24 BP; 5 A; 9 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.2; DB 1; Length 24;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1521 GGGGAAACGTTCTACATGG 1541
Db 22 GGGGAAACGTTCTCCATGG 2

RESULT 1721
ABZ25005/c
ID ABZ25005 standard; DNA; 24 BP.
XX
AC ABZ25005;
XX
DT 14-APR-2003 (first entry)
XX
DE Translation initiation factor eIF-2-11.44 PCR primer #1.
XX
KW Translation initiation factor eIF-2-11.44; diabetes; tumour; infection;
XX
KW cytosstatic; PCR; primer; ss.
XX
OS Unidentified.
XX
XX
PN CN1355189-A.
XX
PD 26-JUN-2002.
XX
PF 01-DEC-2000; 2000CN-00127631.
XX
PR 01-DEC-2000; 2000CN-00127631.
XX
PA (UYFU-) UNIV FUDAN.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2003-000126/01.
XX
PT Polypeptide-translation initiation factor eIF-2-11.44 and polynucleotide
XX for coding it.
XX
PS Example 2; Page 17 (Disclosure); 33pp; Chinese.
XX
CC The present invention relates to translation initiation factor eIF-2-
CC 11.44 (see AB898945). The protein can be used for treating diseases such
CC as diabetes, tumours and infections. The present sequence is a PCR
CC primer, which was used in an example from the invention
XX
SQ Sequence 24 BP; 7 A; 3 C; 2 G; 12 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.2; DB 1; Length 24;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3259 AAAAGACTGATGTTGTTTAA 3279
|||||

Db 24 AAAAGACTGAATGTTTAA 4

RESULT 1722
ACA92709/c
ID ACA92709 standard; DNA; 24 BP.
XX
AC ACA92709;
XX
DT 16-UTL-2003 (first entry)
XX
DE Immunostimulatory Cpg oligonucleotide #52.
XX
KW Immunostimulatory Cpg oligonucleotide; CPG; ss; vaccine; virucide;
KW immunostimulant; cytosstatic; antibacterial; fungicide; viral shedding;
KW oil-in-water emulsion; viral infection; cancer; bone cancer;
KW brain cancer; central nervous system cancer; CNS; eye cancer;
KW connective tissue cancer; oesophageal cancer; Hodgkin's lymphoma;
KW larynx cancer; oral cavity cancer; skin cancer; testicular cancer;
KW bacterial infection; meningitis; HIV infection; AIDS; fungal infection;
KW candidiasis.
XX
OS Synthetic.
XX
PN WO2003030934-A2.
XX
PD 17-APR-2003.
XX
PF 07-OCT-2002; 2002WO-EP011206.
XX
PR 06-OCT-2001; 2001US-0327734P.
XX
PA (QIAG-) QIAGEN GMBH.
XX (UYSA-) UNIV SASAKTCHWAN.
XX
PI Babluk LA, Hecker R;
XX
DR WPI; 2003-381683/36.
XX
PT New compositions comprising an immunostimulatory nucleic acid and an oil-
PT in-water emulsion, useful for reducing viral shedding or tissue damage
PT upon vaccination, or for inducing an immune response against infectious
PT diseases.
XX
PS Claim 32; Page 33; 68pp; English.
XX
CC The invention relates to a composition comprising an immunostimulatory
CC nucleic acid (especially a Cpg dinucleotide containing oligonucleotide)
CC and an oil-in-water emulsion. Also included are reducing viral shedding
CC in a non-human animal (by administering to a non-human animal infected
CC with a virus or at risk of viral infection, an immunostimulatory nucleic
CC acid and an oil-in-water emulsion), reducing tissue damage upon
CC vaccination of a subject by administering to a subject by an invasive
CC route an adjuvanted vaccine and an immunostimulatory nucleic acid to
CC reduce tissue damage arising from the adjuvanted vaccine, where the
CC vaccine is adjuvanted with an oil-in-water emulsion), inducing an immune
CC response (by administering to a subject an oil-in-water emulsion and a
CC Cpg oligonucleotide to produce the immune response) and reducing a dosage
CC of antigen administered to a subject to produce an antigen specific
CC immune response comprising administering to a subject an antigen in a sub
CC therapeutic dosage and an immunostimulatory nucleic acid. The
CC composition is useful for reducing viral shedding in a non-human animal
CC infected with a virus or at risk of viral infection, for reducing tissue
CC damage upon vaccination, for inducing an immune response to treat or
CC prevent infectious diseases, for reducing an antigen specific immune
CC administered to a subject to produce an antigen specific immune response,
CC and for treating or preventing cancer (e.g. bone cancer, brain and CNS
CC (central nervous system) cancer, connective tissue cancer, oesophageal
CC cancer, eye cancer, Hodgkin's lymphoma, larynx cancer, oral cavity
CC cancer, skin cancer, or testicular cancer), bacterial (e.g. meningitis),
CC viral (e.g. HIV infection leading to AIDS) and fungal (e.g. candidiasis)
CC infections. The present sequence is an immunostimulatory oligonucleotide
CC of the invention

XX Sequence 24 BP; 5 A; 9 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 0.2%; Score 16.2; DB 1; Length 24;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1521 GGGGAAACAGTTCTACAAATGG 1541

DB 22 GGGGAAACAGTTCTGCATCG 2

RESULT 1723

ACD99333/c

ID ACD99333 standard; DNA; 24 BP.

XX ACD99333;

DT 25-SEP-2003 (first entry)

XX Immunostimulatory nucleic acid #19.

DE Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;

KW antitumor; gene therapy; vaccine; non-allergic inflammatory disease;

KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;

KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.

XX Synthetic.

PN US2003050266-A1.

PD 13-MAR-2003.

PF 29-MAR-2002; 2002US-00112653.

PR 29-MAR-2001; 2001US-0279642P.

XX (KRIE/) KRIEG A M.

PA (BERG/) BERG D J.

XX Krieg AM, Berg DJ;

DR WPI; 2003-521815/49.

XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,

PT allergic contact dermatitis, latex dermatitis or inflammatory bowel

PT disease by administering an immunostimulatory nucleic acid.

XX Disclosure, Page 9; 22pp; English.

XX The invention describes a method of treating non-allergic inflammatory

CC disease comprising administering to a subject having or at risk of

CC developing a non-allergic inflammatory disease an immunostimulatory

CC nucleic acid for prevention or treatment of the disease. The method is

CC useful for treating non-allergic inflammatory diseases, such as

CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or

CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.

CC This sequence represents an immunostimulatory nucleic acid

XX Sequence 24 BP; 5 A; 9 C; 4 G; 6 T; 0 U; 0 Other;

QY 1521 GGGGAAACAGTTCTACAAATGG 1541

DB 22 GGGGAAACAGTTCTGCATCG 2

XX ADB36402;

XX 04-DEC-2003 (first entry)

XX Immunostimulatory nucleic acid #16.

KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;

KW hypo-responsive subject; immunostimulatory.

XX Synthetic.

PN US2003087848-A1.

PD 08-MAY-2003.

PF 02-FEB-2001; 2001US-0076479.

PR 03-FEB-2000; 2000US-0179991P.

XX (BRAT/) BRATZLER R L.

PA (PETE/) PETERSEN D M.

XX (FOUR/) FOURON Y.

PI Bratzler RL, Petersen DM, Fouron Y;

DR WPI; 2003-657977/62.

XX Treating and/or preventing allergy or asthma using an immunostimulatory

PT nucleic acid alone or in combination with an asthma/allergy medicament.

XX Disclosure, Page 5; 22pp; English.

XX The invention relates to a method of treating or preventing allergy or

CC asthma which comprises administering to a subject a poly-G nucleic acid

CC in an aerosol formulation. The methods and compositions of the present

CC invention are useful for diagnosing and/or treating asthma and allergy

CC especially in a hypo-responsive subject. The present sequence represents

CC an immunostimulatory nucleic acid of the invention.

XX Sequence 24 BP; 5 A; 9 C; 4 G; 6 T; 0 U; 0 Other;

QY 1521 GGGGAAACAGTTCTACAAATGG 1541

DB 22 GGGGAAACAGTTCTGCATCG 2

RESULT 1725

AAAD60216/c

ID AAAD60216 standard; DNA; 24 BP.

XX AAAD60216;

AC 18-DEC-2003 (first entry)

XX Oligonucleotide 1776 used for activating dendritic cells.

XX Dendritic cell activation; cancer immunotherapy; infectious disease;

KW allergy; cell therapy; ss.

OS Unidentified.

PN US2003100527-A1.

XX 29-MAY-2003.

XX 03-JUN-2002; 2002US-00161229.

XX 15-JUL-1994; 94US-00276358.

```
PR 07-FEB-1995; 95US-00386063.
PR 30-OCT-1996; 96US-00738652.
PR 30-OCT-1997; 97US-00960774.
PR 13-NOV-1998; 98US-00191170.
XX
XX (IOWA ) UNIV IOWA RES FOUND.
XX
XX Krieg AM, Hartmann G;
XX WPI; 2003-708674/67.
XX
XX Activating a dendritic cell useful for treating cancer; infectious
XX diseases or allergies, comprises contacting the dendritic cell with an
XX amount of an isolated nucleic acid that contains at least one
XX unmethylated CpG dinucleotide.
XX
XX Example 6; Page 18; 51pp; English.
XX
XX The invention relates to a method of activating a dendritic cell. The
XX method involves contacting the dendritic cell with an isolated nucleic
XX acid containing at least one unmethylated CpG dinucleotide, where the
XX nucleic acid is about 8-80 bases in length, in an amount that activates
XX the dendritic cell. The compositions and methods of the invention are
XX useful for cancer immunotherapy, or for treating an infectious disease
XX (e.g. viral, bacterial or fungal infections) or allergy. The invention is
XX useful in cell therapy. The present sequence is an oligonucleotide used
XX for activating dendritic cells
XX
XX Sequence 24 BP; 5 A; 9 C; 4 G; 6 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 16.2; DB 1; Length 24;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1521 GGGGAAACAGTCTTCATCG 1541
DB 22 GGGGAAACAGTCTTCATCG 2
RESULT 1726
AAT27193
ID AAT27193 standard; DNA; 25 BP.
XX
XX AAT27193;
AC
XX
XX 20-NOV-1996 (first entry)
XX
XX Stem loop oligonucleotide targeted to p53 chromosomal binding site.
XX
XX Stem loop; target; secondary structure; parallel binding domain;
XX antiparallel; replication inhibitor; cell growth inhibitor; p53;
XX detection; stable; strong affinity; nuclease resistant;
XX Watson-Crick bonding; Hoogsteen bonding; ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
XX stem_loop 1..25
XX /tag= a
XX /note= "loop without stem structure"
XX
XX misc_binding 3..10
XX /tag= b
XX /note= "target binding area"
XX
XX misc_binding 16..23
XX /tag= c
XX /note= "target binding area"
XX
XX US514546-A.
XX
XX 07-MAY-1996.
XX
XX 01-SEP-1993; 93US-00115497.
XX
```

```
PR 01-SEP-1993; 93CA-02105364.
XX
XX (RESE ) RESEARCH CORP TECHNOLOGIES INC.
XX
XX Kool ET;
XX
XX WPI; 1995-162088/22.
XX
XX Stem-loop oligo:nucleotide(s) contain parallel and antiparallel binding
XX domains - for binding target nucleic acids, to regulate biosynthesis of
XX nucleic acid or protein in a cell, for treating e.g. cancer.
XX
XX Example 1; Col 30; 34pp; English.
XX
XX AAT27193-r27198 and AAT27200 are stem loop oligonucleotides directed
XX towards chromosomal sites normally bound by p53 (see AAT35519) The stem
XX loop oligonucleotides bind with strong affinity and high selectivity to
XX their target nucleic acids; they are also nuclease resistant. They are
XX used to inhibit cell growth and DNA replication and other processes
XX involving a nucleic acid template. In addition to this the
XX oligonucleotides may be used for the detection and isolation of target
XX nucleic acids and for cell type-specific drug delivery. The stem loops
XX bind to their target via a system of co-operative Watson-Crick bonding
XX and Hoogsteen bonding
XX
XX Sequence 25 BP; 0 A; 7 C; 0 G; 18 T; 0 U; 0 Other;
SQ
Query Match 0.2%; Score 16.2; DB 1; Length 25;
Best Local Similarity 85.7%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4463 CTTTTTTTTTTTTTTTTT 4483
DB 2 CTTTTTTCTCTCTTTTTT 22
RESULT 1727
AAI18367
ID AAI18367 standard; DNA; 16 BP.
XX
XX AAI18367;
AC
XX
XX 11-MAY-1999 (first entry)
XX
XX RT-PCR primer of the invention SEQ ID 8.
XX
XX RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
XX Synthetic.
OS
XX
XX JP11032765-A.
XX
XX 09-FEB-1999.
XX
XX 18-JUL-1997; 97JP-00208312.
XX
XX 18-JUL-1997; 97JP-00208312.
XX
XX (TAKI ) TAKARA SHUZO CO LTD.
XX
XX WPI; 1999-183822/16.
XX
XX Peptides having at least two new nucleotides - useful as primers in RT-
XX PCR.
XX
XX Disclosure; Page 10; 19pp; Japanese.
XX
XX This sequence represents a primer of the invention. The invention relates
XX to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
XX -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
XX a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
XX natural number indicating the repetition of alpha; beta, delta = V or N;
XX V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
XX
```

CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
 CC repetition of gamma, in which thymine expressed by gamma is composed of
 CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
 CC useful as primers for RT-PCR and determination of base sequences. The new
 CC sequences allow for reproductive and highly efficient analysis of gene
 CC sequences

XX Sequence 16 BP; 0 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.2%; Score 16; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 9.6e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4470 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
 Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

RESULT 1728

AAK07568/c

ID AAK07568 standard; cDNA; 16 BP.

AC AAK07568;

DT 21-JUN-1999 (first entry)

XX Homo sapiens fetal kidney clone AK647 secreted protein gene 3' end.

KW Secreted protein; fetal kidney; ds.

XX Homo sapiens.

OS Homo sapiens.

XX MO9900405-A1.

XX 07-JAN-1999.

XX 29-JUN-1998; 98MO-US013530.

XX 30-JUN-1997; 97US-00885610.

XX (GEMV) GENETICS INST INC.

PA Jacobs K, McCoy JM, Lavallie ER, Racie LA, Werberg D, Treacy M;

PI Evans C, Agostino MJ;

XX MPI; 1999-095671/08.

XX New polynucleotides encoding secreted human proteins - are derived from

XX foetal kidney or adult retina cDNA libraries, used as, e.g. potential

XX vaccines.

XX Disclosure; Page 54; 76pp; English.

XX The sequence is that of the 3' end of a sequence encoding a secreted

XX protein from a human fetal kidney clone AK296. Such a sequence is

XX predicted to have biological activities which would make them suitable

XX for treating, preventing or ameliorating medical conditions in humans and

XX CC animals, although no supporting data is given. Suggested activities

XX include nutritional activity, cytokine and cell

XX proliferation/differentiation activity, immune stimulating (e.g. as

XX tissue growth activity, activin/inhibin activity,

XX chemotactic/chemokinetic activity, haemostatic and thrombolytic activity,

XX receptor/ligand activity, anti-inflammatory activity, cadherin/tumour

XX invasion suppressor activity, and tumour inhibition activity. It is also

XX stated to be useful for gene therapy

XX Sequence 16 BP; 16 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 16; DB 1; Length 16;

XX Best Local Similarity 100.0%; Pred. No. 9.6e+02;

XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
 Db 16 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

RESULT 1729

AAK6068/c

ID AAC6068 standard; DNA; 16 BP.

AC AAC6068;

DT 22-FEB-2001 (first entry)

XX DNA chip primer #4.

KW DNA chip; primer; nucleoside derivative; photolabile protecting group;

XX photolithographic nucleic acid chip; ss.

XX Synthetic.

XX MO200061594-A2.

XX 19-OCT-2000.

XX 07-APR-2000; 2000MO-DE001148.

XX 08-APR-1999; 99DE-01015867.

XX 28-JAN-2000; 2000DE-01003631.

XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

XX Beier M, Hoheisel J;

XX MPI; 2000-679457/66.

XX New nucleoside derivatives with photolabile protecting groups, useful in

XX oligonucleotide syntheses, particularly on solid phases, e.g. for

XX hybridization testing.

XX Disclosure; Fig 9; 48pp; German.

XX This invention describes nucleoside derivatives (I) with photolabile

XX protecting groups. (I) are used to synthesize oligonucleotides using the

XX photolithographic nucleic acid chip method, particularly where these are

XX intended for performing enzymatic reactions initiated from a free 3'-

XX CC hydroxy (especially solid-phase polymerase reactions or ligase reactions,

XX CC but also reverse transcription, cDNA synthesis etc.), also for

XX CC hybridization testing, sequencing and in DNA computing. (I) are produced

XX CC with high selectivity by reaction with a mild acylating agent that has

XX CC high specificity for the 3'-position, without significant side-reactions

XX CC (cf. more reactive acylating agents such as chloroformates)

XX Sequence 16 BP; 16 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

XX Query Match 0.2%; Score 16; DB 1; Length 16;

XX Best Local Similarity 100.0%; Pred. No. 9.6e+02;

XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
 Db 16 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

RESULT 1730

ABBA04585

ID ABA04585 standard; DNA; 16 BP.

AC ABA04585;

DT 15-FEB-2002 (first entry)

XX Oligonucleotide #5.

KW Analytical support; genomic sequencing; mutation detection;
KW pharmaceutical development; ss.
OS Synthetic.
FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER = F1(CH2)6-PO-thymine, where F1 is flavine
FT and PO is a phosphate group"
XX
XX FR2805348-A1.
XX
XX PD 24-AUG-2001.
XX
XX PF 23-FEB-2000; 2000FR-00002236.
XX
XX PR 23-FEB-2000; 2000FR-00002236.
XX
XX PA (COMS) COMMISSARIAT ENERGIE ATOMIQUE.
XX
XX PI Cuzin M, Peltie P, Fontecave M, Decout JL, Dueymes C;
XX WPI; 2001-628265/73.
XX
XX DR Support for hybridization analysis of nucleic acids for sequencing
XX techniques, comprises an array of oligonucleotides having a label where
XX the fluorescence changes follow hybridization.
XX
XX PS Example 1; Page 12; 33pp; French.
XX
XX CC The present invention relates to an analytical support, to which a number
XX of oligonucleotides are fixed. The oligonucleotides are labelled with a
XX fluorescent compound, the fluorescence of which varies when the
XX oligonucleotide hybridises to its complement. The analytical support is
XX useful in hybridisation testing for identification of specific nucleic
XX acids, such as genomic sequencing, detecting mutations or pharmaceutical
XX development. The present oligonucleotide was used to illustrate the
XX invention
XX
SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4479
DB 1 TTTT TTTT TTTT TTTT TTTT 16
XX
RESULT 1731
AAF30895
ID AAF30895 standard; DNA; 16 BP.
XX
XX AC AAF30895;
XX
XX DT 09-JUL-2001 (first entry)
XX
XX DE Oligonucleotide-minor groove binder complex.
XX
XX KW ODN-MGB-LF; oligonucleotide; minor groove binder; latent fluorophore;
XX hybridisation; detection; fluorescence; probe; ss.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX modified_base 1
XX /*tag= a
XX /note= "thymine modified by a minor groove binder (2-
XX dimethylaminonaphthalene-6- sulfonamide"

PN WO200131063-A1.
XX
XX PD 03-MAY-2001.
XX
XX PF 26-OCT-2000; 2000WO-US029786.
XX
XX PR 26-OCT-1999; 99US-00428236.
XX
XX PA (EPOC-) EPOCH BIOSCIENCES INC.
XX
XX PI Dempcy RO, Afonina IA, Vermeulen NMJ;
XX WPI; 2001-328656/34.
XX
XX DR Conjugate of oligonucleotide, minor groove binder and latent fluorophore,
XX useful for detecting specific nucleic acids, e.g. for single-nucleotide
XX mismatch discrimination.
XX
XX PS Disclosure; Page 101; 105pp; English.
XX
XX CC The present sequence is that of an oligonucleotide (ODN)-minor groove
XX binder (MGB) complex. MGBs bind in a non-intercalating manner to the
XX minor groove of non-single-stranded DNA, RNA or their hybrids. ODN-MGB-LF
XX conjugates of the invention also comprise a latent fluorophore (LF),
XX which binds similarly to the MGB but in an intercalating manner, or lies
XX in the minor groove, or is oriented in some other way to the DNA molecule
XX by MGB, such that it becomes fluorescent (or its fluorescent properties
XX change detectably). The conjugates are used as hybridisation probes and
XX amplification primers for fluorescent detection of specifically
XX hybridising sequences, for analysis or diagnosis, especially (real-time)
XX PCR, for single-nucleotide mismatch discrimination, target or signal
XX amplification, array-based assays and sequencing, including detection of
XX double-stranded DNA by triplex formation
XX
SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
XX
Query Match 0.2%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4479
DB 1 TTTT TTTT TTTT TTTT TTTT 16
XX
RESULT 1732
AAF30880
ID AAF30880 standard; DNA; 16 BP.
XX
XX AC AAF30880;
XX
XX DT 09-JUL-2001 (first entry)
XX
XX DE Oligonucleotide portion of ODN-MGB-LF conjugate.
XX
XX KW ODN-MGB-LF; oligonucleotide; minor groove binder; latent fluorophore;
XX hybridisation; detection; fluorescence; probe; ss.
XX
XX OS Synthetic.
XX
XX PN WO200131063-A1.
XX
XX PD 03-MAY-2001.
XX
XX PF 26-OCT-2000; 2000WO-US029786.
XX
XX PR 26-OCT-1999; 99US-00428236.
XX
XX PA (EPOC-) EPOCH BIOSCIENCES INC.
XX
XX PI Dempcy RO, Afonina IA, Vermeulen NMJ;
XX WPI; 2001-328656/34.
XX
XX DR


```

XX Conjugate of oligonucleotide, minor groove binder and latent fluorophore,
PT useful for detecting specific nucleic acids, e.g. for single-nucleotide
PT mismatch discrimination.
XX
XX Disclosure; Page 58; 105pp; English.
XX
CC The present sequence is that of the oligonucleotide (ODN) component of an
CC ODN-MGB (minor groove binder)-LF (latent fluorophore) conjugate of the
CC invention. MGBs bind in a non-intercalating manner to the minor groove of
CC non-single-stranded DNA, RNA or their hybrids, while a LF binds similarly
CC but in an intercalating manner, or lies in the minor groove, or is
CC oriented in some other way to the DNA molecule by MGB, such that it
CC becomes fluorescent (or its fluorescent properties change detectably).
CC The conjugates are used as hybridisation probes and amplification primers
CC for fluorescent detection of specifically hybridising sequences, for
CC analysis or diagnosis, especially (real-time) PCR, for single-nucleotide
CC mismatch discrimination, target or signal amplification, array-based
CC assays and sequencing, including detection of double-stranded DNA by
CC triplex formation. Many different targets can be detected a single
CC reaction vessel. The present ODN-MGB-LF conjugate was used to demonstrate
CC hybridisation-triggered fluorescence. Upon hybridisation to the
CC complementary target sequence there was an increase in fluorescence
CC yield, measured as the ratio of the fluorescence emitted by the hybrid
CC between the ODN-MGB-LF conjugate and its target sequence to the
CC fluorescence emitted by unhybridised (i.e. single-stranded) ODN-MGB-LF,
CC of 8.3
XX
SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
XX
Query Match      0.2%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy      4464 TTTTTTTTTTTTTT 4479
Db      1 TTTTTTTTTTTTTT 16

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RESULT 1733
AAH42481
ID AAH42481 standard; DNA; 16 BP.
XX
XX AAH42481;
XX
XX 01-OCF-2001 (first entry)
XX
XX Oligonucleotide used to produce branched chain compounds.
XX
XX Branched chain compound; nucleic acid synthesis; primer extension;
XX reverse transcription; nucleic acid hybridization;
XX nucleic acid amplification; ss.
XX
XX Synthetic.
XX
XX Key
XX modified_base 1 Location/Qualifiers
XX FT /*tag= a
XX FT /note= "COOH attached"
XX FT misc_feature 2..3
XX FT /*tag= C
XX FT /note= "branch present"
XX FT modified_base 2
XX FT /*tag= b
XX FT /note= "COOH attached"
XX
XX BP1111068-A1.
XX
XX 27-JUN-2001.
XX
XX 21-DEC-1999; 99EP-00125484.
XX
XX 21-DEC-1999; 99EP-00125484.
PR

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XX (LION-) LION BIOSCIENCE AG.
PA (VBC-) VBC GENOMICS GMBH.
XX
XX Schmidt W, Hiller R, Huber M, Mueller M;
XX WPI; 2001-466959/51.
XX
XX Example 1; Page 10; 31pp; English.
XX
CC The specification describes branched compounds containing nucleic acid
CC moieties optionally extended by a polymerase. The branched chain
CC compounds of the invention are used in nucleic acid synthesis reaction,
CC primer extension reaction, reverse transcription reaction of RNA into
CC DNA, nucleic acid hybridization experiment (for identifying sequence of a
CC nucleic acid), and nucleic acid amplification experiment (for analysing
CC the expression pattern of genes). The compounds are also used in solid
CC phase enzymatic reactions. The present sequence was used in the course of
CC the invention to produce branched chain compounds
XX
SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
XX
Query Match      0.2%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy      4464 TTTTTTTTTTTTTT 4479
Db      1 TTTTTTTTTTTTTT 16

```

RESULT 1734
ABA97402
ID ABA97402 standard; DNA; 16 BP.
XX
XX ABA97402;
XX
XX 18-JUN-2002 (first entry)
XX
XX Nucleotide sequence of oligomer # 1 used to test thermal stability.
XX
XX Protein nucleic acid molecule; PNA; ds.
XX
XX Synthetic.
XX
XX WO200168673-A1.
XX
XX 20-SEP-2001.
XX
XX 13-MAR-2001; 2001WO-US008111.
XX
XX 14-MAR-2000; 2000US-0189190P.
XX 30-NOV-2000; 2000US-0250334P.
XX
XX (ACT1-) ACTIVE MOTIF.
XX
XX Efimov V, Fernandez J, Archdeacon D, Archdeacon J;
XX Chakmakchaneau O, Buryakova A, Choob M, Hondorp K;
XX WPI; 2002-041177/05.
XX
XX Oligonucleotides analogs useful in detection, separation and purification
XX of nucleic acid molecules, comprise monomers, dimers and oligomers.
XX
XX Example 17; Page 118; 197pp; English.
XX
XX This invention relates to oligonucleotide analogues comprising a protein
XX nucleic acid molecule (PNA) monomer. They are used in the detection and
XX separation of nucleic acid molecules and as probes, primers, linkers,
XX adaptors and antisense agents on solid supports. Modifications enhance
XX

CC their use as capture and detection probes e.g. by the incorporation of
 CC biotin, digoxigenin, radioisotopes, fluorescent labels such as
 CC fluorescein and reporter molecules such as alkaline phosphatase. They are
 CC also used for enhancing or inhibiting the activity of an enzyme or
 CC cellular activity. The compounds are stable to nucleases and proteases,
 CC have high affinity, binding specifically and solubility. The polyamide
 CC backbone of PNA is resistant to both nucleases and proteases. PNAs bind
 CC nucleic acid molecules with greater affinity than DNA or RNA
 CC concentration. The compounds are relatively simple to synthesize and are
 CC used in a wide variety of applications. This sequence represents a DNA
 CC oligomer which is used to represent the thermal stability of the
 CC oligomers of the invention
 XX

SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 0.2%; Score 16; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred.No. 9.6e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4479
 |||||
 Db 1 TTTT TTTT TTTT TTTT TTTT 16

RESULT 1735
 AAD56451
 ID AAD56451 standard; DNA; 16 BP.
 XX
 AC AAD56451;
 XX
 DT 07-AUG-2003 (first entry)
 XX
 DE 2'-F-ANA antisense oligo #6, to elicit RNase H degradation of target RNA.
 XX
 KM Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
 XX antisense; ss.
 XX
 KM
 XX
 OS Unidentified.
 XX
 XX
 FT Key Location/Qualifiers
 FT modified_base 1..16
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "2'-deoxy-2'-fluororabinothymidine"
 FT misc_feature 8..9
 FT /tag= b
 FT /note= "Bases 8 and 9 are linked by two secouridine
 FT linkers which is represented as S in page 49 and X in
 FT page 57 and Fig 7 and 8 of the specification"
 FT
 FT
 PN WO2003037909-A1.
 XX
 XX
 PD 08-MAY-2003.
 XX
 PF 29-OCT-2002; 2002WO-CA001628.
 XX
 PR 29-OCT-2001; 2001US-0330719P.
 XX
 XX (UWMC-) UNIV MCGILL.
 PA
 XX Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;
 PI WPI; 2003-421516/39.
 DR
 XX Novel acyclic linker-containing oligonucleotide useful for preventing or
 PT decreasing translation, reverse transcription and/or replication of a
 PT target RNA in a system, comprises a modified deoxyribonucleotide.
 XX
 XX Example 2; Fig 7; 104pp; English.
 PS
 CC The invention relates to an acyclic linker-containing oligonucleotide
 CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of
 CC the invention are useful for preventing or decreasing translation,

CC reverse transcription and/or replication of a target RNA in a system.
 CC They are useful for selectively preventing gene expression in a sequence-
 CC specific manner, for hybridizing to complementary RNA such as cellular
 CC mRNA or viral RNA, to hybridize to and induce cleavage of complementary
 CC RNA. They are also useful therapeutically in formulations or medicaments
 CC to prevent or treat a disease characterised by the expression of a
 CC particular target RNA. The invention is used in gene therapy. The present
 CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)
 CC H degradation of target RNA. This sequence is used in the exemplification
 CC of the invention
 XX

SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 0.2%; Score 16; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred.No. 9.6e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4479
 |||||
 Db 1 TTTT TTTT TTTT TTTT TTTT 16

RESULT 1736
 AAL54078
 ID AAL54078 standard; DNA; 16 BP.
 XX
 AC AAL54078;
 XX
 DT 06-MAR-2003 (first entry)
 XX
 DE Oligo-homodexoxyribonucleotide sequence, oligo dT.
 XX
 XX
 KM Detection; single-stranded sensor; detectable fluorescence emission;
 KM forensic testing; paternity testing; tissue typing; hereditary disorder;
 KM human population genetics; human evolutionary history; cystic fibrosis;
 KM human haplotype diversity; Tay-Sachs; sickle-cell anaemia; ss.
 XX
 OS Unidentified.
 XX
 XX
 PN WO200284271-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 16-APR-2002; 2002WO-US012176.
 XX
 PR 16-APR-2001; 2001US-00836579.
 XX
 XX (REGC) UNIV CALIFORNIA.
 PA (CHAJ/) CHA J N.
 XX
 XX Cha JN, Morse DE, Stucky GD;
 PI WPI; 2003-103378/09.
 DR
 XX
 XX Detecting polynucleotides, for pharmacogenetic testing, comprises
 PT contacting a target polynucleotide with a complementary single-stranded
 PT sensor polynucleotide and an agent that allows the sensor to fluoresce
 PT upon excitation.
 XX
 XX
 PS Example 1; Page 25; 41pp; English.
 XX
 CC The invention relates to a novel assay for detecting a polynucleotide in
 CC a sample, which comprises: contacting a sample suspected of containing a
 CC target polynucleotide with a predetermined single-stranded sensor
 CC polynucleotide complementary to the target polynucleotide, in a solution
 CC comprising an agent that is a nonaqueous solvent that allows the sensor
 CC polynucleotide to produce a detectable fluorescence emission; exciting
 CC the sensor polynucleotide; and determining fluorescence emission. The
 CC assay is useful for detecting a single or double-stranded target
 CC polynucleotide, such as, DNA or RNA in a sample. The assay finds use in a
 CC wide variety of different applications including pharmacogenetic testing,
 CC forensic testing to identify the species or individual which was the
 CC source of a forensic specimen, in anthropological setting, paternity

CC testing, testing for compatibility between prospective tissue or blood
CC donors and patients and in screening for hereditary disorders. The method
CC is also useful to study alterations of gene expression in response to a
CC stimulus, disease, drug or medication, and other applications include
CC human population genetics, analyses of human evolutionary history and
CC characterization of human haplotype diversity. The method is useful for
CC detecting polynucleotide sequences from contaminants or pathogens
CC including bacteria, yeast, and viruses to detect single nucleotide
CC polymorphisms, which may be associated with particular alleles or subsets
CC of alleles. The method is useful for detection of mutations and to detect
CC nucleotide sequences associated with increased risk of diseases or
CC disorders including cystic fibrosis, Tay-Sachs, and sickle-cell anaemia.
CC This polynucleotide sequence represents an oligonucleotide sequence used
CC in a fluorescence technique of the invention

SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 0.2%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4479
|||||
1 TTTT TTTT TTTT TTTT 16

RESULT 1737

ADB68519
ID ADB68519 standard; DNA; 16 BP.

AC ADB68519;

DT 04-DEC-2003 (first entry)

DE DNA hybridisation oligomer SEQ ID 9.

XX hydroxyproline nucleic acid; HYPNA; PNA; peptide nucleic acid;

KM gene expression; respiration; secretion; signalling;

KW ion-channel activity; cell motility; developmental phenotype;

KM tumour regression; hybridisation; ss.

XX Synthetic.

OS Key Location/Qualifiers

XX misc_difference 1 /*tag= a

FT /note= "Optional N-terminal acetyl"

XX MO2003068798-A2.

XX 21-AUG-2003.

XX 07-FEB-2003; 2003MO-US003904.

XX 09-FEB-2002; 2002US-00072975.

XX (ACTI-) ACTIVE MOTIF.

XX Efimov V, Fernandez J, Archdeacon D, Archdeacon J, Choob M;

XX WPI; 2003-689653/65.

XX Method of inhibiting expression of genes or RNA transcripts, useful for

PT therapy and determining effects of genes, by administering oligomers

XX containing hydroxyproline nucleic acid.

XX Example 17; Page 233; 240pp; English.

XX The invention relates to a novel method of inhibiting the expression of

CC one or more genes or RNA transcripts by administering at least one

CC oligonucleotide analogue that includes at least one hydroxyproline

CC nucleic acid (HYPNA) monomer to a cell or organism or their extracts. The

CC oligonucleotides of the invention may be used to monitor properties

CC including gene expression, respiration, secretion, signalling, ion-
CC channel activity, cell motility, developmental phenotype and tumour
CC regression. Furthermore, they may be utilised to determine the effects of
CC particular genes, as antisense or homologous recombination constructs
CC e.g. for creating animal models of disease and finally, for increasing
CC the activity of some enzymes, such as polymerases. The current sequence
CC is that of the DNA hybridisation oligomer SEQ ID 9 of the invention. This
CC sequence may also comprise a peptide nucleic acid (PNA).

SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 0.2%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4479
|||||
1 TTTT TTTT TTTT TTTT 16

RESULT 1738

AA69798
ID AA69798 standard; RNA; 17 BP.

AC AA69798;

DT 28-UTL-1999 (first entry)

DE Human flt1 VEGF receptor hammethead ribozyme substrate #1093.

XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;

KM KDR; hammethead ribozyme; hairpin ribozyme; cleavage;

KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;

KM fms-like tyrosine kinase 1; kinase insert domain containing receptor;

KW foetal liver kinase 1; ss.

XX Homo sapiens.

OS MO9175662-A2.

XX 01-MAY-1997.

XX 25-OCT-1996; 96MO-US017480.

XX 26-OCT-1995; 95US-0005974P.

XX 11-JAN-1996; 96US-00584040.

XX (RIBO-) RIBOZYME PHARM INC.

XX (CHIR) CHIRON CORP.

XX Pavco P, Mcswigen J, Stinchcomb D, Escobedo J;

XX WPI; 1997-259017/23.

XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA

PT stability - useful for creating e.g. tumour angiogenesis, psoriasis,

PT rheumatoid arthritis, etc., in a human patient.

XX Claim 4; Page 79; 218pp; English.

XX The present invention describes nucleic acid molecules which modulate the

CC synthesis, expression and/or stability of a mRNA encoding 1 or more

CC receptors of vascular endothelial growth factor (VEGF). A patient

CC (preferably human) having a condition associated with the level of the

CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing

CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour

CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be

CC treated by administering the nucleic acid molecule or the expression

CC vector to the patient. AA67275 to AA67572 represent specific examples

CC of nucleic acid molecules from the present invention

SQ Sequence 17 BP; 1 A; 1 C; 0 G; 0 T; 15 U; 0 Other;

Query Match 0.2%; Score 16; DB 1; Length 17;
 Best Local Similarity 12.5%; Pred. No. 1e+03;
 Matches 2; Conservative 14; Mismatches 0; Indels 0; Gaps 0;

QY 4462 ACTTTT TTTT TTTT TTTT 4477
 ||:||||:||||:||||:||||:
 DB 2 ACCUUUUUUUUUUUUUU 17

RESULT 1739

AAK69801
 ID AAK69801 standard; RNA; 17 BP.

XX
 AC AAK69801;

XX
 DT 28-JUL-1999 (first entry)

XX
 DE Human flt1 VEGF receptor hammethead ribozyme substrate #1096.

XX
 KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;

XX
 KW KDR; hammethead ribozyme; hairpin ribozyme; cleavage; ocular disease;

XX
 KW tumor angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;

XX
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;

XX
 KW foetal liver kinase 1; ss.

XX
 OS Homo sapiens.

XX
 PN MO9715662-A2.

XX
 PD 01-MAY-1997.

XX
 PF 25-OCT-1996; 96WO-US017480.

XX
 PR 26-OCT-1995; 95US-0005974P.

XX
 PR 11-JAN-1996; 96US-00584040.

XX
 PA (RIBO-) RIBOZYME PHARM INC.

XX
 PA (CHIR) CHIRON CORP.

XX
 PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;

XX
 DR WPI; 1997-259017/23.

XX
 PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA

XX
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,

XX
 PT rheumatoid arthritis, etc., in a human patient.

XX
 PS Claim 4; Page 79; 218pp; English.

XX
 CC The present invention describes nucleic acid molecules which modulate the

XX
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more

XX
 CC receptors of vascular endothelial growth factor (VEGF). A patient

XX
 CC (preferably human) having a condition associated with the level of the

XX
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing

XX
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour

XX
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be

XX
 CC treated by administering the nucleic acid molecule or the expression

XX
 CC vector to the patient. AAK67275 to AAK75752 represent specific examples

XX
 CC of nucleic acid molecules from the present invention

XX
 SQ Sequence 17 BP; 0 A; 1 C; 0 G; 0 T; 16 U; 0 Other;

XX
 Query Match 0.2%; Score 16; DB 1; Length 17;

XX
 Best Local Similarity 0.0%; Pred. NO. 1e+03; 0; Indels 0; Gaps 0;

XX
 Matches 0; Conservative 16; Mismatches 0;

QY 4464 TTTT TTTT TTTT TTTT 4479
 ||:||||:||||:||||:||||:
 DB 1 UUUUUUUUUUUUUUU 16

RESULT 1740

AAK55054

ID AAK55054 standard; DNA; 17 BP.

XX
 AC AAK55054;

XX
 DT 05-JUL-1999 (first entry)

XX
 DE C/EBP-beta antisense oligonucleotide fragment.

XX
 KW Antisense oligonucleotide; multiple target; antisense treatment;

XX
 KW impaired respiration; inflammation; lung disease;

XX
 KW pulmonary vasoconstriction; inflammation; allergic rhinitis;

XX
 KW acute asthma; allergy; asthma; impeded respiration;

XX
 KW respiratory distress syndrome; pain; cystic fibrosis;

XX
 KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;

XX
 KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;

XX
 KW colon cancer; breast cancer; lung cancer; pancreatic cancer;

XX
 KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;

XX
 KW prostate cancer; ss.

XX
 OS Synthetic.

XX
 PN MO9913886-A1.

XX
 PD 25-MAR-1999.

XX
 PF 17-SEP-1998; 96WO-US019419.

XX
 PR 17-SEP-1997; 97US-0059160P.

XX
 PR 09-JUN-1996; 96US-00093972.

XX
 PA (UYEC-) UNIV EAST CAROLINA.

XX
 PI Nyce JW;

XX
 DR WPI; 1999-229400/19.

XX
 PT New antisense oligonucleotides used in treatment of, e.g. pulmonary

XX
 PT vasoconstriction.

XX
 PS Disclosure; Page 70; 120pp; English.

XX
 CC The specification describes antisense oligonucleotides (AAK52869-X55271)

XX
 CC directed against at least 2 mRNAs selected from target genes, coding and

XX
 CC non-coding regions of RNAs corresponding to target genes, gene initiation

XX
 CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'

XX
 CC end and the juxta-section between coding and non-coding regions and all

XX
 CC segments of RNAs encoding proteins associated with one or more diseases,

XX
 CC conditions or mixtures. The antisense oligonucleotides may be derived

XX
 CC from sequences AAK55272-74. These multiple target oligonucleotides

XX
 CC (specifically AAK55180-271) can be used for the antisense treatment of

XX
 CC diseases and conditions. Typical diseases and conditions are those

XX
 CC associated with impaired respiration and inflammation, including lung

XX
 CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,

XX
 CC acute asthma, allergies, asthma, impeded respiration, respiratory

XX
 CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,

XX
 CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary

XX
 CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.

XX
 CC colon cancer, breast cancer, lung cancer, pancreatic cancer,

XX
 CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as

XX
 CC well as all types of cancers which may metastasize or have metastasized

XX
 CC to the lungs, including breast and prostate cancer

XX
 SQ Sequence 17 BP; 0 A; 5 C; 12 G; 0 T; 0 U; 0 Other;

XX
 Query Match 0.2%; Score 16; DB 1; Length 17;

XX
 Best Local Similarity 100.0%; Pred. NO. 1e+03; 0; Indels 0; Gaps 0;

XX
 Matches 16; Conservative 0; Mismatches 0;

QY 68 GCGGGGGGGGGGGGGG 83
 |||||
 DB 2 GCGGGGGGGGGGGGGC 17